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Supplementary information

The gut microbiome connects nutrition and human health

In the format provided by the authors and unedited

Supplementary Table 1. Large-scale population-based studies of the relationships between food intakes and gut bacteria abundance

Study description	
Reference	**Study name, country and size;** **Food intake assessment tool; Fecal microbiome sequencing method**
1. Asnicar F et al. 2021 10.1038/s41591-020-01183-8	PREDICT 1 study: UK, N=1001 (discovery) and USA, N=97 (validation) 131-item FFQ; Shotgun sequencing
2. Zhernakova A et al. 2016 10.1126/science.aad3369	LifeLines-DEEP cohort: Netherlands, N=1135 Food frequency for 78 items; Shotgun and 16S rRNA gene sequencing
3. Falony G et al. 2016 10.1126/science.aad3503	Flemish Gut Flora Project: Belgium, N=1106; LifeLines-DEEP cohort: Netherlands, N=1135 (replication) Food questionnaire; 16S rRNA gene sequencing
4. Frankenfeld CL et al. 2022 10.1016/j.jand.2021.05.023	Adiposity Phenotype Study (Multiethnic Cohort Study): USA, n=1709 Serum carotenoids and tocopherols (biomarkers of fruit and vegetable dietary intake); 16S rRNA gene sequencing
5. Manor O et al. 2020 10.1038/s41467-020-18871-1	Arivale non-medical lifestyle intervention program (Arivale Inc., Seattle, WA): USA, n=3409 Short food frequency list (Dietary Targets Monitor); 16S rRNA gene sequencing
6. Partula V et al. 2019 10.1093/ajcn/nqz029	Milieu Intérieur study: France, n=862 Food frequency for 19 items; 16S rRNA gene sequencing
7. Maukonen M et al. 2024 10.1007/s00394-024-03406-x	FINRISK/FINDIET 2002 study: Finland, n=1273 48h-dietary recall; Shallow shotgun sequencing
8. Koponen KK et al. 2021 10.1093/ajcn/nqab077	FINRISK 2002 study: Finland, n=4930 Food propensity questionnaire, 42 items; Shallow shotgun sequencing
9. Yu D et al. 2021 10.1093/ajcn/nqaa350	Shanghai Women's Health Study (SWHS) and Shanghai Men's Health Study (SMHS): China, n=1920 Repeated FFQs (81 items); 16S rRNA gene sequencing
10. Borrello K et al. 2022 10.3390/nu14030660	Adiposity Phenotype Study and microbiome Genome-Wide Association Study (Multiethnic Cohort Study): USA, n=5267 180-item FFQ (2003-2008); 16S rRNA gene sequencing (stool collection in 2013-2016)
11. Latorre-Pérez A et al. 2021 10.1038/s41598-021-01002-1	*Microbioma Español* Project: Spain, n=528 Frequency for 43 food items; 16S rRNA gene sequencing
12. Houttu V et al. 2021 10.3390/metabo11120858	HELIUS study: Netherlands, n=1309 Ethnic-specific 200 item-FFQ; 16S rRNA gene sequencing
13. Le Roy CI et al. 2022 10.1186/s12866-021-02364-2	TwinsUK registry: UK, n=1457 131-item FFQ → yogurt consumption; 16S rRNA gene (n=1457) and shotgun (n=544) sequencing
14. Jiang Z et al. 2020 10.1186/s12916-020-01842-0	Guangzhou Nutrition and Health Study: China, n=1879; Guangdong Gut Microbiome Project: China, n=6626 (replication) 79-item FFQ → fruit and vegetables; 16S rRNA gene sequencing
15. Aasmets O et al. 2022 10.1038/s41467-022-28464-9	Estonian Microbiome Project (EstMB): Estonia, n=2509 Dietary preferences (21 items); Shotgun sequencing

Genus or species-level associations with food groups*		
Food group	**Increased relative abundance ▲**	**Decreased relative abundance ▼**
Fruits	-Fruit (incl. berries): Eubacterium spp. (6, 8, 15), [eligens] (1, 2, 4, 6, 7, 15); Ruminococcus spp. (4, 7, 8, 15), [flavefaciens] (15); Faecalibacterium spp. (5, 8, 15), [prausnitzii] (14); Veillonella spp. (2, 5, 8), [parvula] (2); Lachnospira spp. (4, 5, 12, 14); Roseburia spp. (8, 15), [hominis] (2, 7); Bifidobacterium spp. (5, 8), [animalis] (1); Haemophilus spp. (1, 5), [parainfluenzae] (2); Coprococcus spp. (4, 5, 8); Butyrivibrio spp. (8), [crossotus] (7), [proteoclasticus] (15); Acetivibrio spp. (8, 15); Marvinbryantia spp. (8, 12); Coprobacillus spp. (8, 15); Alistipes shahii (2); Barnesiella intestinihominis (2); Lachnospiraceae 8-1-57FAA (2); RF39 spp. (5); Johnsonella spp. (8); Solobacterium spp. (8); Megamonas spp. (8); Megasphaera spp. (8); Enterococcus spp. (8); Streptococcus spp. (8); Anaerostipes spp. (8); Catenibacterium spp. (8); Lactobacillus spp. (8); Tannerella spp. (8); Mitsuokella spp. (8); Butyricicoccus spp. (12); Ruminococcaceae UCG-010 (12); Akkermansia muciniphila (14); Acidaminococcus spp. (14); Prevotella spp. [stercorea, copri] (14) -Berries (8): Intestinibacter spp.; Turicibacter spp.; Subdoligranulum spp.; Lactococcus spp.; Dorea spp. -Fruit, fresh or raw: Parasutterella spp. [excrementihominis] (6); Clostridium spp. (15); Anaeroplasma sp. (15); Blautia spp. (15); Bacteroides pectinophilus (15); -Fruit, juice (8): Dialister spp.; Parasutterella spp. -Fruit, cooked (6): Bacteroides spp. [stercoris]; Sutterella spp. [wadsworthensis] -Total blood carotenoids (4): Clostridium sensu stricto 11 spp., Lachnospiraceae ND3007	-Fruit (incl. berries): Clostridium spp. (15), [CAG_58] (1), [spiroforme] (1, 7), [phoceensis] (7), [XlVa saccharolyticum] (6); Parabacteroides spp. (3, 8, 11, 15), [distasonis, gordonii, merdae, sp. CAG_2, johnsonii] (15); Bifidobacterium [bifidum] (7, 12, 15), [spp., animalis, adolescentis, pseudocatenulatum, longum] (15); Bacteroides spp. (5, 8, 15), [pyogenes, finegoldii, caccae, fragilis, intestinalis, fluxus, uniformis, clarus, CAG_144, stercoris, ovatus, cellulosilyticus] (15); Collinsella spp. (3, 5), [aerofaciens] (12, 15); Eubacterium spp. (4, 7), [hallii] (2); Ruminococcus spp. (5, 6), [torques] (2); Dorea spp. (3, 5), [longicatena] (15); Roseburia spp. (3), [inulinivorans] (7, 12); Alistipes spp. (8, 15), [putredinis] (7); Blautia spp. (3), [hydrogenotrophica] (7); Pseudoflavonifractor An184 (1, 15); Holdemania spp. (5, 8); Sutterella spp. (5, 15); Bilophila spp. (5, 8); Streptococcus [gordonii, mitis, mutans] (7), [pneumoniae] (15); Negativibacillus spp. (11, 12); Anaerotruncus colihominis (1); Oscillospira spp. (5); Ruthenibacterium spp. (8); Escherichia spp. (8); Phocea spp. (8); Butyricimonas spp. (8); Acidaminococcus spp. (11); Flavonifractor spp. (11); Faecalitalea spp. (11) -Berries (8): Tyzzerella spp.; Erysipelatoclostridium spp. -Fruit, fresh or raw: Christensenella spp. (5); Oscillibacter spp. (15); Pseudomonas spp. (15); Enterobacter [spp., cloacae] (15); Eggerthella sp. (15); Klebsiella [spp., oxytoca] (15); Acinetobacter sp. (15); Prevotella spp. (15); Salmonella enterica (15); Porphyromonas spp. (15); Odoribacter splanchnicus (15); Coprobacter sp. (15); Lawsonibacter asaccharolyticus (15); Tannerella spp. (15); -Fruit, cooked (6): Alloprevotella sp.; Prevotella spp. [shahii]
Vegetables	Eubacterium spp. (8, 11), [eligens] (1, 2, 4, 7, 11), [ruminantium] (11); Lachnospira spp. (4, 5, 7, 14); Ruminococcus spp. (4, 5, 8, 10); Clostridium spp. (5, 15), [CAG_417] (15), [sensu stricto 11] (4); Lachnospiraceae [UCG-001] (12), [UCG-008] (11), [ND3007] (4, 10); Prevotella spp. (7, 11), [buccalis] (7); Anaerostipes spp. (8), [hadrus] (1, 7); Bacteroides spp. (5), [cellulosilyticus, fluxus] (7), [pectinophilus] (11); Butyrivibrio spp. (8, 11); Megasphaera spp. (5, 8); Coprococcus spp. (4, 5); RF39 spp. (5, 11); Dorea spp. (5); Faecalibacterium spp. (5); Veillonella spp. (5); Oxalobacter spp. (5); RF32 spp. (5); Oscillospira spp. (5); Dielma (7); Parabacteroides [distasonis, goldsteinii] (7); Parasutterella spp. (8); Acetivibrio spp. (8); Tannerella spp. (8); Solobacterium spp. (8); Johnsonella spp. (8); Megamonas spp. (8);	Bifidobacterium spp. (7, 8, 11), [bifidum] (1, 7), [longum] (7, 15), [dentium] (7), [adolescentis] (15); Collinsella spp. (5, 8, 11), [aerofaciens] (1); Actinomyces spp. (5, 8); Bacteroides spp. (5, 11); Megasphaera spp. (5, 11); Bilophila spp. (5, 11); Ruminococcus spp. (5), [torques] (11); Oscillibacter spp. (11, 15); Eubacterium spp. (4); Coprobacillus spp. (5); Coprococcus spp. (5); Lachnospira spp. (5); Faecalibacterium spp. (5); Parabacteroides spp. (5); Lactobacillus spp. (5); Oscillospira spp. (5); Lactococcus spp. (5); Catenibacterium sp. (6); Roseburia faecis (7), Streptococcus [spp., mutans, salivarius] (7); Turicibacter sp. (7); Blautia spp. (8); Ruthenibacterium spp. (8); Erysipelatoclostridium spp. (8); Eggerthella spp. (8); Acidaminococcus spp. (11); Flavonifractor spp. (11); Coprobacter spp. (11); Pseudomonas sp. (15); Lawsonibacter asaccharolyticus (15)

	Enterococcus spp. (8); Alistipes spp. (8); Barnesiella spp. (8); Porphyromonas spp. (8); Akkermansia spp. (8); Oscillibacter sp. (1); Roseburia sp. (1); Oscillospiraceae NK4A214 (11); Butyricicoccus spp. (12); Tyzzerella-3 spp. (12)	
	Vegetables mediate differences in Anaerostipes, Flavonifractor, Lachnospira, Lachnospiraceae ND307, Ruminiclostridium and Ruminococcus (African Am. and/or Latino vs Native Haw.) (10)	
Legumes Nuts and seeds	-Legumes: Faecalibacterium spp. (5); Prevotella spp. [stercorea] (6); RF39 spp. (9); Bacteroides ovatus (1); Bifidobacterium pseudocatenulatum (1); Haemophilus parainfluenzae (1); Coprococcus spp. (11) -Nuts and seeds: Eubacterium spp. (8), [eligens] (1, 2, 11), [hallii] (1); Clostridium spp. (1, 5); Roseburia [spp., hominis] (1, 2); Parabacteroides spp. (8); Tannerella spp. (8); Anaerostipes hadrus (1); Blautia wexlerae (1); Coprococcus sp. (1); Oscillibacter sp. (1); Oxalobacter spp. (11); Oscillospiraceae spp. [UCG-005, NK4A214, UCG-003] (11); Christensenellaceae R-7 (11); Marvinbryantia spp. (11); Lachnospiraceae UCG-001 (12); Lactobacillus ruminis (12); Ruminococcaceae spp. [NK4A214, UCG-003] (12) -Nuts/legumes: RF39 (9)	-Legumes: Clostridium [spp., CAG_58, spiroforme] (1), [leptum] (2); Dorea spp. (5); Oscillospira spp. (5); Butyricimonas sp. (1); Coprococcus comes (1) -Nuts and seeds: Alistipes spp. (12), [finegoldii] (1); Bifidobacterium spp. (11), [catenulatum] (1); Flavonifractor spp. (11), [plautii] (1); Ruminococcus [gnavus] (1), [torques] (11); Negativibacillus spp. (11, 12); Bacteroides spp. (5); Christensenella spp. (5); Turicibacter spp. (8); Eggerthella spp. (8), [lenta] (1); Dialister spp. (8); Anaerotruncus colihominis (1); Bilophila wadsworthia (1); Clostridium [spp., bolteae, leptum, saccharolyticum, spiroforme] (1); Escherichia coli (1); Pseudoflavonifractor An184 (1); Ruthenibacterium lactatiformans (1); Acidaminococcus spp. (11); Oscillibacter spp. (11); Megasphaera spp. (11); Lactobacillus spp. (11); Faecalitalea spp. (11); Parasutterella spp. (12); Parabacteroides johnsonii (12)
	Nuts/seeds/legumes mediate differences in Coprococcus (Native Haw. vs White) (10)	
Potatoes	Alistipes finegoldii (1); Anaerotruncus colihominis (1); Bacteroides uniformis (1); Clostridium leptum (1); Ruthenibacterium lactatiformans (1)	Anaerostipes hadrus (1); Bifidobacterium animalis (1); Roseburia sp. (1); Ruminococcus lactaris (1); Veillonella spp. (5); RF32 spp. (5); RF39 spp. (5); Enterococcus sp. (7)
Grain products	-Grain products: Bifidobacterium spp. (7, 8, 11, 15), [adolescentis] (2, 7, 15), [bifidum, longum] (7, 15), [animalis] (11), [catenulatum] (2), [pseudocatenulatum] (15); Haemophilus spp. (5, 7), [influenzae] (7), [parainfluenzae] (11, 2, 15); Roseburia spp. (5, 8, 15), [faecis] (7), [hominis] (11); Lactobacillus spp. (8), [ruminis] (7, 12); Subdoligranulum spp. (8, 11, 15); Ruminococcus spp. (5, 15), [gnavus] (11); Veillonella spp. (2, 5); Faecalibacterium spp. (8), [prausnitzii] (15); Bacteroides spp. (3), [plebeius] (15); Dorea spp. (8, 11); Clostridium sp. (15), [leptum] (11); Lachnospiraceae 8-1-57FAA (2); Alistipes spp. (3); Prevotella spp. (7); Oscillibacter spp. (11); Dialister spp. (11); Collinsella spp. (11); Megasphaera spp. (12); Blautia sp. (15); Lachnospira spp. (15); Eubacterium sp. (15) -Fiber-rich bread (8): Methanobrevibacter spp.; Acetivibrio spp.; Butyrivibrio spp.; Megamonas spp.; Cellulomonas spp.; Johnsonella spp.	-Grain products: Bacteroides spp. (5, 3, 8, 15), [clarus] (12), [uniformis] (15); Ruminococcus spp. (5, 7, 15), [torques] (7, 15); Clostridium [spp., phoceensis] (7, 15), [citroniae, spiroforme] (7), [CAG_58] (15); Eubacterium [ramulus] (7), [eligens] (11); RF32 spp. (9, 5); Oscillospira spp. (5, 15); Lachnospiraceae spp. [NK4A136, UCG-010] (12), [UCG-008] (11); Bilophila spp. (5, 8); Lactobacillus sp (2); Dorea spp. (5); Sutterella spp. (5); Desulfovibrio spp. (5); RF39 spp. (5); Actinomyces [spp., oris] (7); Adlercreutzia equolifaciens (7); Faecalitalea cylindroides (7); Holdemania massiliensis (7); Hungatella hathewayi (7); Phocea massiliensis (7); Streptococcus spp. [gordonii, mitis, mutans] (7); Anaerostipes hadrus (11); Oscillospiraceae UCG-003 (11); Odoribacter splanchnicus (12); Lachnospira spp. (15) -Bread: Alistipes spp. (3); Christensenella spp. (5); Dielma spp. (8); Ruthenibacterium spp. (8); Eggerthella spp. (8); Succinivibrio spp. (11); Oscillibacter spp. (15); Lawsonibacter asaccharolyticus (15); Parabacteroides spp. (15); Negativibacillus sp. (15); Pseudomonas sp. (15); Porphyromonas sp. (15)
Dairy	-Dairy: Streptococcus spp. (7, 8, 11, 13), [parasanguinis] (7), [thermophilus] (1, 2, 7, 13, 15), [salivarius] (6, 7); Bifidobacterium spp. (9, 11), [animalis] (1,	-Dairy: Prevotella spp. (8, 7); Lachnospira spp. (5, 7); Bacteroides stercoris (6)

	7, 13), [longum] (7); Lactococcus spp. (5, 8, 15), [lactis] (2, 7, 15); Lactobacillus spp. (5, 7), [delbrueckii] (2, 7); Eubacterium spp. (7, 8), [ramulus] (2), [xylanophilum] (7); Ruminococcus spp. (13, 8); Erysipelatoclostridium (8, 7); Leuconostoc [spp., mesenteroides] (7, 2); Lachnospira sp. (7); Lachnospiraceae UCG-001 (13); Christensenellaceae R-7 (13); Ruminococcaceae [NK4A214, UCG-010, UCG-005] (13) -Milk/cream/ice cream (7): Actinomyces oris; Enterobacter [spp., cloacae]; Faecalitalea sp.; Klebsiella [spp., oxytoca]; Pseudomonas sp.; Salmonella enterica -Cheese: Clostridium spp. (7), [XlVb lactatifermentans] (6); Anaerostipes spp. (8), [hadrus] (7); Butyrivibrio spp. (8), [proteoclasticus] (7); Ruminococcus [spp., gauvreauii] (7); Blautia obeum (7); Dorea longicatena (7); Shuttleworthia sp. (7) -Low-fat cheese (8): Enterococcus spp.; Acetivibrio spp.; Intestinibacter spp.; Adlercreutzia spp.; Veillonella spp.; Solobacterium spp.; Turicibacter spp.; Parasutterella spp.; Coprobacillus spp.; Marvinbryantia spp.; Hungatella spp.; Johnsonella spp.; Faecalibacterium spp.; Anaerotruncus spp.; Megamonas spp.; Tyzzerella spp.; Subdoligranulum spp.	-Yogurt (5): Dorea spp.; Ruminococcus spp. -Cheese: Akkermansia muciniphila (6); Butyricimonas spp. (8); Phascolarctobacterium spp. (8); Desulfovibrio spp. (8); Bifidobacterium spp. (8); Sutterella spp. (8) -Milk (11): Butyricicoccus spp. -Fermented milk (7): Megasphaera sp. -Milk/cream/ice-cream (7): Alistipes [spp., ihumii, putredinis]; Megamonas funiformis; Oscillibacter sp.; Parabacteroides distasonis; Selenomonas sp.; Clostridium sp.; Eubacterium eligens -Avoid dairy (5): Collinsella spp.; Lactococcus spp.; Streptococcus spp.
	Dairy mediate differences in Bifidobacterium (Japanese Am. vs White) (10)	
Egg	-Egg: Eubacterium eligens (1); Mitsuokella spp. (12); Mogibacterium spp. (12); Prevotella spp. (12); Succinivibrio spp. (12); Phascolarctobacterium sp. (12)	-Egg: Bifidobacterium spp. [catenulatum, longum] (5); Clostridium bolteae (1); Bacteroides clarus (12); Phascolarctobacterium faecium (12)
Meat Processed meat Poultry Fish	-Red meat: Clostridium spp. [saccharolyticum, CAG_58] (1), sensu stricto (6); Dorea spp. (5), [formicigenerans] (12); Ruminococcus spp. (1), [torques] (11); Collinsella spp. (3); Parasutterella excrementihominis (7); Alistipes spp. [finegoldii, putredinis] (1); Bilophila wadsworthia (1); Barnesiella intestinihominis (1); Blautia hydrogenotrophica (1); Odoribacter splanchnicus (1); Ruthenibacterium lactatiformans (1); -Processed meat: Lactococcus spp. (5); Oxalobacter spp. (5); Streptococcus pneumoniae (7); Coprococcus sp. (7); Acinetobacter spp. (9); Bifidobacterium bifidum (15) -Poultry: Alloprevotella spp. (8, 12); Oscillospira spp. (5); Parabacteroides spp. (8); Parasutterella spp. (8); Enterococcus spp. (8); Mitsuokella spp. (8); Alistipes spp. (8); Tannerella spp. (8); Eubacterium spp. (8); Anaerostipes spp. (8); Methanobrevibacter spp. (8); Solobacterium spp. (8); Marvinbryantia spp. (8); Butyrivibrio spp. (8)	-Red meat: Haemophilus spp. (5), [parainfluenzae] (1); Lactococcus lactis (2); Bifidobacterium spp. (5); Blautia wexlerae (6); Cellulomonas sp. (7); Porphyromona ssp. (7); Prevotella spp. (7); Eubacterium eligens (11); Ruminococcus spp. (11) -Processed meat and ham: Lachnospira spp. (5); Roseburia spp. (5, 9), [faecis] (9), [hominis] (7, 12); Haemophilus spp. (5); Johnsonella sp. (7); Anaerostipes hadrus (7); Dorea sp. (7); Clostridium spp. (7, 15); Eubacterium xylanophilum (11); Bacteroides pectinophilus (11); RF39 spp. (11); Ruminococcus spp. (11) -Poultry: Clostridium spp. (5); Bifidobacterium spp. (8); Cellulomonas spp. (8); Prevotella spp. (8) -Red and processed meat (low use) (8): Collinsella spp.; Paraprevotella spp.; Phocea spp.; Cellulomonas spp.; Prevotella spp.; Actinomyces spp.; Oscillibacter spp.; Bilophila spp. -Meat, poultry, fish (12): Anaeroplasma spp. -Fish and seafood: Ruminococcus spp. (5); Prevotella stercorea (6); Clostridium spp. XlVa (6); Butyricicoccus (8)

	-Fish and seafood: Lachnospira spp. (5); Paraprevotella spp. (8); Coprococcus spp. (9), [comes] (12) -Meat, poultry, fish (12): Prevotella spp.; Acidaminococcus spp.; Veillonella spp. -Red and processed meat (low use) (8): Anaerostipes spp.; Klebsiella spp.; Streptococcus spp.; Butyrivibrio spp.; Eubacterium spp.; Johnsonella spp.; Acetivibrio spp.; Eggerthella spp.	
	Red meat mediate differences in Coprococcus-2, Lachnospira, Ruminiclostridium-5 and Ruminococcus-11 (Native Haw. and/or Japanese Am. vs African Am.) (10)	
Sweet products (sweets, desserts, sugar, pastry, savoury, fatty sweet products)	Bifidobacterium spp. (12), [catenulatum, longum] (1), [adolescentis] (6), [pseudocatenulatum] (15); Ruthenibacterium lactatiformans (1); Streptococcus spp. [mutans] (2), [salivarius] (2); Blautia sp. (6); Ruminococcus spp. [gauvreauii, flavefaciens] (6); Clostridium leptum (1); Dialister invisus (1); Lactobacillus ruminis (12);	Bacteroides finegoldii (1); Ruminococcus torques (2); Bilophila spp. (6); Lactococcus spp. (6); Oscillospiraceae NK4A214 (11); Lachnospiraceae UCG-010 (12)
Savoury snacks, pizza, fried products	Blautia sp. (6); Eubacterium hallii (6); Flavonifractor spp. (11)	Eubacterium spp. (5), [eligens] (11); Coprococcus spp. (5); Veillonella spp. (5); Haemophilus spp. (5); RF39 spp. (11); Lachnospiraceae UCG-008 (11)
Sugar-sweetened beverages, soda	Flavonifractor spp. (11), [plautii] (1); Bifidobacterium bifidum (1); Clostridium spp. [leptum, spiroforme] (1); Oscillibacter spp. (1, 15); Ruthenibacterium lactatiformans (1); Collinsella spp. (3); Christensenella spp. (5); Ruminococcus spp. (5); Parasutterella spp. (11); Pseudoflavonifractor An184 (15)	Roseburia spp. (15), [hominis] (2); RF39 spp. (5, 11); Haemophilus parainfluenzae (1); Streptococcus spp. (1), [parasanguinis] (6); Veillonella sp. (1); Coprococcus spp. (5); Lachnospira spp. (5); Shuttleworthia spp. (5); Faecalibacterium spp. (5); RF32 spp. (5); Prevotella sp. (6); Eubacterium spp. [eligens, xylanophilum] (11); Bacteroides pectinophilus (11); Akkermansia spp. (11); Oxalobacter spp. (11)
Alcoholic beverages	-Alcoholic beverages: Roseburia spp. (1, 3), [inulinivorans] (12); Clostridium spp. [spiroforme] (1), sensu stricto 11 (12); Faecalibacterium spp. (3), [prausnitzii] (2); Bacteroides spp. (6), [plebeius] (12); Coprobacter sp. (1); Lawsonibacter asaccharolyticus (1); Oscillibacter sp. (1); Parabacteroides spp. [distasonis, goldsteinii] (1); Pseudoflavonifractor capillosus (6); Mogibacterium spp. (12); Lachnospiraceae UCG-008 (12); Butyrivibrio crossotus (12); Ruminiclostridium-9 (12); Intestinibacter bartlettii (12) -Red wine (2): Eubacterium eligens; Lactococcus lactis -Beer (3): Collinsella spp.; Dorea spp. -Spirits (3): Ruminococcus spp.	-Alcoholic beverages: Akkermansia spp. (3, 11); Clostridium sp. (1); Haemophilus parainfluenzae (1); Selenomonas sp. (6); Lachnospiraceae UCG-001 (12); Tyzzerella 3 (12); Parabacteroides johnsonii (12); Alistipes finegoldii (12); Streptococcus spp. (12); Bilophila wadsworthia (12); Bacteroides ovatus (12) -Wine: Clostridium leptum (2); Acidaminococcus spp. (11); Bifidobacterium spp. (11) -Beer (3): Oscillibacter spp. -Spirits (11): RF39 spp., Ruminococcus spp., Paraprevotella spp.
	Alcohol mediate differences in Bifidobacterium (White vs Japanese Am.) (10)	
Coffee, caffeinated beverages, tea	-Coffee: Eubacterium biforme (2); Oscillibacter spp. (2); Lachnospiraceae 7_1_58FAA (2); Eggerthella sp. (15); Prevotella spp. (15); Clostridium phoceensis (15); Lawsonibacter asaccharolyticus (11, 15) -Tea, coffee (1): Alistipes sp. -Caffeinated beverages: Methanobrevibacter spp.; Lactococcus spp. (5)	-Coffee: Veillonella spp. [parvula] (2); Eggerthella sp. (2); Roseburia spp. (15); Haemophilus parainfluenzae (2, 15) -Tea, coffee: Clostridium sp. (1); Phascolarctobacterium faecium (1) -Caffeinated beverages: Bifidobacterium (5)

*Associations at genus or species level only; only genus or species associated with any food group in at least 2 different studies are shown; sp./spp. are used when genus-level associations were reproduced but not at the level of one or several particular species; species are indicated into square brackets [species] when several species were found or a combination of genus level associations with unspecified species (spp.) and specified species. Studies of more than 500 participants are included.
The number of occurrences of the following genera in the Table, reflecting their associations with several food ítems or groups is as follows (in decreasing order): Clostridium (n=24), Ruminococcus (n=22), Eubacterium (n=19), Bifidobacterium (n=19), Bacteroides (n=16), Prevotella (n=15), Oscillibacter (n=13), Lachnospiraceae (n=13), Coprococcus (n=12), Alistipes (n=12), Roseburia (n=11), Streptococcus (n=11), Dorea (n=11), Parabacteroides (n=10), Anaerostipes (n=10), Lachnospira (n=10), RF39 (n=10), Blautia (n=10), Veillonella (n=9), Haemophilus (n=9), Lactococcus (n=9), Lactobacillus (n=8), Faecalibacterium (n=8), Oscillospira (n=8), Ruthenibacterium (n=8), Collinsella (n=8), Bilophila (n=8), Parasutterella (n=7), Butyrivibrio (n=7), Eggerthella (n=7), Johnsonella (n=6), Megasphaera (n=6), Acidaminococcus (n=6), Flavonifractor (n=6), Acetivibrio (n=5), Megamonas (n=5), Enterococcus (n=5), Tannerella (n=5), Akkermansia (n=5), Lawsonibacter (n=5), Marvinbryantia (n=4), Oxalobacter (n=4), RF32 (n=4), Solobacterium (n=4), Butyricicoccus (n=4), Turicibacter (n=4), Dialister (n=4), Sutterella (n=4), Pseudoflavonifractor (n=4), Anaerotruncus (n=4), Faecalitalea (n=4), Christensenella (n=4), Cellulomonas (n=4), Tyzzerella (n=4), Pseudomonas (n=4), Actinomyces (n=4), Oscillospiraceae (n=4), Phascolarctobacterium (n=4), Coprobacillus (n=3), Barnesiella (n=3), Mitsuokella (n=3), Ruminococcaceae (n=3), Intestinibacter (n=3), Subdoligranulum (n=3), Negativibacillus (n=3), Phocea (n=3), Butyricimonas (n=3), Erysipelatoclostridium (n=3), Klebsiella (n=3), Porphyromonas (n=3), Odoribacter (n=3), Coprobacter (n=3), Ruminiclostridium (n=3), Methanobrevibacter (n=3), Paraprevotella (n=3), Anaeroplasma (n=2), Holdemania (n=2), Catenibacterium (n=2), Enterobacter (n=2), Acinetobacter (n=2), Salmonella (n=2), Escherichia (n=2), Alloprevotella (n=2), Dielma (n=2), Desulfovibrio (n=2), Adlercreutzia (n=2), Hungatella (n=2), Christensenellaceae (n=2), Succinivibrio (n=2), Shuttleworthia (n=2), Selenomonas (n=2), Mogibacterium (n=2), Leuconostoc (n=1)

References

1. Asnicar, F. *et al.* Microbiome connections with host metabolism and habitual diet from 1,098 deeply phenotyped individuals. *Nat. Med.* **27**, 321–332 (2021).

2. Zhernakova, A. *et al.* Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. *Science* **352**, 565–569 (2016).

3. Falony, G. *et al.* Population-level analysis of gut microbiome variation. *Science* **352**, 560–564 (2016).

4. Frankenfeld, C. L. *et al.* The Gut Microbiome Is Associated with Circulating Dietary Biomarkers of Fruit and Vegetable Intake in a Multiethnic Cohort. *J. Acad. Nutr. Diet.* **122**, 78–98 (2022).

5. Manor, O. *et al.* Health and disease markers correlate with gut microbiome composition across thousands of people. *Nat. Commun.* **11**, 5206 (2020).

6. Partula, V. *et al.* Associations between usual diet and gut microbiota composition: results from the Milieu Intérieur cross-sectional study. *Am. J. Clin. Nutr.* **109**, 1472–1483 (2019).

7. Maukonen, M. *et al.* Associations of plant-based foods, red and processed meat, and dairy with gut microbiome in Finnish adults. *Eur. J. Nutr.* (2024) doi:10.1007/s00394-024-03406-x.

8. Koponen, K. K. *et al.* Associations of healthy food choices with gut microbiota profiles. *Am. J. Clin. Nutr.* **114**, 605–616 (2021).

9. Yu, D. *et al.* Long-term diet quality is associated with gut microbiome diversity and composition among urban Chinese adults. *Am. J. Clin. Nutr.* **113**, 684–694 (2021).

10. Borrello, K. *et al.* Dietary Intake Mediates Ethnic Differences in Gut Microbial Composition. *Nutrients* **14**, 660 (2022).

11. Latorre-Pérez, A. *et al.* The Spanish gut microbiome reveals links between microorganisms and Mediterranean diet. *Sci. Rep.* **11**, 21602 (2021).

12. Houttu, V. *et al.* Physical Activity and Dietary Composition Relate to Differences in Gut Microbial Patterns in a Multi-Ethnic Cohort-The HELIUS Study. *Metabolites* **11**, 858 (2021).

13. Le Roy, C. I. *et al.* Yoghurt consumption is associated with changes in the composition of the human gut microbiome and metabolome. *BMC Microbiol.* **22**, 39 (2022).

14. Jiang, Z. *et al.* Dietary fruit and vegetable intake, gut microbiota, and type 2 diabetes: results from two large human cohort studies. *BMC Med.* **18**, 371 (2020).

15. Aasmets, O., Krigul, K. L., Lüll, K., Metspalu, A. & Org, E. Gut metagenome associations with extensive digital health data in a volunteer-based Estonian microbiome cohort. *Nat. Commun.* **13**, 869 (2022).