

Supplementary Table S1: PRISMA 2020 Main Checklist

Topic	No.	Item	Location where item is reported
TITLE			
Title	1	Identify the report as a systematic review.	Page 1
ABSTRACT			
Abstract	2	See the PRISMA 2020 for Abstracts checklist	Page 3
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of existing knowledge.	Pages 4-5
Objectives	4	Provide an explicit statement of the objective(s) or question(s) the review addresses.	Page 5
METHODS			
Eligibility criteria	5	Specify the inclusion and exclusion criteria for the review and how studies were grouped for the syntheses.	Pages 6
Information sources	6	Specify all databases, registers, websites, organisations, reference lists and other sources searched or consulted to identify studies. Specify the date when each source was last searched or consulted.	Page 7
Search strategy	7	Present the full search strategies for all databases, registers and websites, including any filters and limits used.	Supplementary Material Table 2
Selection process	8	Specify the methods used to decide whether a study met the inclusion criteria of the review, including how many reviewers screened each record and each report retrieved, whether they worked independently, and if applicable, details of automation tools used in the process.	Page 7
Data collection process	9	Specify the methods used to collect data from reports, including how many reviewers collected data from each report, whether they worked independently, any processes for obtaining or confirming data from study investigators, and if applicable, details of automation tools used in the process.	Page 7
Data items	10a	List and define all outcomes for which data were sought. Specify whether all results that were compatible with each outcome domain in each study were sought (e.g. for all measures, time points, analyses), and if not, the methods used to decide which results to collect.	Page 7-8

Topic	No.	Item	Location where item is reported
Study risk of bias assessment	10b	List and define all other variables for which data were sought (e.g. participant and intervention characteristics, funding sources). Describe any assumptions made about any missing or unclear information.	Pages 8
	11	Specify the methods used to assess risk of bias in the included studies, including details of the tool(s) used, how many reviewers assessed each study and whether they worked independently, and if applicable, details of automation tools used in the process.	Pages 8
Effect measures	12	Specify for each outcome the effect measure(s) (e.g. risk ratio, mean difference) used in the synthesis or presentation of results.	Page 8-9
Synthesis methods	13a	Describe the processes used to decide which studies were eligible for each synthesis (e.g. tabulating the study intervention characteristics and comparing against the planned groups for each synthesis (item 5)).	Page 8-9 Supplementary Table 3
	13b	Describe any methods required to prepare the data for presentation or synthesis, such as handling of missing summary statistics, or data conversions.	Page 8-9
	13c	Describe any methods used to tabulate or visually display results of individual studies and syntheses.	Page 9
	13d	Describe any methods used to synthesize results and provide a rationale for the choice(s). If meta-analysis was performed, describe the model(s), method(s) to identify the presence and extent of statistical heterogeneity, and software package(s) used.	Page 9
	13e	Describe any methods used to explore possible causes of heterogeneity among study results (e.g. subgroup analysis, meta-regression).	NA
	13f	Describe any sensitivity analyses conducted to assess robustness of the synthesized results.	NA
Reporting bias assessment	14	Describe any methods used to assess risk of bias due to missing results in a synthesis (arising from reporting biases).	NA
Certainty assessment	15	Describe any methods used to assess certainty (or confidence) in the body of evidence for an outcome.	NA
RESULTS			

Topic	No.	Item	Location where item is reported
Study selection	16a	Describe the results of the search and selection process, from the number of records identified in the search to the number of studies included in the review, ideally using a flow diagram.	Page 9 & Figure 1
	16b	Cite studies that might appear to meet the inclusion criteria, but which were excluded, and explain why they were excluded.	NA
Study characteristics	17	Cite each included study and present its characteristics.	Page 9-11, Table 2 and Supplementary Table 4
Risk of bias in studies	18	Present assessments of risk of bias for each included study.	Page 11 and Figure 2
Results of individual studies	19	For all outcomes, present, for each study: (a) summary statistics for each group (where appropriate) and (b) an effect estimate and its precision (e.g. confidence/credible interval), ideally using structured tables or plots.	Supplementary material S3
Results of syntheses	20a	For each synthesis, briefly summarise the characteristics and risk of bias among contributing studies.	Page 11-12
	20b	Present results of all statistical syntheses conducted. If meta-analysis was done, present for each the summary estimate and its precision (e.g. confidence/credible interval) and measures of statistical heterogeneity. If comparing groups, describe the direction of the effect.	Page 11-12 and Figure 3
	20c	Present results of all investigations of possible causes of heterogeneity among study results.	Page 12
	20d	Present results of all sensitivity analyses conducted to assess the robustness of the synthesized results.	NA
Reporting biases	21	Present assessments of risk of bias due to missing results (arising from reporting biases) for each synthesis assessed.	NA
Certainty of evidence	22	Present assessments of certainty (or confidence) in the body of evidence for each outcome assessed.	NA
DISCUSSION			
Discussion	23a	Provide a general interpretation of the results in the context of other evidence.	Pages 15-19
	23b	Discuss any limitations of the evidence included in the review.	Page 19

Topic	No.	Item	Location where item is reported
	23c	Discuss any limitations of the review processes used.	Page 19
	23d	Discuss implications of the results for practice, policy, and future research.	Page 20
OTHER INFORMATION			
Registration and protocol	24a	Provide registration information for the review, including register name and registration number, or state that the review was not registered.	Page 5
	24b	Indicate where the review protocol can be accessed, or state that a protocol was not prepared.	Page 5
	24c	Describe and explain any amendments to information provided at registration or in the protocol.	NA
Support	25	Describe sources of financial or non-financial support for the review, and the role of the funders or sponsors in the review.	Page 29
Competing interests	26	Declare any competing interests of review authors.	Page 29
Availability of data, code and other materials	27	Report which of the following are publicly available and where they can be found: template data collection forms; data extracted from included studies; data used for all analyses; analytic code; any other materials used in the review.	Page 29-30

From: Page MJ, McKenzie JE, Bossuyt PM, Boutron I, Hoffmann TC, Mulrow CD, et al. The PRISMA 2020 statement: an updated guideline for reporting systematic reviews. MetaArXiv. 2020, September 14. DOI: 10.31222/osf.io/v7gm2. For more information, visit: www.prisma-statement.org

Supplementary Table S2. Complete search strategy strings (updated until 1st September 2025)

Database	Search Strategy	Filters applied	Articles Retrieved
MEDLINE/Pubmed	(("gut microbiome"[All Fields] OR "gut microbiomes"[All Fields] OR "gut microflora"[All Fields] OR "gut microbiota"[All Fields] OR "gut microbiotas"[All Fields] OR "gastrointestinal flora"[All Fields] OR "gut flora"[All Fields] OR "gastrointestinal microbiotas"[All Fields] OR "gastrointestinal microbiota"[All Fields] OR "gastrointestinal microbial community"[All Fields] OR "intestinal microbiome"[All Fields] OR "intestinal microbiomes"[All Fields] OR "intestinal microbiota"[All Fields] OR "intestinal microbiotas"[All Fields] OR "intestine flora"[All Fields] OR "intestinal microbe"[All Fields] OR "intestinal microbes"[All Fields] OR "gut bacteria"[All Fields]) AND ("moduation"[All Fields] OR "modulate"[All Fields] OR "effect"[All Fields] OR "effects"[All Fields] OR "change"[All Fields] OR "changes"[All Fields] OR "influence"[All Fields] OR "influences"[All Fields] OR "stability"[All Fields] OR "dysbiosis"[All Fields] OR "impact"[All Fields] OR "impacts"[All Fields] OR "instability"[All Fields] OR "alterations"[All Fields] OR "alteration"[All Fields] OR "control"[All Fields] OR "controls"[All Fields] OR "shape"[All Fields] OR "shaping"[All Fields] OR "regulation"[All Fields] OR "regulate"[All Fields] OR "modification"[All Fields] OR "modify"[All Fields] OR "modifications"[All Fields]) AND ("prebiotics"[MeSH Terms] OR "supplements"[All Fields] OR "supplement"[All Fields] OR "supplementation"[All Fields] OR "diet"[MeSH Terms] OR "dietary intervention"[Affiliation] OR "dietary fiber"[MeSH Terms] OR "diet therapy"[MeSH Terms] OR "diet regimen"[All Fields] OR "dietary exposure"[MeSH Terms] OR "dietary effect"[All Fields] OR ("diet"[MeSH Terms] OR "diet"[All Fields] OR "diets"[All Fields] OR "diet s"[All Fields] OR "dieted"[All Fields] OR "dieting"[All Fields]) OR "dietary influence"[All Fields] OR "nutrition intervention"[All Fields] OR "dietary impact"[All Fields]))	allchild[Filter]	1672
Embase	('gut microbiome'/exp OR 'gut microbiome' OR 'gut microbiomes' OR 'gut microflora' OR 'gut microbiota'/exp OR 'gut microbiota' OR 'gut microbiotas' OR 'gastrointestinal flora'/exp OR 'gastrointestinal flora' OR 'gut flora' OR 'gastrointestinal microbiotas' OR 'gastrointestinal microbiota'/exp OR 'gastrointestinal microbiota' OR 'gastrointestinal microbial community' OR 'intestinal microbiome'/exp OR 'intestinal microbiome' OR	(([adolescent]/lim OR [child]/lim OR [infant]/lim OR [preschool]/lim OR [school]/lim) AND	2033

	'intestinal microbiomes' OR 'intestinal microbiota'/exp OR 'intestinal microbiota' OR 'intestinal microbiotas' OR 'intestine flora'/exp OR 'intestine flora' OR 'intestinal microbe'/exp OR 'intestinal microbe' OR 'intestinal microbes' OR 'gut bacteria'/exp OR 'gut bacteria') AND ('modulation'/exp OR 'modulation' OR 'modulate' OR 'effect' OR 'effects' OR 'change'/exp OR 'change' OR 'changes' OR 'influence' OR 'influences' OR 'stability'/exp OR 'stability' OR 'dysbiosis'/exp OR 'dysbiosis' OR 'impact'/exp OR 'impact' OR 'impacts' OR 'instability'/exp OR 'instability' OR 'alteration' OR 'alterations' OR 'control'/exp OR 'control' OR 'controls' OR 'shape'/exp OR 'shape' OR 'shaping' OR 'regulation'/exp OR 'regulation' OR 'regulate' OR 'modification'/exp OR 'modification' OR 'modifications' OR 'modify') AND ('prebiotic agent'/exp OR 'prebiotic agent' OR 'supplement' OR 'supplements' OR 'supplementation'/exp OR 'supplementation' OR 'diet'/exp OR 'diet' OR 'dietary intervention'/exp OR 'dietary intervention' OR 'diet therapy'/exp OR 'diet therapy' OR 'diet regimen'/exp OR 'diet regimen' OR 'dietary effect'/exp OR 'dietary effect' OR 'dieting'/exp OR 'dieting' OR 'dietary influence'/exp OR 'dietary influence' OR 'dietary fiber'/exp OR 'dietary fiber' OR 'nutrition intervention' OR 'dietary exposure'/exp OR 'dietary exposure' OR 'dietary impact')	[embase]/lim NOT ([embase]/lim AND [medline]/lim)	
Cochrane CENTRAL	"gut microbiome" OR "gut microbiomes" OR "gut microflora" OR "gut microbiota" OR "gut microbiotas" OR "gastrointestinal flora" OR "gut flora" OR "gastrointestinal microbiotas" OR "gastrointestinal microbiota" OR "gastrointestinal microbial community" OR "intestinal microbiome" OR "intestinal microbiomes" OR "intestinal microbiota" OR "intestinal microbiotas" OR "intestine flora" OR "intestinal microbe" OR "intestinal microbes" OR "gut bacteria" in Title Abstract Keyword AND "modulation" OR "modulate" OR "effect" OR "effects" OR "change" OR "changes" OR "influence" OR "influences" OR "stability" OR "dysbiosis" OR "impact" OR "impacts" OR "instability" OR "alterations" OR "alteration" OR "control" OR "controls" OR "shape" OR "shaping" OR "regulation" OR "regulate" OR "modification" OR "modify" OR "modifications" in All Text AND "prebiotic" OR "supplements" OR "supplement" OR "supplementation" OR "diet" OR "dietary intervention" OR "dietary fiber" OR "diet therapy" OR "diet regimen" OR "dietary effect" OR "dieting" OR "dietary influence" OR "nutrition intervention" OR "dietary exposure" in Title Abstract Keyword - (Word variations have been searched)	NOT ([embase]/lim AND [medline]/lim)	55

Supplementary Table S3. Reason for exclusion from the meta-analysis evaluating the impact on nutritional intervention on gut microbiota's alpha diversity.

Alpha diversity index	Study (Author, year, country)	Study Design	Exclusion Reason		Inclusion in final meta- analysis
			Available data for meta-analysis	Study design	
Chao	Huang J., 2020, China	RCT	YES	Adequate study design (intra group differences)	✓
	Ruiz A., 2017, Spain	non-RCT	YES	Adequate study design (intra group differences)	✓
	Catherine C. Cohen, 2023, USA	RCT	YES	Different study design (inter group differences)	X
	Moran-Ramos S., 2022, Mexico	non-RCT	YES	Adequate study design (intra group differences)	✓
	Santacruz A., 2009, Spain	non-RCT	NO		X
	Zhou M., 2024, China	non-RCT	NO		X
	Aqeel A., 2024, USA	RCT pilot	YES	Adequate study design (intra group differences)	✓
	Peng et al, 2024, China	non-RCT	YES	Adequate study design (intra group differences)	✓
Shannon	Huang J., 2020, China	RCT	YES	Adequate study design (intra group differences)	✓
	Ruiz A., 2017, Spain	non-RCT	YES	Adequate study design (intra group differences)	✓
	Catherine C. Cohen, 2023, USA	RCT	YES	Different study design (inter group differences)	X
	Moran-Ramos S., 2022, Mexico	non-RCT	YES	Adequate study design (intra group differences)	✓
	Santacruz A., 2009, Spain	non-RCT	NO		X
	Zhou M., 2024. China	non-RCT	NO		X
	Aqeel A., 2024, USA	RCT pilot	YES	Adequate study design (intra group differences)	✓
	Peng et al, 2024, China	non-RCT	YES	Adequate study design (intra group differences)	✓
Simpson	Huang J., 2020, China	RCT	YES	Adequate study design (intra group differences)	✓
	Ruiz A., 2017, Spain	non-RCT	YES	Adequate study design (intra group differences)	✓
	Catherine C. Cohen, 2023, USA	RCT	NO	Different study design (inter group differences)	X
	Moran-Ramos S., 2022, Mexico	non-RCT	NO	Adequate study design (intra group differences)	X
	Santacruz A., 2009, Spain	non-RCT	NO	Different study design (inter group differences)	X
	Zhou M., 2024. China	non-RCT	NO		X
	Aqeel A., 2024, USA	RCT pilot	YES	Adequate study design (intra group differences)	✓

	Peng et al, 2024, China	non-RCT	YES	Adequate study design (intra group differences)	✓
ACE index	Huang J., 2020, China	RCT	YES*	Adequate study design (intra group differences)	✓
	Ruiz A., 2017, Spain	non-RCT	NO	Adequate study design (intra group differences)	X
	Catherine C. Cohen, 2023, USA	RCT	NO	Different study design (inter group differences)	X
	Moran-Ramos S., 2022, Mexico	non-RCT	NO	Adequate study design (intra group differences)	X
	Santacruz A., 2009, Spain	non-RCT	NO	Different study design (inter group differences)	X
	Zhou M., 2024. China	non-RCT	YES*	Adequate study design (intra group differences)	✓
	Aqeel A., 2024, USA	RCT pilot	NO		X
	Peng et al, 2024, China	non-RCT	NO		X

*For ACE index it was not possible to carry out the metanalysis due to insufficient number of articles and according to our criteria of data synthesis.

Abbreviations: RCT, randomized controlled trials

For other outcomes the criteria for performing the metanalysis were not met.

- I. Have at least three articles with sufficient detail for the pooled analysis
- II. Have a similar definition of the exposure and measurement of the outcome
- III. Include mean and confidence interval, association or regression coefficient

Supplementary Table S4. Extraction table of the included articles extended version

AUTHOR NAME, YEAR	Type of study (RCT, intervention trial)	Population (age and sex)	Healthy/Obesity/N AFLD/metabolic alterations	SAMPLE SIZE (n° groups)	NUTRITIONAL INTERVENTION	Methodology to implement the interventions	DURATION intervention	CONTROL/COMPARISO N GROUP	Alpha Diversity (richness evennes)
Huang J., 2020	Intervention Trial PRE- POST	9-16 years (12.88 ± 0.41 y; 15M, 9F)	Obesity	n= 24 (1 group)	A calorie-restricted diet (60% CH, 20% P, and 20% F) Calories were distributed as 30%, 40%, and 30% at breakfast, lunch, and dinner, respectively + endurance and strength training exercise	Dedicated weight loss camp (6-week program of endurance and strength exercises along with dietary restriction), dietary plan supervised from dietitians. Adherence not reported.	6 weeks	no control (PRE-POST)	POST INTERVENTION > Observed species (PRE 203.59 ± 10.53 vs POST 240 ± 12.00, p=0.002) > Chao (PRE 259.77 ± 14.15 vs POST 299.77 ± 16.33, p=0.007) > Ace (PRE 265.66 ± 15.33 vs POST 298.70 ± 14.87, p=0.023) > Shannon (PRE 2.93 ± 0.09 vs POST 3.19 ± 0.10, p= 0.009) < Simpson (PRE 0.14 ± 0.02 vs POST 0.11 ± 0.01, p=0.01)
Alicia Ruiz, 2017	Intervention Trial PRE- POST	13-16 years (mean age 14.8y; sex NA)	Obesity	n= 13	A calorie restricted diet and an educational assessment on nutrition concepts and physical activity	From the original study (face-to-face interviews, FFQ, 3-day food diary, nutrition knowledge) [Martinez- Gomez, D., et al. BMC Public Health 9: 414]. Adherence not reported.	1 year	no control (PRE-POST)	POST INTERVENTION > Fisher index (not significant) > taxa, Chao and Shannon indexes (not significant) > evenness index (not significant)
Catherine C. Cohen, 2023	RCT (secondary)	11-16 years (13 ± 1.9 y; sex NA)	NAFLD. Overweight or obesity	n= 40 (20 intervention, 20 control); analysis of microbiota (8 intervention; 10 control)	Low free-sugar version of their habitual diet (goal:<3% of TEI from free sugars)	From the original study Twice-weekly telephone calls assessed diet adherence [Schwimmer, J.B.; et al. JAMA 2019, 321, 256–265]. Adherence not reported.	8 weeks	control: usual diet	Less change in richness in the phylum level, in treatment group VS control, after intervention Richness: There is a higher mean chande al phylum level, in tratment VS control (no difference class, order, family, genus). Shanon, simpson, evenness index: no significant differences
Morán-Ramos S., 2022	Intervention Trial PRE- POST	11-14 years (mean age 12.9y IQR 2; only M)	Children with obesity defined as (SDS>+1,64)	n=6 children (20 originally)	hypo-caloric dietary plan (60% energy from CHO, 20-25% from fats, and 15-20% from proteins) + physical activity plan and recommendations to achieve at least 150 min/week	No information	6 weeks	no control (PRE-POST)	Chao and Shannon index showed no significant differences PRE-POST

Santacruz A., 2009	Intervention trial PRE-POST	13-15 years (18 M, 18 F; mean age 14.5 y)	Adolescents with obesity defined accordng to IOTF cutoffs	n=36 Identified 2 groups: responders to weight loss (GROUP A, n=23) and not responders (GROUP B, n=13)	hypo-caloric dietary plan (10–40% reduction) with a repartition of 50%CHO, 30% from fat, 20% from protein + increased physical activity (15–23 kcal/kg body weight/week)	No information	10 weeks	no control (PRE-POST and also GROUP A vs GROUP B)	NA
Zhou M., 2024	Intervention trial PRE-POST	6-12 years (18 M, 22 F; mean age 9.1 ± 1.6)	Obesity according to China's reference growth charts	n=30 (37 originally)	calorie-restricted dietary plan (80% of EER for school-age children) with a repartition of 45-50%CHO, 25-30% from fat, 20-25% from protein	Parents were required to record their children’s diet during the intervention, and they could communicate with dietitians online and receive online nutrition education during the whole process. Adherence not reported.	12 weeks	no control (PRE-POST)	POST INTERVENTION < ACE and Chao index
Aqeel A., 2024	RCT (pilot)	6-11 years (16 M; 17 F; mean age 8.9 ± 1.5)	Obesity (BMI>95th percentile for age and sex)	n=33 (randomized 50; control group n=17; intervention n=16)	CHILD-1 diet (evidence-based adaptation of the DASH diet), promotion of high fiber intake (vegetables, fruits, whole grains), restriction on animal dairy and limited consumption of processed meat, processed carbohydrates/sugary foods, foods high in sodium and fast foods. Participants received weekly groceries shops chosen by dieticians.	Participants received weekly groceries chosen under guidance from a registered dietitian. Adherence not reported.	4 weeks	control: usual diet (standard health behaviour and lifestyle treatment)	INTERVENTION vs CONTROL no significant changes observed BEFORE INTERVENTION VS AFTER INTERVENTION (N=16) Chao1 (118,3±26,62; 118,55±22,45) Shannon (3,64±0,21; 3,46±0,31) Simpson (0,95±0,01; 0,92±0,05)
Peng et al, 2024	Intervention trial PRE-POST	<15 yers (65 M; 21 F; mean age total sample 9.53 ± 1.78)	Obesity according to China's reference growth charts	n= 86 children with obesity; study group subsample n=39	Six-week of dietary and exercise intervention. Training: 6 days a week (aerobic exercise 4h per day). Calorie restricted diet (approx between 1300-1500 kcal) constiuted by 50% CHO, 20-25% of fat and 20-25% of protein.	Daily diet, exercise training and accommodation were provided by the summer camp. Each children had a dedicated teacher and management coach. Adherence not reported.	6 weeks	no control (PRE-POST)	BEFORE INTERVENTION VS AFTER INTERVENTION (N=39) Chao1 (425.17±154.57; 526.73±151.04 p=0.016) OBS(320.44±129.01; 402.06±132.67 p=0.028) PD_ whole_tree (24.64±8.43; 29.96±8.13 p=0.020) Shannon (4.54±0.72; 5.02±0.73 p=0.020) Simpson (0.88±0.07; 0.92±0.04 p0.025)

Microbiota Outcomes					
Beta Diversity	F/B	SCFA	Phylum mod	Class mod	Order mod
No significant differences	POST INTERVENTION <F/B ratio (POST 0.737 ± 0.09 vs. PRE 1.11 ± 0.205; P = 0.011).	NA	POST intervention < Firmicutes abundance > Bacteroidetes abundance (not significant)	POST INTERVENTION < Bacilli and > Lentisphaeria abundance (LDA effect size at P < 0.05, and LDA score >2)	POST INTERVENTION > Victivallales abundance (LDA effect size at P < 0.05, and LDA score >2)
B-diversity showed different clustering at baseline compared to 12-month follow up (p<0,05 for weighted, unweighted and Unifrac metrics)	POST INTERVENTION < F/B ratio (p=0.063)	NA	INTERVENTION: PRE vs DURING (3months) vs POST (12months) (mean ± SEM) < Actinobacteria relative abundance (PRE 0.89 ±0.32 vs POST 0.15± 0.04, p=0.02) (DURING 0.86 ± 0.30 vs POST 0.15±0.04, p<0.001) < Proteobacteria relative abundance (PRE 0.32 ±0.17 vs DURING 0.06 ± 0.02, P=0.04) > Bacteroidetes relative abundance (DURING 0.81 ±0.41 vs POST 8.24 ± 4.93, p= 0.04) No differences to Firmicutes, Verrucomicrobia	NA	
Significant correlation in family r=0,719 (p<0,001) and genus r=0,787 (p<0,001) level between baseline and endline.	NA	NA	No significant differences	No significant differences	No significant differences
NA	NA	NA	Bacteroidetes (median relative abundance = 46.5%), Firmicutes (median relative abundance = 45.7%), Proteobacteria (median relative abundance = 3.7%). No differences PRE-POST	NA	NA

NA	NA	NA	NA	NA	NA
No significant differences	NA	POST INTERVENTION > AA/TE, PA/TE and BA/TE vs baseline (p<0.0001, 0=0.0012, p=.026, respectively) No significant difference in IBA/TE, VA/TE, and IVA/TE	POST INTERVENTION (mean ± SEM or median (IQR)) > Actinobacteria relative abundance (PRE 4.3(1.6-10.0) vs POST 13.9(7.1-32.0), p<0.001) < Bacteroidetes relative abundance (PRE 31.3±13.3 vs POST 10.5(4.9-14.2), p<0.001) No differences in Firmicutes (PRE 52.0±17.4 vs 55.3±15.0, p ns), Verrucomicrobia, Proteobacteria	NA	NA
NA	NA	NA	NA	NA	NA
PERMANOVA Analysis revealed that obesity had significatn effects on the communities (p<0,01). The dietary intervention did not showed significant effect in PERMANOVA analysis.	NA	NA	NA	NA	NA

FAMILY mod	GENUS mod	SPECIES mod	Others?	METHODS of assessment
POST INTERVENTION < Lactobacillales, Streptococcaceae and > Victivallaceae abundance (LDA effect size at p<0.05, and LDA score >2) > Christensenellaceae (LDA effect size at p<0.05, and LDA score >2)	POST INTERVENTION < Veillonella, Streptococcus and > Victivallis, Butyricimonas abundance (LDA effect size at p<0.05, and LDA score >2) > Christensenellaceae R-7 group (LDA effect size at p<0.05, and LDA score >2)		NA	16S rRNA gene sequencing
POST INTERVENTION (mean ± SEM) < Coriobacteriaceae relative abundance (PRE 0.70 ± 0.29 vs POST 0.12 ±0.04, p=0.03) < Crostidiales_incertae sedis XIII relative abundance (PRE 0.53 ± 0.09 vs POST 0.21 ± 005, p=0.007) < Eubacteriaceae relative abundance (PRE 0.0083 ± 0.0038 vs POST 0.0008 ±0.0006, P=0.03) < Erysipelotrichaceae relative abundance (PRE 7.11 ±1.50 vs POST 2.91 ± 0.94, p=0.03) > Bacteroidaceae relative abundance (PRE 1.33 ± 0.73 vs POST 6.87 ± 4.26, p=0.05) > Veillonellaceae relative abundance (PRE 1.01± 0.80 vs POST 1.1 ± 0.31, p=0.03)	POST INTERVENTION (mean ± SEM) < Streptococcus relative abundance (PRE 0.45 ± 0.22 vs POST 0.16 ± 0.07,p=0.01) < Eubacterium (PRE 0.0083 ± 0.0038 vs POST 0.0008 ± 0.0006, p= 0.03) < Dorea (PRE 3.93 ± 1.01 vs POST 1.79 ± 0.50, p= 0 0.03) > Bacteroides (PRE 1.33 ± 0.73 vs POST 6.87 ± 4.26, p = 0.04) > Barnesiella (PRE 0.026 ± 0.014 vs POST 0.256 ± 0.166 p=0.02) > Clostridium XIVa (PRE 0.0085 ± 0.0048 vs POST 0.0659 ± 0.019, p= 0.005) > Coprococcus (PRE 0.94 ± 0.22 vs POST 1.65 ± 0.55, p= 0.05) > Roseburia (PRE 0.83 ± 0.56 vs POST 2.54 ± 0.63, p=0.02) > Faecalibacterium (PRE 0.80 ± 0.26 vs POST 6.39 ±3.03, p= 0.01) > Holdemania (PRE 0.0058 ± 0.0029 vs POST 0.0273 ± 0.0083, p<0.001) > Veillonella (PRE 0.0015 ± 0.0009 vs POST 0.0152 ± 0.0076, p=0.04)	NA	NA	16S rRNA gene sequencing
No significant differences	Significant differences in abundance (significant increase in treatment VS control) - Unclassified genus, Ruminococcaceae Family (p = 0.006) - Phascolarctobacterium genus, Veillonellaceae Family (p = 0.035) Abundance of two genera (Ruminococcaceae (p = 0.006) and Phascolarctobacterium (p = 0.035) and three OTUs, including Ruminococcus bromii (p = 0.026), were increased in treatment VS control at endline.	Significant differences in the mean changes (significant increase in treatment VS control) - Unclassified species of Ruminococcaceae Family - Ruminococcus bromii - Unclassified species of Phascolarctobacterium Genera	NA	16S rRNA gene sequencing. Plasma metabolomics (HILIC with mass spectrometry).
No differences PRE-POST	No differences PRE-POST.	NA	NA	16S rRNA gene sequencing

NA	ALL GROUPS PRE POST >Lactobacillus groups COUNT (p=0.030) total Bifidobacterium group counts were similar GROUP A >Lactobacillus groups (P=0.007) after intervention GROUP B No significant differences	ALL GROUP PRE-POST >counts of B. fragilis group (p=0.001) <counts of C. coccoides group (p=0.028). No significant differences for B. fragilis group (R = 0.55, p<0.001) and C. leptum group (R = 0.52, p<0.001) < counts B. longum (p=0.031) < counts B. adolescentis (p=0.044). GROUP A >B. fragilis (p=0.001) <B. longum (p=0.044) and <C.coccoides (p=0.001) after intervention GROUP B No significant differences POST GROUP A VS B -In group A >Total bacteria, >B. fragilis group, >C. leptum group counts, > B.catelunatum (p=0.015, p=0.001, p<0.001, p=0.036) vs B after intervention -In group A <C. coccoides group, <Lactobacillus group, and <Bifidobacterium (p<0.001, p<0.001, and p=0.008, respectively) vs B after intervention -In group B > B.bifidum and > B.breve vs A after intervention (p<0.001)	GROUP A PRE-POST >ratio Bifidobacterium to C. coccoides group counts (p=0.022) <ratio of Bifidobacterium to B. fragilis group counts (p=0.001).	16S rRNA-gene-targeted group specific primers
NA	POST INTERVENTION (mean ± SEM) > Bifidobacterium, Collinsella, Streptococcus, Blautia, and Escherichia-Shigella (18.37%, 3.16%, 5.53%, 5.61% and 1.38%, respectively; p<0.05) <Bacteroides and Megamonas (8.05% and 0.26%, respectively; p<0.001) >Ruminococcus_gnavus_group (1.48%; p<0.01) Akkermansia increasing trend (3.19%), not significant	NA	NA	16S rRNA gene sequencing. Faecal SCFA levels, gas chromatography–mass spectrometry (GC-MS)
NA	>Faecalibacterium, Eubacterium coprostanoligenes group, Oscillospiraceae group-002 (UCG-002), Bifidobacterium	> F. prausnitzii strains, Bacteroides uniformis, Prevotella copri	NA	16S rRNA gene sequencing (axonomy assignment were conducted using a DADA2 + SILVA)
BEFORE INTERVENTION VS AFTER INTERVENTION (N=39) Rikenellaceae (0.01±0.01 vs. 0.02±0.03) Enterobacteriaceae (0.03±0.04 vs. 0.06±0.04)	BEFORE INTERVENTION VS AFTER INTERVENTION (N=39) Sutterella (0.03±0.03 vs. 0.02±0.01)	BEFORE INTERVENTION VS AFTER INTERVENTION (N=39) Akkermansia muciniphila (0.00±0.02 vs. 0.02±0.05)	NA	16S rRNA gene sequencing

HEALTH-IMPACT				
Anthropometry (BMI, FM,WC)	Hematological parameters	NAFLD/other metabolic	Nutritional impacts	Anthropometry (BMI, FM,WC)
POST INTERVENTION < body weight (PRE 82.64 ± 3.40 kg vs. POST 74.00 ± 3.56 kg, P < 0.001) < BMI (PRE 31.02 ± 0.94 kg/m2 vs. POST 27.78 ± 0.88 kg/m2, P < 0.001) < body fat (PRE 34.35 ± 2.05 kg vs. POST 26.30 ± 1.73 kg, P < 0.001) < waist-to-hip ratio (PRE 0.93 ± 0.01% vs. POST 0.88 ± 0.12%, P < 0.001).	POST INTERVENTION < fasting blood glucose (PRE 4.37 ± 0.08 mmol/L vs. POST 4.14 ± 0.07 mmol/L, P < 0.05) < serum TGs (PRE 4.15 ± 0.18 mmol/L vs. POST 3.25 ± 0.07 mmol/L, P < 0.001) < LDL-C (PRE 2.30 ± 1.14 mmol/L vs. POST 1.73 ± 0.08 mmol/L, P < 0.001). No significant changes in levels of serum TC or HDL-C were found.	POST INTERVENTION > SEVR (PRE 112.21 ± 6.89% vs POST 163.08 ± 8.61%, P <0.001) < A1x75 (PRE 9.45 ± 1.49% vs. POST 3.13 ± 2.18%, P = 0.006) < resting heart rate (PRE 77.08 ± 2.87 beats/min vs. POST 60.88 ± 2.65 beats/min, P < 0.001) No significant changes in levels of SBP and DBP	NA	NA
POST INTERVENTION (mean, range) < BMI significantly (PRE 32.0 kg/m2, range 24.8-39.7 vs 29.4 kg/m2, range 23.0-34.2)	POST direct correlation BMI and: - serum LDL (r=0.5, q-value <0.2) - total cholesterol (r=0.4, q-value <0.2) - triglycerides (r=0.5, q-value <0.2) - insuline (r=0.5, q-value <0.2) - fasting glucose (r=0.3, q-value <0.2) - HOMA-IR index (r=0.5, q-value <0.2) POST inverse correlation BMI and HDL (r= -0.3, q-value <0.2) POST inverse correlation HDL and - Insulin (r= -0.5, q-value <0.2) - HOMA-IR (r= -0.5, q-value <0.2) - Tryglicerides (r= -0.4, q-value <0.2)	NA		POST direct correlation species richness (Taxa and Chao1) with BMI (r= 0.5, q-value<0.2) POST inverse correlation eveness index and BMI (r=-0.3, q-value <0.2) [*See articlesupplementary information for expanded results]
POST INTERVENTION Adjusted endpoint mean diference between groups (95% CI): - Weight (kg), higher change in intervention group, mean difference between group end treatment -2.0 (-3.3, -0.79) p=0,002 - BMI (kg/m2): higher change in intervention group, mean difference between group end treatment -0.78 (-1.2, -0.35) p=0,001 - BMI z-score: higher change in intervention group, mean difference between group end treatment -0.06 (-0.09, -0.03) p<0,001 - Waist Circumference (cm): decrease in intervention, no significant difference between groups - Systolic (mm Hg): higher change in intervention group, mean difference between group end treatment -6.9 (-13.4, -0.38) p=0,04 - Diastolic (mm Hg): decrease in intervention, no significant difference between groups	Adjusted mean diference (post intervention) between groups (95% CI): - Glucose (mg/dL): higher change in intervention group, mean difference between group end treatment -4,90 (-9,87 to 0,07) p=0,05 - Total Col (mg/dL): higher change in intervention group, mean difference between group end treatment -15,16 (-25,67 to -4,65) p=0,006 - LDL Col (mg/dL): higher change in intervention group, mean difference between group end treatment -9,58 (-19,30 to 0,15) p=0,05 - HDL Col (mg/dL): decrease in intervention, no changes in controls, no significant difference between groups - Insulin (µIU/mLe): no significant difference between groups - HOMA-IR: no significant difference between groups - Triglycerides (mg/dL):no significant difference between groups	Assessment of metabolomic changes in the amino acid and fatty acids pathways. Enriched metabolic pathways with increase for serine, glycine, acetylcine, and 2-aminobutyric acid, indole-3-acetic acid, ketone body 3-hydroxybutric acid; decrease of kynurenine and linolenic acid in the treated group compared to controls at 8 weeks. Intervention VS control at endpoint: Adjusted ratio of geometric means (95% CI): ALT (U/L): 0,65 (0,53-0,81) p<0,001 AST (U/L): 0,78 (0,65-0,92) P=0,005 GGT (U/L): 0,77 (0,68-0,87) p<0,001 Decrease in hepatic fat (p<0,001) Intervention: 25% to 17% Control: 21% to 20%	Intervention: decreased free-sugar intake from 11% to <1% TEI Control: from 14% to 10% TEI (Adjusted endpoint mean difference (95% CI): - 7,8% (-10,4 to -5,1) p<0,001)	Moderate correlation between change in weight and change in MRI-PDFF (hepatic steatosis) (r=0,42: 95% CI, 0,12 to 0,65)
<WC after intervention (98.05 ± 11.2 cm vs. 94.95 ± 7.82 cm, p = 0.031)	No differences PRE-POST	NA	Intervention: greater mean decrease in hepatic fat (25% to 17%) than the control (21% to 20.0%)	Odoribacter abundance showed a negative and significant correlation with the change in WC (delta WC PRE-POST): the quantity of Odoribacter increased significantly in those with a more substantial reduction in WC (r = -0.94, p = 0.0167).

GROUP A median weight loss 6.8 (4.8–9.0) kg, corresponding to 7.5% (IQR 5.8–9.3%)+ significant differences in BMI (p=0.030) and BMI SDS (p=0.035) GROUP B median weight loss 1.4 (0.75–2.00) kg, corresponding to 1.3% (IQR 0.85–2.25%) of body weight, no differences in BMI and BMI SDS	NA	NA	Between groups: no significant differences in dietary intake of energy, macronutrients, or on food group level before and after the intervention program. Within same group PRE-POST significant reduction: energy, protein, fat, PUFA, CHO, sugars, complex CHO.	POST Positive correlation B. fragilis counts group (R = 0.55, P < 0.001) and C. leptum group counts (R = 0.52, P < 0.001) with higher weight loss. POST Inverse correlation for higher weight loss with count of -Lactobacillus group (R = –0.40, P = 0.001) -Bifidobacterium (R = –0.37, P = 0.001) - E. coli (R = –0.26, P = 0.025) - C. coccoides group (R = –0.61, P < 0.001) POST inverse correlation lower weight loss (kg) and counts of B. breve (R = -0.56, P < 0.001) and B. bifidum (R = -0.76, P < 0.001) GROUP A POST direct correlation higher weight loss (kg) and B. fragilis (R = 0.27, P = 0.055) and Lactobacillus (R = 0.55, P < 0.001) POST inverse correlation higher weight loss(kg) and E.coli group count (R = –0.37, P = 0.010) and C. coccoides group levels (R = –0.611, P = 0.001) POST direct correlation body weight loss% and Lactobacillus group
POST INTERVENTION: significant reduction weight, BMI, BMI z score, WC, WHtR and FM% (p<0.001). No changes in FFM, BMR, skeletal muscle mass	NA	NA	Intervention: significant decreased total energy, fat energy ratio and intake, CHO, protein intake, vitamin B1 and E; significant increase protein energy ratio, DFI, Ca, vitamin B6, B12, C, and A	NA
INTERVENTION GROUP vs CONTROL: no significant changes in anthropometric parameters	NA	NA	Study of Dietary Screener Questionnaire (DSQ) score. Control vs. Intervention: <DSQ predicted intake of total added sugars. Within intervention: >DSQ predicted intake of whole grain, and fiber; <DSQ predicted dairy intake	NA
BEFORE INTERVENTION VS AFTER INTERVENTION (N=39) Weight: 61.12 ± 15.05 VS 55.46±13.9 BMI: 27.33 ± 5.54 vs 24.16 ± 3.15	NA	NA	NA	NA

CORRELATION RELATED HEALTH-IMPACT						
Hematological parameters	NAFLD/other metabolic	Nutritional impacts	CONFOUNDERS IDENTIFIED (Y/N)	LIST ADJUSTMENTS	STATISTICAL ANALYSIS CORRECTIONS	COMMENTS
POST direct correlation higher fasting glucose level and - Eubacterium ruminantium group (R = 0.432, P = 0.035) -Paraprevotella (R=0.559, P=0.004) POST inverse correlation higher fasting glucose level and Eubacterium ventriosum group (R= -0.600, P= 0.004) POST direct correlation higher TG levels and Family XIII UCG-001 (R= 0.498, P=0.013) POST direct correlation higher TC level and - Alloprevotella (R=0.567, P=0.004) - Eubacterium coprostanoligenes group (R=0.453, P=0.026) - Family XIII UCG-001 (R=0.430, P=0.036) - Ruminococcus torques group (R=0.535, P=0.007) POST inverse correlation higher TC level and Bacteroides (R=-0.412, P=0.045) POST inverse correlation higher HDL-C and Ruminococcaceae UCG-003 (R=-0.407, P=0.049) POST direct correlation higher LDL-C and	POST direct correlation higher SEVR and - Akkermansia (R=0.636, p<0.001) - Ambiguos taxa (R=0.636, p<0.039) - Anaerotruncus (R=0.563, p=0.004) - Helicobacter (R=0.558, p=0.005) - Ruminococcaceae UCG-014 (R=0.554, p=0.005) - Victivallis (R= 0.650, p<0.001) POST inverse correlation higher SEVR and - Cronobacter (R= -0.540, p=0.006) - Lachnospira (R= -0.546, p=0.006) - Lachnospiraceae UCG-003 (R= -0.558, p=0.005) - Prevotella 2 (R=-0.555, p=0.005) -Sutterella (R= -0.486, p=0.016) POST direct correlation higher Alx75 and - Cronobacter (R=0.592, p=0.002) - Lachnospiraceae UCG-003 (R=0.610, P=0.002) - Sutterella (R=0.567, p=0.004) POST inverse correlation higher Alx75 and Helicobacter (R= 0.608, p= 0.003)	NA	N	NA	N	
POST direct correlation higher Chao 1 index and glucose levels (r=0.5, q-value <0.2) POST direct correlation microbial metabolic performance (glycosidase) and: - HOMA-IR (r=0.5, q-value <0.2) - Insulin (r=0.5, q-value <0.2) - plasma LDL (r=0.3, q-value <0.2)			N	NA	Benjamini–Hochberg correction for multiple testing	
NA	Metabolic pathway of: Acetylglycine (r = 0.38, p = 0.03, q = 0.18) and creatine (r = 0.35, p = 0.04, q = 0.19) were positively correlated with the unclassified genera in Ruminococcaceae Disaccharide (r = -0.41, p = 0.02, q = 0.19) and taurine (r = -0.46,p = 0.008, q = 0.14) were negatively correlated with the unclassified genera in Ruminococcaceae Kynurenine (r = -0.52, p = 0.006, q = 0.14) was negatively correlated with Phascolarcotobacterium	NA	Y	Adjustment for baseline value	Benjamini-Hochberg correction test	Secondary study to the RCT "Effect of a Low Free Sugar Diet vs Usual Diet on NonalcoholicFatty Liver Disease in Adolescent Boys" MAIN STUDY (primary outcome-> health effects) SECONDARY STUDY (secondary outcome -> gut microbiota)
NA	NA	NA	N	NA	N	

NA	NA	POST reduction in complex CHO intake was significantly and negatively correlated (R= -0.334; P=0.050) to changes in B. fragilis group	Y	sex, age (only for dietary intake analysis)	N	
NA	NA	NA	N	NA	Benjamini–Hochberg correction for multiple testing	
NA	NA	NA	Y	Adjustments for repeated measure and relevant covariates	N	
NA	NA	NA	N	NA	Y	

Supplementary Table S5. Taxa-level changes in gut microbiota after dietary interventions in children and adolescents with obesity

Taxa level	Intra-variability			Inter-variability		
	Observed change	Intervention	Author	Observed change	Intervention	Author
Phylum	<i>Firmicutes</i>	↓	STCR	Huang	-	-
	(syn <i>Bacillota</i>)	=	STCR	Zhou	-	-
	<i>Bacteroidetes</i>	↑	STCR	Huang		
	(syn <i>Bacteroidota</i>)	↑	LTCR	Ruiz	-	-
		↓	STCR	Zhou	-	-
	<i>Actinobacteria</i>	↓	LTCR	Ruiz	-	-
	(syn <i>Actinomycetota</i>)	↑	STCR	Zhou	-	-
	<i>Proteobacteria</i>	↓	LTCR	Ruiz	-	-
	(syn <i>Pseudomonadota</i>)	=	STCR	Zhou	-	-
Class	<i>Verrucomicrobia</i>	=	LTCR	Ruiz	-	-
	(syn <i>Verrucomicrobiota</i>)	=	STCR	Zhou	-	-
Order	<i>Bacilli</i>	↓	STCR	Huang	-	-
	<i>Lentisphaera</i>	↑	STCR	Huang	-	-
Family	<i>Lactobacillales</i>	↓	STCR	Huang	-	-
	<i>Victivallales</i>	↑	STCR	Huang	-	-
Family	<i>Streptococcaceae</i>	↓	STCR	Huang	-	-
	<i>Christensenellaceae</i>	↑	STCR	Huang	-	-
	<i>Victivallaceae</i>	↑	STCR	Huang	-	-
	<i>Veillonellaceae</i>	↑	LTCR	Ruiz	↑	Low free sugar Cohen
	<i>Ruminococcaceae</i>	-	-	-	↑	Low free sugar Cohen
	<i>Coriobacteriaceae</i>	↓	LTCR	Ruiz	-	-
	<i>Crosidiales Incerae Sedis XIII</i>	↓	LTCR	Ruiz	-	-
	<i>Eubacteriaceae</i>	↓	LTCR	Ruiz	-	-
	<i>Erysipelotrichaceae</i>	↓	LTCR	Ruiz	-	-
	<i>Bacteroidaceae</i>	↑	LTCR	Ruiz	-	-
	<i>Rikenellaceae</i>	↑	STCR	Peng	-	-
	<i>Enterobacteriaceae</i>	↑	STCR	Peng	-	-
	<i>Alcaligenaceae</i>	↓	STCR	Peng	-	-
Genus	<i>Veillonella</i>	↓	STCR	Huang	-	-
		↑	LTCR	Ruiz	-	-
	<i>Victivallis</i>	↑	STCR	Huang	-	-
	<i>Christensenellaceae R7 group</i>	↑	STCR	Huang	-	-
	<i>Lactobacillus group</i>	↑	STCR	Santa Cruz	-	-
	<i>Phascolarctobacterium</i>	-	-	-	↑	Low free sugar Cohen
	<i>Streptococcus</i>	↓	LTCR	Ruiz	-	-

		↑	STCR	Zhou			
	<i>Dorea</i>	↓	LTCR	Ruiz	-	-	-
	<i>Bacteroides</i>	↑	LTCR	Ruiz	-	-	-
		↓	STCR	Zhou	-	-	-
	<i>Barnisella</i>	↑	LTCR	Ruiz	-	-	-
	<i>Holdemania</i>	↓	LTCR	Ruiz	-	-	-
	<i>Sutterella</i>	↓	STCR	Peng	-	-	-
	<i>Akkermansia</i>	=	STCR	Zhou	-	-	-
	<i>Prevotella</i>	=	STCR	Zhou	-	-	-
	<i>Ruminococcus gnavus</i> group	↑	STCR	Zhou	-	-	-
	<i>Collinsella</i>	↑	STCR	Zhou	-	-	-
	<i>Megamonas</i>	↓	STCR	Zhou	-	-	-
	<i>Escherichia-Shigella</i>	↑	STCR	Zhou	-	-	-
	<i>Eubacterium coprostanoligenes</i> group	-	-	-	↑	CHILD-1 diet	Aqeel
	<i>Oscillospiraceae</i> group-002 (UCG-002)	-	-	-	↑	CHILD-1 diet	Aqeel
	<i>Bifidobacterium</i>	↑	STCR	Zhou	↑	CHILD-1 diet	Aqeel
Species	<i>B. fragilis</i>	↑	STCR	Santa Cruz	-	-	-
	<i>B. longum</i>	↓	STCR	Santa Cruz	-	-	-
	<i>B. adolescentis</i>	↓	STCR	Santa Cruz	-	-	-
	<i>Akkermansia muciniphila</i>	↑	STCR	Peng	-	-	-
	<i>Bacteroides uniformis</i>	-	-	-	↑	CHILD-1 diet	Aqeel
	<i>Prevotella copri</i>	-	-	-	↑	CHILD-1 diet	Aqeel
	<i>Unclassified species of phascolarobacterium</i>	-	-	-	↑	Low free sugar	Cohen
Butyrate producing bacteria							
Genus	<i>Butyricimonas</i>	↑	STCR	Huang	-	-	-
	<i>Eubacterium</i>	↓	LTCR	Ruiz	-	-	-
	<i>Clostridium XVI</i>	↑	LTCR	Ruiz	-	-	-
	<i>Coprococcus</i>	↑	LTCR	Ruiz	-	-	-
	<i>Roseburia</i>	↑	LTCR	Ruiz	-	-	-
	<i>Faecalibacterium</i>	↑	LTCR	Ruiz	↑	CHILD-1 diet	Aqeel
		=	STCR	Zhou	-	-	-
	<i>Fusobacterium</i>	=	STCR	Zhou	-	-	-
	<i>Subdoligranulum</i>	=	STCR	Zhou	-	-	-
	<i>Blautia</i>	↑	STCR	Zhou	-	-	-
	<i>Megasphaera</i>	=	STCR	Zhou	-	-	-
Species	<i>C. coccoides</i>	↓	STCR	Santa Cruz	-	-	-
	<i>F. prausnitzii</i> strains	-	-	-	↑	CHILD-1 diet	Aqeel
	<i>Ruminococcus bromii</i>	-	-	-	↑	Low free sugar	Cohen