## Supplementary Material S1: Search Strings for Pubmed and Embase Databases

### 1. PubMed (n=5,828)

(((("gastrointestinal tract"[MeSH Terms] OR "gastrointestin*"[Title/Abstract] OR "Gut"[Title/Abstract] OR "intestin*"[Title/Abstract] OR "colon*"[Title/Abstract] OR "feces"[MeSH Terms] OR "feces"[Title/Abstract] OR "faecal"[Title/Abstract]) AND ("microbiota"[MeSH Terms] OR "gastrointestinal microbiome"[MeSH Terms] OR "dysbiosis"[MeSH Terms] OR ("alpha diversity"[Title/Abstract] OR "alpha diversity"[Title/Abstract] OR "Acetate"[Title/Abstract] OR "Bacteroides"[Title/Abstract] OR "Bacteroidetes"[Title/Abstract] OR "beta diversity"[Title/Abstract] OR "beta diversity"[Title/Abstract] OR "Bifidobacterium"[Title/Abstract] OR "Butyrate"[Title/Abstract]) OR ("bacteria"[Title/Abstract] OR "flora"[Title/Abstract] OR "Microbial"[Title/Abstract] OR "microflora"[Title/Abstract] OR "dysbiosis"[Title/Abstract] OR "microbial profile"[Title/Abstract] OR "Firmicutes"[Title/Abstract] OR "microbial communit*"[Title/Abstract] OR "microbes"[Title/Abstract] OR "metabolom*"[Title/Abstract] OR "microbial 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OR ("pretest"[Title/Abstract] AND "posttest"[Title/Abstract]) OR ("program*"[Title/Abstract] AND ("evaluat*"[Title/Abstract] OR "effectiveness"[Title/Abstract])) OR "intervention"[Title/Abstract]))) AND ((english[Filter]) AND (2008:2021[pdat]))

### 2. Embase (n=9,695)

('crossover procedure':de OR 'double-blind procedure':de OR 'randomized controlled trial':de OR 'single-blind procedure':de OR random*:de,ab,ti OR factorial*:de,ab,ti OR crossover*:de,ab,ti OR ((cross NEXT/1 over*):de,ab,ti) OR placebo*:de,ab,ti OR ((doubl* NEAR/1 blind*):de,ab,ti) OR ((singl* NEAR/1 blind*):de,ab,ti) OR assign*:de,ab,ti OR allocat*:de,ab,ti OR volunteer*:de,ab,ti OR 'controlled clinical trial'/exp OR trial:ti,ab OR 'clinical article'/exp OR 'controlled study'/exp OR 'major clinical study'/exp OR 'prospective study'/exp OR 'cohort analysis'/exp OR 'cohort':ti,ab OR 'compared':ti,ab OR 'groups':ti,ab OR 'multivariate':ti,ab OR 'program evaluation'/exp OR 'follow-up studies'/exp OR 'cross-over studies'/exp OR 'pretest posttest control group design'/exp OR 'control group'/exp OR 'parallel design'/exp) AND ('gastrointestinal tract'/exp OR 'gastrointestinal tract' OR gastrointestin*:ab,ti OR gut:ab,ti OR 'intestine'/exp OR 'intestine' OR intestin*:ab,ti OR colon:ab,ti OR 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## Supplementary Material 2: Gut Microbiota Outcomes

- Change in alpha diversity (microbial diversity within each subject) and beta diversity (difference between each subject's) – Increase indicates beneficial effect, and the reverse indicates harmful effect
    - α-diversity indices (Observed species, Shannon index, Simpson index, and Chao 1 index)
    - β-diversity dissimilarity based on Bray-Curtis distance
- Change in fecal short chain fatty acid (SCFA) levels
    - Beneficial change - Increase in total SCFA, butyrate, acetate, propionate, and Isobutyrate
- Change at phyla level – change in abundance of phyla Bacteroidetes, Firmicutes, Proteobacteria, Actinobacteria, Verrucomicrobia, Tenericutes, Fusobacteria, Saccharilbacteria, Chloroflexi, Acidobacteria, and Cyanobacteria
    - Beneficial phyla
        - Bacteroidetes (gram-negative bacteria - Bacteroides, Prevotella, Porphyromonas, Alistipes and Parabacteroides)
        - Firmicutes (gram-positive bacteria - butyrate producers – Lactobacillus (pro), Faecalibacterium (pro), Eubacterium, Roseburia, Anaerostipes, Clostridium perfringens and Ruminococcus)
        - Actinobacteria (Bifidobacteria)
    - Not beneficial when excess phyla
        - Proteobacteria (Enterobacteriaceae family, Escherichia genus, Collinsella genus)
        - Fusobacteria - Fusobacterium nucleatum

- Change in ratios of phyla – change in Firmicutes/Bacteroidetes ratio
    - Balanced Firmicutes/Bacteroidetes ratio – Beneficial
    - Increase in Firmicutes/Bacteroidetes ratio – associated with obesity
- Change in bacteria that are shown to be associated with inflammation, obesity, postprandial glucose metabolism, cardiometabolic health
    - Beneficial bacteria - Prevotella copri , Blastocystis spp., Faecalibacterium prausnitzii, Haemophilus parainfluenzae , Firmicutes bacterium CAG95, Eubacterium. eligens, Roseburia CAG182, Oscillibacter sp 57_20, Firmicutes bacterium CAG170, Oscillibacter sp PC13, Clostridium sp CAG167, Bifidobacterium. animalis, Romboutsia ilealis, Veillonella atypica, V. infantium, V. dispar
    - Harmful bacteria - Clostridia (C. spiroforme, C.bolteae CAG59, C. bolteae, Clostridium CAG58, C. symbiosum, C. innocuum, C. leptum), Flavonifractor plautii, Rumminococcus. gnavus, Eggerthella lenta, E coli, Ruthenibacterium. lactatiformans, Collinsella intestinalis, Blautia hydrogenotrophica, Anaerotruncus colihominis, Bacteroides thetaiotaomicron
- Change in bacteria that are shown to be associated with different cancers (colorectal cancer, breast cancer, other cancers) Beneficial bacteria - Bifidobacterium, Lactobacillus, Lactococcus, Roseburia, Akkermansia, Faecalibacterium prausnitzii, Eubacterium rectale, Roseburia faecis, Eulonchus halli, Prevotella copri, Parabacteroides distasonis, Sphingomonadaceae
- Harmful bacteria - Bacteroides fragilis, Enterobacteriaceae spp., Listeria monocytogenes, Fusobacterium nucleatum, Streptococcus gallolyticus, Clostridium difficile, Clostridium

septicum, Enterococcus faecalis, Escherichia coli, Peptostreptococcus stomatis, Helicobacter pylori, Ruminococcus torques, Bilophila wadsworthia, Streptococcus agalactiae, Pseudomonas, Alistipes, Atopobium, Hydrogenophaga, Gluconacetobacter, Bacillus cereus.

- Most reported bacteria from the studies included in the review
- Beneficial - Faecalibacterium, Bifidobacterium, Lactobacillus, Lactococcus, Parabacteroides, Roseburia, Eubacterium rectale, Eubacterium hallii, Akkermansia, Akkermansia muciniphila, Prevotella, Prevotella copri, Anaerostipes, Anaerostipes hadrus, Veillonellaceae, Parabacteroides distasonis, Gemmiger, Moraxellaceae
- Harmful - Bacteroides, Bacteroides fragilis, Fusobacteria, Streptococcus, Clostridium, Clostridium symbiosum, Clostridium perfringens, Dialister, Alistipes, Bilophila, Ruminococcus gnavus, Dorea, Actinomyces, Odoribacter, Blautia, Lachnospira, Lachnospiraceae, Sutterella, Enterobacteriaceae, Klebsiella sp
- Not clearly known - Ruminococcus bromi, Oscillospira

## Table S1: Summary Tables Presenting Extracted Evidence from Reviewed Articles

Table S1.a. Summary tables – Dairy

| **Specific foods -** Dairy (n=8) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Kefir - 180 mL/day - Bellikci-Koyu_2019 | 1 | Randomized, Controlled Study | Increase in the Actinobacteria | | No effect on other phyla or diversity |
| High dairy (HD: 1500 mg calcium/day) versus low dairy (LD: 600 mg calcium/day). -Bendtsen_2018<br><br>(HD, consumed ≥4 servings of dairy/day vs AD ≤2/day) - Khorraminezhad_2021<br><br>High-dairy diet (HDD) (5–6 dairy portions per day) and a low-dairy diet (LDD) (≤1 dairy portion - Swarte 2020 | 3 | 2 x A randomized controlled parallel design<br><br>A randomized, crossover Study | The abundance of Lactococcus were significantly increased during the HDD, while the relative abundance of Bilophila significantly decreased.<br>Increase in Faecalibacterium after HD | The abundance of Streptococcus significantly increased during the HDD | No significant changes from the phylum to the genus level or in diversity<br><br>Ratio Bacteroidetes /firmicutes showed no differences. |
| Total dairy intake - highest (≥0.5 serving/d) and second highest (1 serving/wk-0.5 serving/d) total dairy intake category, compared with lowest category (<1 serving/mo - Shuai_2021 | 1 | Prospective cohort study | High dairy intake - higher levels of Shannon, Simpson index and beta-diversity.<br>Yogurt consumption was positively associated with Shannon and Observed species.<br>Bifidobacterium were enriched in in the highest total dairy intake group | Streptococcus, and Clostridium were enriched in in the highest total dairy intake group | |
| Whole-fat liquid yogurt - 220 g/day - Chen_2019<br><br>Three types of yogurts (cow’s whole-milk yogurt, ewe’s semi-skimmed-milk yogurt, ewe’s whole-milk yogurt) - Redondo_2019 | 2 | A randomized, controlled trial | Decreased the relative abundance of the Firmicutes phylum | | No differential effect by type of yogurt |

| **Specific foods -** Dairy (n=8) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Whole milk – 250ml/day - Li_2018 | 1 | Intervention study | | | No effect on diversity or on SCFA |

Table S1.b. Summary tables – Meat and fish products

| **Specific foods -** Meat and fish products (n=7) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| A standard diet enriched with 100 g of sardines 5 d/wk - Balfegó_2016 | 1 | A pilot randomized trial | A decrease in Firmicutes/Bacteroidetes ratio<br>An increase in Bacteroides–Prevotella | 1 | A pilot randomized trial |
| Atlantic cod in weekly doses of 750 g, Atlantic salmon in weekly doses of 750 g, and no-fish intake - Bratlie_2021 | 1 | A randomized, controlled parallel group design | Higher counts for a few bacteria in the Firmicutes phylum | In the Cod and Salmon groups - lower counts for bacteria that belong to the Bacteroidales order in the Bacteroidetes phylum and the Clostridiales order of the Firmicutes phyla | |
| Fried meat - 4 times/week vs no fried meat intake - Gao_2021 | 1 | Randomized controlled-feeding trial | The ratio of Firmicutes and Bacteroidetes was decreased in both groups, and it was significantly lower in the control group | | No difference in microbial community richness |
| Consume 2x150 g portions of farmed salmon per week or habitual diet - Urwin_2014 | 1 | A single-blind, randomized, controlled intervention | | | No significant effects on any of the bacteria enumerated in maternal fecal samples |
| High-protein/high red meat (HP) diet (35% protein, 40% carbohydrate, and 25% fat) VS High-carbohydrate/low red meat (HC) diet (17% protein, 58% carbohydrate, and 25% fat) - Benassi-Evans_2010 | 1 | A Parallel-Group, Randomized, Controlled Study | | | No change in SCFA |

| **Specific foods -** Meat and fish products (n=7) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| 'Animal-based diet'- composed of meats, eggs, and cheeses VS 'Plant-based diet'- rich in grains, legumes, fruits, and vegetables - David_2014<br><br>Mediterranean diet - including meat and meat products, poultry, and fish VS Vegetarian diet - abstinence to consume meat and meat products, poultry, fish, seafood and flesh from any other animal, but included eggs and dairy products - Pagliai_2020 | 2 | Dietary intervention<br><br>Dietary intervention study | Decrease in the levels of Firmicutes that metabolize dietary plant polysaccharides (Roseburia, Eubacterium rectale and Ruminococcus bromii) in animal-based diet<br><br>MD led to an increase of 10% in propionate<br>Carbohydrate was positively correlated with butyric acid in MD | Reduction in fecal propionate and an increase in both branched chain SCFA, isobutyric and isovaleric acid after vegetarian diet<br>Increase in the abundance of bile-tolerant microorganisms (Alistipes, Bilophila and Bacteroides) after animal-based diet<br>Fat intake was negatively correlated with acetic acid, propionic acid, valeric acid and isobutyric acid | No change in alpha diversity<br>No change in alpha diversity |

Table S1.c. Summary tables – Legumes and nuts

| **Specific foods- Legumes_nuts** (n=15) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Daily intake of flaxseed mucilage (10 g) or placebo for 6 wks - Brahe_2015<br><br>Flax Seed ground - 10 g/d of for 6 weeks - McCann_2021 - McCann_2021 | 2 | RCT, a single-blinded, parallel-group<br><br>A randomized, crossover intervention study | Fusobacteria, Pyramidobacter and Odoribacter -reduced in the FS | alpha diversity- Shannon diversity index and Simpson's inverse index decreased<br>Clostridium genus – increased<br>Faecalibacterium prausnitzii species & Ruminococcuslactaris - decreased | Did not differ in Alpha and beta diversity (Shannon Diversity Index) |
| Almonds -1.5oz daily for 3wks - Burns 2016<br><br>Almonds - 56g/day for 8wks - Choo 2021<br><br>Almond - 57 g/d for 8 wk - Dhillon_2019<br><br>Almonds – 42 g/day for 3wks - Holscher_2018_2<br><br>Almond-based low carbohydrate diet (a-LCD) - 56 g/day almonds vs a low-fat diet (LFD) - Ren_2020<br><br>No nuts vs 1.5 servings/d either almonds or pistachios (42.5 g/d) vs 3 servings/d of | 6 | 3x A randomized, crossover study<br><br>A randomized, parallel controlled trial<br><br>2xA randomized, controlled, parallel arm | Increases in bacterial community richness, evenness (Simpson's index(1−D), P=.003) and diversity (Faith's phylogenetic diversity<br><br>Increase in alpha diversity & beta-diversity<br><br>Decrease in Bacteroides fragilis<br>Increased Lachnospira, Roseburia, Clostridium, and Dialister<br><br>Increase in Roseburia, Ruminococcus, and Eubacterium in the a-LCD arm<br><br>β-diversity larger for pistachio | Increases in the relative abundance of OTUs assigned to three members in the Ruminococcaceae family and one member of the Lachnospiraceae family<br><br>Decreased Actinobacteria, Bifidobacterium and Parabacteroides<br><br>Decrease in Firmicutes in the a-LCD arm<br>Decrease in Bacteroidetes and Bacteroides in the a-LCD arm<br><br>Decrease in lactic acid bacteria after 42.5 or 85 g/d of pistachios | No significant differences in alpha diversity<br><br>No significant change at phylum level<br><br>No change in SCFA<br><br>α-diversity was not affected by either almonds or pistachios<br><br>No change at phyla level |

| **Specific foods- Legumes_nuts** (n=15) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| either almonds or pistachios (85 g/d) - Ukhanova_2014 | | | | | |
| Canned Chickpea - 200 g/d for 3wks - Fernando_2010 | 1 | A randomized crossover intervention | Increase in Faecalibacterium prausnitzii<br>A decrease in Clostridium clusters (C. histolyticum, C. lituseburense and relatives) | | No change in alpha diversity, SCFA |
| Walnut - 1.5 servings (42g)/day for 3 wks - Holscher_2018<br><br>Whole walnuts (WD; 57–99 g/d walnuts; 2.7% α-linolenic acid (ALA)), vs a fatty acid–matched diet devoid of walnuts (walnut fatty acid–matched diet; WFMD; 2.6% ALA), vs a diet replacing ALA with oleic acid without walnuts - Tindall_2020 | 2 | A controlled-feeding, randomized crossover study | Change in beta-diversity<br>Increased Faecalibacterium, and Roseburia<br><br>Decreased Ruminococcus, Dorea, and Oscillospira<br><br>Increase in Roseburia, Eubacterium eligens group in WD arm | Increased Firmicutes and decreased Actinobacteria<br><br>Increase Clostridium, Dialister<br><br>Decrease in Bifidobacterium<br><br>Increase in Lachnospiraceae, Gordonibacter in WD | No change in alpha diversity<br>No change in alpha diversity<br>No change in Bacteroidetes, Firmicutes, or Proteobacteria |
| Non-fermented soybean milk (NFSM - 100 g/day) or fermented soybean milk (FSM-100 g/day) for 2 weeks - Inoguchi_2012<br><br>One Revival soy bar per day (160 mg of soy isoflavones and 1 g saponin) - Nakatsu_2014<br><br>Low glycinin soymilk - 500 mL/day(LGS, 49.5% β-conglycinin/6% glycinin) VS conventional soymilk (S, 26.5% β-conglycinin/38.7% glycinin) VS bovine milk (M, 0% β-conglycinin/0% glycinin) - Fernandez-Raudales_2012 | 3 | Randomized controlled-feeding trial<br><br>Experimental design<br><br>Randomized, double-blind trial | Increase in bifidobacteria during NFSM intake.<br>Increase in bifidobacteria and lactobacilli and clostridia decreased during FSM intake.<br><br>Decrease in unclassified Clostridiaceae<br>Firmicutes decreased for both soy-milk groups (LGS and S) | Decrease in Lactobacillus<br><br>Decrease in bacterial diversity and richness (ACE and Chao1 indices) in all arms while unchanged in the M group<br><br>Bifidobacterium decreased within LGS and S and increased within the M group | No change in alpha diversity & in beta-diversity |

| **Specific foods- Legumes_nuts** (n=15) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| | | | Bacteroidetes increased in both soymilk groups and decreased in the M group<br>Firmicutes to Bacteroidetes ratio decreased in both the LGS and S groups and remained relatively unchanged in the M group<br>Bacteroides-Prevotella increased significantly in LGS but not S or M<br>Faecalibacterium increased in LGS group | Lactobacillus increased within M but not in LGS and S<br>Roseburia tended to increase whereas Prevotella tended to decrease in bovine milk arm and opposite for S group | |
| Legume consumption, including peanuts, soy foods, and other beans - total legume consumption (in grams/day) - Wang_2021 | 1 | Population-based cohort study | Enterobacteriales positively associated with high legume intake | | α-diversity or β-diversity was not associated with legume consumption |

Table S1.d. Summary tables – Grains

| **Specific foods - Grain** (n=20) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| A diet high in Whole Grains (>80 g/d) or low in WGs (<16 g/d, RG diet) - Ampatzoglou, 2015<br><br>Whole grain daily (WW - 105 g) or no whole grain (RW) both in energy-restricted diet (deficit of at least 1250 kJ/day) - Christensen_2013<br><br>Whole grain oat Granola (WGO – 45g/day) or non-whole grain (NWG) - Connolly_2016<br><br>Whole grain (WG - 48 g/d, 1442 kJ/100 g, 18 g/100 g fiber) or wheat bran (WB - 48 g/d, 1184 kJ/100 g, 27 g/100 g fiber) - Costabile_2008<br><br>Durum wheat (75%) and whole-grain barley (25%) pasta containing 3 g of barely beta-glucans - 100 g/day - DeAngelis_2015 | 6 | Crossover study<br><br>Dietary intervention, open-label parallel, randomized<br><br>A randomized, controlled, crossover, double-blinded design<br><br>A double-blind, randomised, placebo-controlled, crossover study<br><br>Dietary intervention<br><br>A placebo-controlled, | Increase in abundance of Bifidobacterium after whole grain daily<br>Decrease in abundance of Bacteroides after no whole grain diet<br><br>Increase in bifidobacterial, lactobacilli, and total bacteria population after WGO<br><br>Increase in bifidobacteria during the ingestion of the WG<br>Increase in fecal lactobacilli/enterococci with ingestion of either WB or WG<br><br>Increase in SCFA (2-methyl-propanoic acid, acetic acid, butanoic acid, and propanoic acid) after the intervention<br>Increase in Roseburia hominis<br><br>Increase in Prevetolla after WG intake<br>Decrease in Dialister, Blautia, and | Decrease in bifidobacteria and total bacteria population after NWG<br><br>Increase in clostridia during WB intake<br><br>Fewer total anaerobes, decrease in Firmicutes after the intervention<br><br>Increase in Clostridiaceae (Clostridium orbiscindens and Clostridiumsp.), and Ruminococcus sp<br><br>Decrease in Bifidobacterium | No significant change in SCFA or bacterial groups<br><br>No significant changes in SCFA<br><br>No change in Chao1 and Shannon index<br><br>No change at phyla level<br><br>No change in α-diversity or β-diversity |

| **Specific foods - Grain** (n=20) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Whole grain (WG) product - 70 g/d(3 biscuits/d) VS Control - 1 package (33 g) of crackers and 3 slices of toasted bread (˜27 g) Vitaglione_2015 (C) | | parallel-group randomized trial | Collinsella after WG intake | | |
| Whole grain market basket -13.7 g of fiber/day VS refined grain market basket - 4.2 g of fiber/day - Cooper_2017<br><br>Whole grain diet (≥75g/day whole grain) VS a refined grain diet (<10g/day whole grain) - Roager_2019<br><br>Whole grain wheat (WGW) (98 g/d - 17.6 g fiber/100 g) VS colored refined wheat (RW) products (98 g/d - 7.2 g fiber/100 g) - vanTrijp_2021<br><br>A whole-grain (WG) diet (16 g/1000 kcal - 35 g/d) VS refined grains (RGs) diet (8 g/1000 kcal) - Vanegas_2017 | 4 | A six-week intervention trial<br><br>A randomized, controlled crossover<br><br>Double-blind, randomized, controlled, parallel<br><br>Randomized, controlled, parallel-design human trial | Increase in relative abundance of Akkermansia and Lactobacillus in the high fiber group<br><br>Increase in Faecalibacterium prausnitzii, one Prevotella copri after whole grain<br><br>Decrease in Bacteroides thetaiotaomicron after whole grain<br><br>Decreased in bacterial taxon within the Lachnospiraceae family after WGW diet<br><br>Increase in acetate and total SCFA in the WG<br><br>Decrease in Enterobacteriaceae after WG<br>Increase in Roseburia after WG | Increase in Clostridiales after whole grain<br><br>Increased 3 bacterial taxa within the Ruminococcaceae family) after WGW diet<br><br>Increase in Lachnospira after WG | No significant difference in the relative abundance of any taxa<br><br>No change in richness or evenness<br><br>No change in α-diversity or β-diversity<br><br>No change in α-diversity or β-diversity<br><br>No change at phyla level |
| Intervention arm - Rye breads with a high-fiber content (7–15%), whole-meal pasta [3.5 dL/wk and high-fiber oat biscuits VS controls - refined white wheat breads with | 4 | A randomized, parallel, 2-arm 12-wk intervention | Increase in Actinobacteria, Bifidobacterium, Bifidobacteriales, | Decrease in Bacteroidetes phylum and increase in the members of Clostridium | No change in microbiota composition |

| **Specific foods - Grain** (n=20) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| a low fiber content (4%) and restricted rye intake to 1–2 portions/d.- Lappi_2013<br><br>Whole-grain wheat (WGW) VS Whole-grain rye (WGR), or Refined wheat (RW) - Vuholm_2017<br><br>White bread period VS a white rice period - Mano_2018<br><br>Brown rice flakes 60g (4.4g total dietary fiber) VS Brown rice and barley (consisting of 30 g each - 11.5 g total dietary fiber) VS Barley (consisting of 60 g - 18.7 g total dietary fiber) - Martínez_2013 | | A randomized parallel researcher-blinded parallel intervention study<br><br>Randomized, crossover trial<br><br>Randomized cross-over trial | Bifidobacteriaceae after bread period compared to rice period<br><br>Increase in community evenness (Shannon's and Simpson's), after all interventions<br><br>Increase in Roseburia, Bifidobacterium and the species E. rectale after intake of diets containing barley | cluster IV (Firmicutes) in the control arm<br><br>Butyrate decreased in in the refined wheat arm<br><br>Firmicutes increased and bacteroidetes decreased in all three dietary treatments<br><br>Increase in Firmicutes/Bacteroidetes ratio<br>Increase in Dialister | No change in the relative abundance of any bacterial taxa after the intervention arm<br><br>No changes in alpha- and beta-diversity<br><br>No change at genera level<br><br>No change in Bacteroidetes and Firmicutes<br><br>No significant change in SCFA |
| Oatmeal porridge- 60 g/d oatmeal (contained per 100 g - 8.5g dietary fiber, including 4.7g β-glucans - Valeur_2016<br><br>Oatmeal - 80 g/day VS refined white rice 80 g/day - Ye_2020 | 2 | Pilot study - dietary intervention<br><br>A secondary analysis of a randomized, controlled clinical trial | | Decrease in the relative abundance of Bacteroides phylum (and Proteobacteria phylum in the oatmeal arm<br>Increase in the relative abundance of Firmicutes phylum in the oatmeal arm | No significant change in SCFA<br><br>No changes in alpha- and beta-diversity |
| Himalaya 292 (96g/d - a novel hull-less barley - higher total dietary fiber) VS whole-wheat (97 g/d) VS refined cereal foods (99 g/d) - Bird_2008 | 1 | A randomized cross-over design | Higher excretion of butyrate or higher faecal total SCFA excretion during the consumption of Himalaya 292<br>Excretion of anaerobes was significantly | | |

| **Specific foods - Grain** (n=20) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| | | | higher during the consumption of Himalaya 292 | | |
| Foods produced from unrefined flour mix composed an equal percentage of “Tim-ilia”, “Margherito”, and “Russello” (all ancient grains) VS refined flour from “Simeto wheat - Carroccio_2021 | 1 | A non-randomized, nutrition intervention | Increase in abundance of culturable enterococci, lactic acid bacteria (LABs) and total anaerobes after diet containing ancient grains | | No change in Shannon species diversity index<br><br>No change at the high taxonomic levels, specifically phyla, families, and genera |
| Simple (a higher proportion of foods containing sucrose and/or high-fructose corn syrup) VS Refined (foods made from refined grains, such as white rice, white bread, and white pasta), VS Unrefined (foods made from whole grains) carbohydrate-containing foods - Faits_2020 | 1 | A post hoc analysis of a randomized clinical trial, crossover design | Increase in Roseburia and Anaerostipes after consumption of the unrefined carbs | | No change in α-diversity or β-diversity<br>No significant change in SCFA |
| Whole grain (WG) diet - 40g/d dietary fiber & ≤ 30g/d red meat products VS Red meat (RM) diet -200g/d - Foerster_2014 | 1 | Randomized Crossover design | Increase in diversity after WG diet | | No significant change in SCFA<br>No change at phylum level |

Table S1.e. Summary tables – Fiber

| **Specific foods – Fiber** (n=3) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| 'African style' foods increasing their average fiber intake from 14 to 55 g per day and reducing their fat from 35% to 16% of total calories VS 'Western-style' diet reducing their fiber from 66 to 12 g per day and increasing their fat from 16% to 52% - Okeefe_2015 | 1 | food exchange intervention | Increase in butyrate in colonic evacuates 2.5 times after 'Africanization' of the diet<br>High-fibre, low-fat dietary intervention in African Americans - associated with an increase of Firmicutes, and E. rectaleet rel. | Low-fibre, high-fat intervention in Africans - associated with an increase of F. nucleatum<br>High-fibre, low-fat dietary intervention in African Americans - associated with Clostridium symbiosumet rel | |
| dietary fiber intake 40 g/day - 50 g/day - Oliver_2021 | 1 | dietary fiber intervention | A trend to increase in acetate, propionate, butyrate, and valerate<br>Increase in Bifidobacterium, Lactobacillus, Coprococcussp and Anaerostipes hadrus after intervention<br>Decrease in Lachnospiraceae after intervention | Decrease in alpha diversity after intervention | |
| High-fiber diet (increased fiber consumption to 45.1±10.7 g /day) or High-fermented-foods diet (increased consumption to an average of 6.3±2.9 servings/day) - Wastyk_2021 | 1 | randomized, prospective study | Increase in microbiota diversity after high-fermented-food diet | Increase in the genus Lachnospira in the high-fiber-diet arm and a decrease in the high-fermented-food arm | No change in butyrate in high-fiber diet arm |

Table S1.f. Summary tables – Fruits

| **Specific foods - Fruits** (n=19) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Green olives - 12 table green olives/day - Accardi_2016 | 1 | Pilot nutritional intervention | A trend towards an increase of Lactobacilli after green olive intake | | |
| Mango 400g/day for 6 wks - Barnes_2019 | 1 | Clinical pilot trial | A trend toward increased levels of butyric acid and valeric acid | | No significant change in SCFA<br>No change in microbiota composition at the genus level for Lactobacillus or Bifidobacterium |
| A dried daily portion (equivalent to one apple) of the red-fleshed or placebo (white-fleshed) apple - Barnett_2021 | 1 | A randomized, placebo-controlled, crossover | Decrease in Streptococcus, Ruminococcus, Blautia, and Roseburia<br>Increase in Butyricicoccus, and Lactobacillus after red apple intake | Increase in Sutterella, after red apple intake | No change in alpha diversity |
| Sweetened dried cranberries - 42 g daily - Bekiares_2018 | 1 | A prospective clinical study | Decrease in Firmicutes, Firmicutes:Bacteroidetes ratio<br>Increase in Bacteroidetes & Akkermansiain | | |
| Cranberry diet (basal/animal-based diet plus 30 g/day of freeze-dried whole cranberry powder) VS control diet (basal/animal-based diet plus 30 g/day of matched placebo powder) - Rodríguez-Morató_2018 | 1 | Randomized, double-blind, cross-over, controlled design trial | A decrease in acetic and butyric acids after animal-based diet was attenuated by cranberry powder<br>Increase in Bacteroidetes and a decrease in Firmicutes after addition of cranberries | Decrease in the gram-negative Bacteroidetes and an increase in gram-positive Firmicutes after animal-based diet | No changes in alpha diversity and beta diversity |

| **Specific foods - Fruits** (n=19) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Orange juice from Cara Cara or Bahia juices (500ml/day) or an isocaloric control drink containing water sucrose, and vitamin C - Brasili_2019<br><br>Orange juice 300 mL/day - Cesar_2020<br><br>Flavonoid-rich orange juice (190mL each 600 ±5.4 mg flavonoids 2 times/day) VS Flavonoid-low orange flavored cordial drink (190mL each 108 ±2.6 mg flavonoids 2 times/day) - Park_2020 | 3 | A randomized, crossover and controlled trial<br><br>A controlled nonrandomized clinical study with temporal series intergroup design<br><br>A Randomized Controlled single-blind Study | Increase of Lactobacillus spp., Bifidobacterium spp and Total anaerobic bacteria | Increase in Clostridia OTUs after orange intake<br><br>Increase in Lachnospiraceae family after intake flavonoid-rich orange juice | No change in Clostridium spp |
| Dates (7/day - 50 g) VS a control group (maltodextrin–dextrose, 37.1 g) - Eid_2015 | 1 | A randomized, controlled, cross-over intervention | | | No changes in SCFA<br>No significant alterations in faecal microbiota |
| Standardized freeze-dried strawberry powder (SBP) (2×13g/day) - Ezzat-Zadeh_2021 | 1 | Intervention study | | | No change in α-diversity or β-diversity<br>No changes in SCFA<br>No changes on the phylum level |
| Avocado one/day VS no avocado - Henning_2019<br><br>Avocado 175 g (men) or 140 g (women) daily VS isocaloric control meal-Thompson_2021 | 2 | Randomized, parallel-controlled, open-label, 2-arm intervention study<br><br>An investigator-blinded, parallel- | A trend to increase in Firmicutes after avocado intake<br><br>Increase in Veillonellaceae and Prevotellaceae after avocado intake<br><br>Increased Phylogenetic Diversity, a measure of microbiota α-diversity in the avocado group | Increases in Dialister, Sutterella, Bilophila, Holdemanella, Herbaspirillum, and Acetivibrio after avocado intake<br><br>A trend to increase for Ruminoccocaceae after avocado intake<br><br>Increase in Alistipes, Ruminococcus, and | No change in α-and β-diversity<br>No change in Bacteroidetes<br><br>No significant change in other phyla after avocado intake |

| **Specific foods - Fruits** (n=19) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| | | arm, randomized controlled trial | Weighted Unifrac distances, a measure of β-diversity, tended to be greater in the avocado group<br><br>Increase in Fecal acetate in the avocado group<br><br>Increase in Faecalibacterium (P=0.07) in the avocado group<br>Decrease in Roseburia and Ruminococcus in the avocado group | Lachnospira in the avocado group | |
| A (poly)phenol-rich extract (116 mg, 75 g berries), a whole fruit powder (12 mg, 10 g berries), or placebo (maltodextrin) daily - Istas_2019 | 1 | A double-blind, parallel design, randomized controlled trial | Increase in Anaerostipes after consumption of aronia extract | Increases in Bacteroides after aronia whole fruit | No changes in gut microbiota diversity |
| Fruits and vegetables (FV) group 3 servings/d VS whole grain (WG) servings/d VS refined grain 3 servings/d - Kopf_2018<br><br><br>Fruit and vegetable intake in quartiles with the lowest quartile indicating low intake - Jiang_2020 | 2 | A randomized controlled - parallel arm feeding trial<br><br>Prospective cohort study | Increase in α-diversity in FV groups but no change in other group<br><br>Habitual fruit intake was positively associated with Observed species, Shannon index and Chao 1 index<br><br>Fruit in-take was prospectively positively associated with 31 gut microbial OTUs assigned to Faecalibacterium prausnitzii, Akkermansia | Fruit in-take was prospectively positively associated with gut microbial OTUs assigned to Ruminococcaceae, Clostridiales, Acidaminococcus, and Enterobacteriaceae.<br><br>Vegetable intake was positively associated with 1 OTU belonging to Lachnospira | No changes in SCFA<br>No significant change in bacterial genera |

| **Specific foods - Fruits** (n=19) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| | | | muciniphila, Prevotella stercorea, and Prevotella copri. | | |
| One medium banana (120gm) VS one cup of banana-flavoured drink (170 ml) VS one cup of water (170 ml) - Mitsou_2011 | 1 | A randomised, controlled trial | Increase in bifidobacterial levels in the banana group | | No change SCFA |
| Boysenberry juice beverage (350ml/d - 750 mg polyphenols), VS apple fiber beverage (350ml/d - 7.5 g dietary fiber) VS Boysenberry juice plus apple fiber beverage (350ml/d - 750 mg polyphenols plus 7.5 g dietary fiber) VS placebo beverage - Wallace_2015 | 1 | Placebo-controlled crossover | | | No change SCFA<br>No differences in fecal levels of total bacteria, Bacteroides-Prevotella-Porphyromonas group, Bifidobacterium species, Clostridiumperfringens, or Lactobacillus species |
| Sun dried raisins 3X28.3 g each daily - Wijayabahu_2019 | 1 | Dietary intervention | A trend towards an increased relative abundance of Bacteroidetes and decreased relative abundance of Firmicutes<br><br>Increased in Faecalibacterium prausnitzii.<br><br>Decrease in Klebsiella spp. | Decrease in Prevotella sp. and Bifidobacterium spp<br><br>Increased in Bacteroidetes sp. and Ruminococcus sp. | No changes in alpha diversity and beta diversity |
| Two SUNGold Kiwifruit every day - Wilson_2018 | 1 | Pilot intervention trial | Increase in the relative abundance of bacterial family Coriobacteriaceae | | No changes in alpha diversity |

Table S1.g. Summary tables – Vegetables

| **Specific foods - Vegetables** (n=10) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Green leafy vegetables (GLV) - 1 cup/day (including spinach, kale, collards, mustard greens, and turnip greens) VS habitual diet (high in red meat) - Frugé_2021 | 1 | Randomized controlled crossover trial | | | No changes in alpha diversity<br>No significant differences within phyla b/n groups or across time |
| Fresh (180 g/day) vs fermented kimchi (180 g/day) group - Han_2015<br><br>Fermented kimchi intake (100g/day) - Park_2021 | 2 | A randomized controlled clinical<br><br>Dietary intervention | Decrease in Firmicutes/Bacteroidetes ratio in response to both groups of kimchi intervention<br><br>Increase in Actinobacteria after kimchi intervention in both group<br><br>Increase in Bacteroides and Prevotella and a decrease Blautia after intake of fermented kimchi<br>Increased in observed index, Chao1 Richness index and Shanon index after fermented kimchi intake<br><br>Decrease in Enterococcua, Coryobacteriaceau in patients with advanced colon adenoma after kimchi intake | Increase in Proteobacteria after kimchi intervention in both group<br><br>Decrease in Roseburia, Bifidobacterium spp., and Akkermansia in patients with advanced colon adenoma after kimchi intake | |

| **Specific foods - Vegetables** (n=10) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Inulin-type Fructans-rich Vegetables (ITF-rich - artichoke, artichoke bottoms, Onion, garlic, shallot, salsify, Leek, scorzonera, gratin, Celery root) - ≥9 g/day of fructans VS habitual diet - Hiel_2019 | 1 | A single group-design intervention | Increase in Actinobacteria phylum and class, Actinobacteridae subclass, Bifidobacteriales order, Bifidobacteriaceae family, and Bifidobacterium genus in ITF-rich veggies arm<br><br>Decrease in the Alistipes genus and Oscillibacter genus, and an increase in the Prevotellaceae family in ITF-rich veggies arm | Decrease in observed species index of richness | No change in SCFA production, at phylum and family levels |
| Broccoli plus base diet (200 g/day (20 g daikon radish) vs base diet (control diet – American foods) - Kaczmare_2019<br><br>Low-Brassica diet (84 g frozen broccoli, 84 g frozen cauliflower, and a single portion of the participant's choice per wk) VS High-Brassica diet (6X 84 g of frozen broccoli, 6X 84 g of frozen cauliflower and 6X300 g of a broccoli and sweet potato soup containing 84 g broccoli. - Kellingray_2017<br><br>Broccoli sprouts (20 g/day - 4.4 mg/g sulforaphane glucosinolates) Vs the alfalfa sprouts (AS) group (20 g/day – no sulforaphane glucosinolates) - Yanaka_2018 | 3 | Randomized crossover a single-blind, design<br><br>Randomized crossover study<br><br>A placebo-controlled semi-open label intervention trial | Increase in Bacteroidetes phylum & Bacteroides genus after broccoli consumption<br>Decrease in Firmicutes after broccoli consumption<br>Increase in ratio of Bacteroidetes to Firmicutes after broccoli | Decrease in beta diversity after broccoli consumption<br><br>Decrease in sulphate-reducing bacteria, Rikenellaceae, Ruminococcaceae, Mogibacteriaceae, Clostridium and unclassified Clostridiales after increased Brassica consumption.<br><br>Decrease in Bifidobacterium after broccoli intake | No change in alpha diversity<br><br>No change gut microbiota composition<br>No changes in lactobacilli |
| Low-phytochemical basal diet VS Single-cruciferous diet (basal diet + 7 g | 1 | Randomized, crossover,controlled | Eubacterium hallii, Phascolarctobacterium | | |

| **Specific foods - Vegetables** (n=10) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| cruciferous vegetables/ (kg body weight a day)) VS Double-cruciferous diet (basal diet + 14 g cruciferous vegetables/(kg body weight a day)) VS Mixed diet (basal diet + 7 g cruciferous vegetables/(kg body weight a day) + 4 g apiaceous vegetables/(kg body weight a day)) - Li_2009 | | | faecium, Alistipes putredinis, and Eggerthella spp. were associated with cruciferous vegetable intake. | | |
| Tomato juice (330 ml/d - provided 37.0 mg lycopene and 1.6 mg β-carotene) VS Carrot juice (330 ml/d – 27.1 mg β-carotene and 13.1 mg α-carotene) - Schnäbele_2008 | 1 | A randomized crossover trial | No change in SCFA | | |
| Ginger juice (20 ml/d) VS sterile 0.9% sodium chloride - Wang_2020 | 1 | Randomized controlled crossover trial | Anti-inflammatory Faecalibacterium after ginger intake<br><br>A decreased relative abundance of the Prevotella-to-Bacteroides ratio and pro-inflammatory Ruminococcus_1 and Ruminococcus_2 after ginger intake | Decrease in evenness and in richness after ginger intake<br><br>Increase in Proteobacteria, Firmicutes-to-Bacteroidetes ratio, after ginger intake | |

Table S1.h. Summary tables – Macronutrients

| **Specific foods** – **Macronutrients** (n=14) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| **Protein**<br>Very-low-calorie ketogenic diets (VLCKD-780 kcal/day) with whey protein VS vegetable protein VS animal protein - Basciani_2020<br><br>A moderately high-protein diet (MHP - 40% energy from carbohydrates, 30% from proteins, and 30% from lipids) VS A low fat diet (LF - 60% of total energy from carbohydrates, 18% from proteins, and 22% from lipids) - Cuevas-Sierra_2021<br><br>Calorie-restricted high protein diet (HPD)(30% calorie intake) VS Calorie-restricted normal protein diet (NPD) (15% calorie intake) - Dong_2020<br><br>Recommended dietary intake (RDA) of protein (0.8 g protein/kg body weight per d) VS 2RDA (1.6 g protein/kg body weight per d) - Mitchell_2020<br><br>High-protein and low-carbohydrate (HPLC; 29% protein, 5% carbohydrate, and 66% fat as calories) diet VS High-protein and moderate-carbohydrate (HPMC; 28% protein, 35% carbohydrate, and 37% fat) diet - Russell_2011 | 5 | A prospective, open, nutritional intervention pilot study<br><br>Weight loss intervention study<br><br>A dietary intervention trial<br><br>A Parallel-Group, Randomized, Controlled Study<br><br>A randomized, crossover design, 9-wk dietary intervention study | Higher reduction in Firmicutes in whey protein and vegetable protein<br>Higher increase in Bacteroidetes after whey protein<br><br>Decrease in Negativicutes, Selenomonadales, Acidaminococcus, Bacteroides clarus, Bifidobacterium adolescentis in both diets<br>Increase in Peptococcaceae in both diets<br><br>Higher Shannon index in HPD<br><br>Decreased in Lachnospiraceae_UCG-004 in the HPD<br>Gemella is enriched in the HPD<br>Increase in Branched-chain fatty acids (BCFAs) isovalerate and isobutyrate after both diets | Decrease in the relative abundance of Firmicutes and Actinobacteria & an increase in Bacteroidetes and Proteobacteria after all VLCKD diets<br><br>Effect on diversity depend on sex<br>A minor trend of increasing Firmicutes and decreasing Bacteroides in both diets<br><br>Decreased in Prevotella_2, Faecalibaculum in the HPD<br><br>Decrease in total SCFA, butyrate after the HPLC diet<br><br>Decrease in total bacteria, Bacteroides, Roseburia/Eubacterium rectale group of butyrate producers with the HPLC diet | no change in beta-diversity<br><br>No change in α-diversity and β-diversity |

| Specific foods – Macronutrients (n=14) | No of studies | Type of design | Beneficial effect | Harmful effect | No effect |
|---|---|---|---|---|---|
| **Fat**<br>Diet with high monounsaturated fat/high glycemic index VS Diet with high monounsaturated fat/low glycemic index VS Diet with high carbohydrate/high glycemic index VS Diet with high carbohydrate/low glycemic index VS Diet with high saturated fat/high glycemic index (control diet) - Fava_2013 | 6 | Dietary intervention study | Increase in acetate, propionate, and n-butyrate only after the high saturated fat (control diet)<br>Increase in Bifidobacterium after high carbohydrate diets<br>Increase in Bacteroides after high carbohydrate/high glycemic index diet.<br><br>Increase in Faecalibacterium prausnitzii after high carbohydrate/low glycemic index diet and high saturated fat diets | Decrease in total bacterial numbers in the high monounsaturated fat diets | |
| Low-calorie low-carbohydrate high-fat weight loss diet (WLD - diet plan with energy restriction of 30±10%) - Jaagura_2021 | | Dietary intervention study | | Decrease in Bifidobacteriaceae<br>Increase in Enterobacteriaceae, Rikenellaceae,Desulfovibrionaceae<br><br>Increase in Lachnospira, Dialister and an undefined genus of Clostridiaceae, Anaerotruncus after low-fat diet | No change in alpha diversity |
| Low-fat diet - 50-60% of carbohydrates, 15-20% of protein per day, and maintain the intake of fat at a level of <25% - Liu_2020 | | long-term dietary intervention | Increase in Acinetobacter, Roseburia after low-fat diet | | No change in at the phylum level |
| Lower-fat diet (fat 20% energy and carbohydrate 66% energy) VS Moderate-fat diet (fat 30% energy and carbohydrate | | Randomized controlled-feeding trial | Increase in α-diversity after lower-fat diet | | |

| **Specific foods** – **Macronutrients** (n=14) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| 56% energy) VS Higher-fat diet (fat 40% energy and carbohydrate 46% energy) - Wan_2019 | | | Decrease in Firmicutes after higher-fat diet<br>Decrease in ratio of Firmicutes to Bacteroidetes after moderate-fat and high-fat diet<br>Increase in Faecalibacterium with lower-fat diet | | |
| Diets rich in saturated fat (SAT, 59E% fat), VS rich in unsaturated fat (UNSAT, 60E%fat), VS rich in simple sugars (CARB, 24E% fat), all diets were excess of 1000 kcal/day - Jian_2021 | | A randomized trial | Increase in Lactococcus and Escherichia coli after CARB<br>Increase in butyrate producers and Roseburia after UNSAT | Increase in Proteobacteria after SAT diet<br>Increase in Lachnospira and unclassified Ruminococcaceae after UNSAT | No change in alpha diversity or Firmicute to Bacteroidetes ratio |
| Overfeeding program - High-fat diets (HFDs) - 48 energy percent (EN%) from fat (mainly SFAs - whipping cream (341 mL/d)), 34 EN% from carbohydrates, and 18EN% from protein; a surplus of 1000 kcal/d - Ott_2018 | | A single-arm, prospective intervention study | | | No change in α-diversity & β-diversity<br>No change in fecal bacterial populations after HFD |
| **Carbohydrates**<br>Very low-carbohydrate, high-fat diet- (LC, 35 % of total energy as protein, 61 % as fat and 4 % as carbohydrate) VS High-carbohydrate, high-fiber, low-fat diet- (HC, 24 % as protein, 30 % as fat and 46 % as carbohydrate) - Brinkworth_2009 | 2 | A Parallel-Group, Randomized, Controlled Study | Fecal total SCFA concentration was positively correlated with the intake of fiber and carbohydrate<br>Faecal bifidobacteria levels decreased in the LC group<br><br>Increase in proportions of branched chain | Decrease in acetate, butyrate, and total SCFA concentration in the LC group<br>Total fecal anaerobes increased in the HC group<br><br>Decrease in alpha diversity, richness, and evenness of the microbiota after the RS diet | No change in fecal propionic concentrations<br>No change in lactobacilli or anaerobe:aerobe ratio |

| **Specific foods** – **Macronutrients** (n=14) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Diet high in type 3 resistant starch (RS) VS diet high in non-starch polysaccharides (NSPs)<br>- Salonen_2014 | | Randomized cross-over design | SCFA (isobutyrate and isovalerate) after RS diet | Decrease in total SCFA, acetate, propionate and butyrate in RS diet<br>Increase in Ruminococcaceae phylotypes on the RS diet<br>Increase in Lachnospiraceae phylotypes on the NSP diet | |
| **Multiple macronutrients and other nutrients**<br>Diet records from 24 hr dietary recall - Carrothers_2015 | 1 | Prospective, longitudinal investigation | Higher Spirochaetes is associated with higher protein intake<br>Higher Firmicutes is associated with high n–3, n–6 FAs and higher beta-carotene<br>Higher Faecalibacterium is associated with higher insoluble fiber intake | Higher Firmicutes and lower Bacteroidetes associated with higher Carbohydrate, protein intake | |

Table S1.i. Summary tables – Oils and seasonings

| **Specific foods – Oils and seasonings** (n=5) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| 14% (0.425 g) of the ADI for aspartame and 20% (0.136 g) of the ADI for sucralose - Ahmad_2020 | 1 | Randomized, double-blind crossover and controlled clinical trial | | | No change in richness and evenness, SCFA, bacteria phyla and genius-level taxa |
| No spices VS Low spices - a mixture of 7 dried spice powders at doses 6 g VS high spices- 12g spices<br>Polyphenol-rich mixed spices - turmeric, cumin, coriander, amla (Indian gooseberry), cinnamon, clove, and cayenne pepper - KhineWWT_2021 | 1 | Randomized, crossover, acute, food based intervention trial | Decrease in Bacteroides was with increasing spice doses<br>Increase in Bifidobacterium with increasing spice doses | | No change in alpha-diversity |
| Daily containing 25 mL of one of the test oils: soybean oil, extra virgin olive oil or coconut oil - NettoCândido_2021 | 1 | Randomized, parallel, double-blind clinical trial | Increase in microbial richness (Chao 1 index) after the soybean oil | | No change in Shannon and Simpson indices, in beta-diversity, in SCFA<br>No change at phyla level, in Firmicutes/Bacteroidetes ratio |
| 50 g Extra Virgin Olive Oil (EVOO) daily - Olalla_2019<br><br>Mediterranean Diet (MD) rich in High Quality-Extra Virgin Olive Oil (HQ-EVOO) - (55–60% carbohydrates, mainly complex ones, 25–30% polyunsaturated and monounsaturated fats, 15–20% proteins and received a low-calorie MD (Kcal 1,552 ± 160). Utilized 40 g/die of HQ-EVOO - Luisi_2019 | 2 | Experimental single arm open study<br><br>Dietary intervention | Increase in Gardnerella, and a decrease of Mogibacterium, Dethiosulfovibrionaceae, and Coprococcus after intervention<br><br>Increase in Bulleidia moorei and a decrease of the Bacilli species after intervention<br><br>Increase in Lactic Acid Bacteria after the intervention | | No change alpha diversity, beta diversity |

Table S1.j. Summary tables – Coffee and Tea

| **Specific foods - Coffee and Tea** (n=3) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| A single-dose serving of sugar free black coffee (30ml; ~8g Coffea arabica ground coffee powder) - Chong_2020<br><br>Coffee (3 cups/day, 3.4 g of instant coffee powder) - Jaquet_2009 | 2 | A non-randomized, nutrition intervention<br><br>A single group-design intervention | Increase in Prevotella and reduction in Bacteroidetes after coffee intake<br><br>Increase in Bifidobacterium spp. after coffee intake | | <br><br>No change in diversity after coffee intake |
| Green tea liquid (GTL) (400 mL per day) - Yuan_2018 | 1 | Intervention study | Increase in α-diversity & β-diversity with GTL Increase in Firmicutes and Actinobacteria, and Increase in Bifidobacterium and Bifidobacterium to Enterobacteriacea ratio Decrease in Bacteroidetes, Prevotellaceae, proinflammatory Fusobacterium genus, & uncultured Prevotella 9 Increase in SCFA-producing Lachinospiraceae, Ruminococcaceae, Erysipelotrichaceae, Bifidobacteriaceae and Coriobacteriaceae Increase in SCFA-producing Roseburia, Feacalibacterium, Eubacterium, Blautia, Coprococcus, and Dorea | | Increase in Firmicutes to Bacteroidetes ratio (FIR:BAC) |

Table S1.k. Summary tables – Alcohol and wine

| **Specific foods - Alcohol and wine** (n=2) | **No of studies** | **Type of design** | **Beneficial effect** | **Harmful effect** | **No effect** |
|---|---|---|---|---|---|
| Red wine 250 mL/day (439.5 mg of equivalents of polyphenols per day) VS no wine - Belda_2021 | 1 | Randomized and controlled trial | | Less dispersion in beta-diversity in the wine arm | No change in alpha-diversity in the wine arm<br>No significant changes in the relative abundance of Firmicutes, Bacteroidetes, Actinobacteria, Proteobacteria, Euryarchaeota, Verrucomicrobia phyla, Bacteroidetes/Firmicutes ratio |
| De-alcoholized red wine (272 mL/d), red wine (272 mL/d), or gin (100 mL/d) - Queipo-Ortuño_2012 | 1 | Randomized, crossover, controlled intervention | Increase in Firmicutes and Bacteroidete after red wine intake | Increase in Proteobacteria, and Fusobacteria after red wine intake<br>Increased in Fusobacteria after de-alcoholized red wine | |