

Systematic qualitative synthesis of the impact of physical activities and other lifestyle factors on the gut microbiome

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Abstract

This systematic review synthesises current evidence on the clinical implications of physical activity and other lifestyle factors in adjusting gut microbial profile. While many studies have explored the relationship between lifestyle factors such as dietary fibre intake, red meat consumption, physical activity, and smoking with colorectal cancer risk, comparatively fewer have examined how these factors influence the gut microbiome itself, particularly in relation to physical activity. This review aims to target this gap and focuses on the impact of lifestyle factors, especially exercise and physical activity, on the gut microbiome. A search of four databases (PubMed, MEDLINE, ScienceDirect, and Scopus) was conducted using a population-intervention-comparison-outcome (PRISMA) framework, with duplicates removed and records independently screened. Risk of bias was assessed for each primary paper, and findings were synthesised qualitatively to contextualise microbial dysbiosis and host–microbiome interactions. We found that notably, exercise increased expression of various beneficial gut microbiota, particularly regarding commensal small-chain fatty acid producers and anti-inflammatory modulators. Other lifestyle factors, including diet, body mass index (BMI) and smoking, also significantly modulated microbiota expression.

INTRODUCTION

The human gut microbiome comprises the entire gastrointestinal tract and is influenced by factors such as the local microenvironment, pH, nutrient and oxygen availability. Consequently, the gut microbiome of the colon differs markedly from that of the oral cavity, oesophagus, stomach, and small intestine. The oxygen gradient along the intestinal tract plays a key role in shaping microbial distribution. Partial oxygen pressure progressively declines from the duodenum to the colon, which modulates bacterial survival along the epithelial surface [1]. As a result, the sparsely populated small intestine is predominantly dominated by facultative anaerobes, whereas the densely colonised large intestine harbours obligate anaerobic fermenters adapted to a hypoxic environment [2]. The four dominant phyla within the colonic microbiome include Firmicutes, Bacteroidetes, Actinobacteria, and Proteobacteria, of which Firmicutes and Bacteroidetes predominate [3]. Microbial dysbiosis is a cornerstone of CRC pathogenesis due to key metabolic and immunomodulatory effects within the gastrointestinal tract and host intestinal cells [4].

The carcinogenic potential of the gut microbiota is mediated through virulence factors, polymicrobial synergy, metabolic activity, invasion and disruption of host mucosal barriers, and prolonged inflammatory effects [5]. Specific microbial species, such as *F. nucleatum*, *E. faecalis* and *B. Fragilis* have been linked to CRC through enrichment of faecal or colonic mucosa samples of CRC patients relative to healthy individuals [6]. This study aims to build upon these established connections by providing context between lifestyle factors and gut microbiota changes.

Although numerous studies have investigated associations between lifestyle factors and CRC risk, few have examined how these factors directly modulate the gut microbiome, particularly in relation to physical activity. This review systematically synthesises current evidence regarding the effects of physical activity and other modifiable lifestyle factors on gut microbial composition, diversity, and metabolic function, with emphasis on taxa relevant to colorectal carcinogenesis.

MATERIALS AND METHODS

Search strategy

Study selection was conducted in accordance with PRISMA guidelines. The original scope of this project included CRC dysbiosis and the investigation of the relationship between lifestyle and CRC, which were subsequently refined and separated into separate papers. Databases were systematically searched and screened to identify all relevant studies examining the relationship between lifestyle factors and gut microbiota.

The original database search was conducted in 2024. An updated search using the identical search strategy and databases was performed in June 2026 to identify studies published since the initial search. All newly identified records were screened according to the same predefined eligibility criteria. A summary of this process, including a PRISMA flow diagram, is presented in Fig. 1.

Systematic review screening: inclusion and exclusion criteria

Studies were eligible for inclusion if they: (1) included adult populations aged 18–90 years; (2) investigated the effects of physical activity and other lifestyle factors on the gut microbiome; and (3) were published in or after 2000.

Eligible study designs included randomised controlled trials (RCTs), cross-sectional studies, and cohort studies. Relevant literature and systematic reviews identified during the search were used for contextual and background purposes; however, they were not included in the PRISMA flow diagram.

Studies were excluded if they: (1) included participants aged < 18 or > 90 years; (2) were not published in English; (3) were published before 2000; (4) had a sample size of < 20 participants; and (5) were not peer-reviewed or indexed in Scopus or PubMed.

Following title and abstract screening, 459 studies underwent full-text review, with two independent reviewers assessing each article. Discrepancies were resolved by consultation with a third reviewer. After full-text screening, 31 primary studies met eligibility criteria and were included for data extraction. Data were synthesised narratively according to recurring themes, including microbial diversity, metabolic pathways, and taxonomic alterations associated with physical activity and lifestyle exposures. A 2025-26 rescreen was conducted in a similar fashion, using one reviewer to include novel literature.

Risk of bias assessment for systematic narrative synthesis:

Primary studies investigating microbial dysbiosis in CRC or the effects of physical activity and other lifestyle factors on gut microbial populations were assessed for risk of bias following inclusion using the ROBINS-E, ROBINS-I, or ROB-2 Cochrane Risk of Bias tools, as appropriate to the study design (see Table 1 of the Appendix). Existing systematic reviews, narrative reviews, and relevant educational materials were used to contextualise and inform the interpretation of the findings.

Table 1
Risk of bias assessment of primary studies linking exercise and lifestyle factors to gut microbiome alterations.

Primary Studies Author, Year	Study type and ROB tool	Domains of Concern	Risk of Bias:
Allen 2018	RCT ROB 2 Criteria	Confounding bias	Moderate-serious
Baldanzi 2024	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Selection bias	Low-Moderate
Bressa 2017	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias	Low-Moderate
Castro-Mejia 2020	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias	Low-Moderate
Clarke 2014	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias	Low-Moderate
Cronin 2018	RCT ROBINS-I Criteria	Confounding bias Selection bias Missing data	Moderate-serious
Cui 2021	Observational/Cross-Sectional ROBINS-E Criteria	N/A	Low-Moderate
Cullen 2024	RCT ROB 2 Criteria	Missing data	Low-Moderate
Duan 2024	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Selection bias	Moderate-serious
Durk 2019	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Selection bias	Low-Moderate
Estaki 2016	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Missing data	Low-Moderate
Fart 2020	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Selection bias	Low-Moderate
Fiorilli 2025	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias	Moderate-Serious
Fontana 2023	Systematic Review/Meta Analysis ROBINS-I Criteria	Lack of adjustments Heterogeneity of participant groups and measurements	Moderate-serious
Iwasaka 2023	Observational/Cross-Sectional ROBINS-E Criteria	Selection bias	Low-Moderate
Jang 2019	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias	Low-Moderate
Jie 2021	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias	Low-Moderate
Jung 2020	Observational/Cross-Sectional ROBINS-I Criteria	Selection bias	Low-Moderate
Kang 2023	RCT ROB 2 Criteria	N/A	Low-Moderate
Kern 2020	Cohort Study ROBINS-E Criteria	Confounding bias Selection bias	Moderate-serious

Primary Studies Author, Year	Study type and ROB tool	Domains of Concern	Risk of Bias:
Langsetmo 2019	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias	Low-Moderate
Li 2026	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias	Moderate-Serious
Liu 2025	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias Classification of exposure bias Missing data bias	Moderate-Serious
Martinez-Tellez 2025	RCT ROB 2 Tool	Bias due to deviations from intended interventions Missing outcome data	Low-Moderate
Memili 2023	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias	Low-Moderate
Morita 2019	Non-randomised Intervention ROBINS-I Criteria	Confounding bias	Low-Moderate
Perez-Prieto 2024	Observational/Cross-Sectional ROBINS-E Criteria	Confounding bias Selection bias	Low-Moderate
Petersen 2017	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias	Low-Moderate
Resende 2021	RCT ROB 2 Criteria	Bias due to deviations from intended interventions Missing outcome data	Low-Moderate
Shah 2023	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias	Low-Moderate
Shi 2022	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Classification of exposure bias	Low-Moderate
Urban 2024	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias	Low-Moderate
Whisner 2018	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias Classification of exposure bias	Moderate-Serious
Zheng 2025	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias Selection bias Classification of exposure bias	Moderate-Serious
Zhong 2021	Observational/Cross-Sectional ROBINS-I Criteria	Confounding bias	Low-Moderate

RESULTS

Exercise and lifestyle-induced changes on gut microbiome composition

This section explores the interplay between physical activity and other lifestyle factors, with the changes observed in the gut microbiome. We have observed studies in three key domains: metabolic pathways, microbiome diversity, and specific gut microbiota. The collection of primary studies and their findings, which will be referenced throughout, are summarised in Tables 2 and 3 of the Appendix. Following this section, we will discuss the role of other lifestyle factors in gut microbiome modulation, summarised in Table 4 of the Appendix.

Table 2
Effects of physical activity on gut microbiota part 1

Authors	Country	Age (Years)	Population Demographic	Gender	Level(s) of Fitness	Metabolic Pathways	Microbiota Diversity Outcomes	Microbiota Specific Outcomes
Allen 2018	USA	Lean: 25.1 ± 6.52 Obese: 31.14 ± 8.57	Lean and obese, previously sedentary	F	6-week progressive endurance-based exercise program	↑SCFA in lean group, reversed once exercise ceased ↑Butyrate with lean body composition	↑β-diversity with leaner body composition	↑Clostridiales, Lachnospira, Roseburia, Lachnospiraceae, Faecalibacterium genera after exercise
Baldanzi 2024	Sweden	57.6 ± 3.8	Healthy women	F	Sedentary (SED), moderate (MPA), vigorous (VPA)	↑SCFA & butyrate in MPA/VPA	↑B-diversity & A-diversity in MPA/VPA	↑ F. prausnitzii, Roseburia spp in MPA/VPA ↑ E. coli, R. torques, E. lenta, R. gnavus in SED
Bressa 2017	Spain	Active: 30.7 ± 5.9 Sedentary: 32.2 ± 8.7	Healthy premenopausal Caucasian women	F	Sedentary; Active (3hr+ weekly PA)	↑Butyrate in active ↑Anti-inflammatory (F. prausnitzii) in active	No significant changes	↑F:B ratio in active ↑Barnesiellaceae & Odoribacteraceae in SED women ↑F. prausnitzii, R. homini, & A. muciniphila in active
Castro-Mejia 2020	Denmark	70.2 ± 3.9	Healthy older adults	Both	High fitness (HF); Low fitness (LF)	No difference in SCFA concentrations between HF and LF	↑A-diversity in HF phenotypes	↑Bifidobacteriales, Clostridiales
Clarke 2014	Ireland	29 ± 4	Healthy Irish males	M	Elite athletes; Low BMI controls; High BMI controls	↓Inflammatory and ↑metabolic markers in elite athletes compared to controls	↑A-diversity in elite athletes	↑Firmicutes, Ruminococcaceae, Succinivibrionaceae, Akkermansiaceae in elite athletes ↓ Bacteroidetes in athletes
Cronin 2018	Ireland	33.7	Healthy Caucasian volunteers	Both	8-week moderate exercise group (mixed aerobic & resistance)	-	No significant changes	-
Cui 2021	Denmark	70 ± 5	Healthy older adults	Both	High fitness (HF); Low fitness (LF)	↓SCFAs (propionic acid, lactic acid) and AAs (methionine, leucine, glutamic acid, threonine) in the HF group	-	-
Cullen 2024	USA	RT: 28.4 ± 4.1 CT: 28.5 ± 4.4	Sedentary adults with overweight & obesity	Both	6-wk resistance program; control aerobic program	↑SCFA & butyrate in RT	No significant changes	↑R. faecis, F. prausnitzii, Holdemania genus in resistance
Duan 2024	China	49 ± 3.75	Middle-aged healthy individuals	Both	Serious runners; sedentary healthy controls	↑Starch, sucrose, glycerolipid, cysteine and methionine metabolism in runner	↑ β-diversity in runner No changes in A-diversity	↑F:B ratio in runners ↑Ruminococcus, Coprococcus in runners ↑Bacteroides, Lachnospiraceae, Lachnospira in control
Durk 2019	USA	25.7 ± 2.2	Healthy young adults	Both	Levels based on VO2 max	-	-	↑F: B ratio in those with higher VO2 max.

Authors	Country	Age (Years)	Population Demographic	Gender	Level(s) of Fitness	Metabolic Pathways	Microbiota Diversity Outcomes	Microbiota Specific Outcomes
Estaki 2016	Canada	Low: 25.5 ± 3.3 Avg: 24.3 ± 3.7 Hi: 26.2 ± 5.5	Healthy young adults	Both	Low, average or high fitness based on VO2 peak (cardiorespiratory fitness)	↑Butyrate production and fecal butyric acid with higher fitness	↑A-diversity in higher fitness individuals Higher fitness did not promote distinct clustering of β-diversity data	↑Coprococcus, Roseburia, Adlercreutzia, Clostridiales, Lachnospiraceae, Erysipelotrichaceae with higher fitness
Fart 2022	Sweden	Community-dwelling: 72 (69–76) Orienteering Athletes 68.5 (67–72)	Elderly healthy individuals	Both	Community-dwelling; Orienteering Athletes	↑Butyrate in orienteers	Homogenous microbiota in orienteers No changes in A-diversity	↑Faecalibacterium prausnitzii in orienteers ↓Parasutterella excrementihominis, Bilophila wadsworthia in orienteers
Fontana 2023	Italy	N/A	Healthy individuals	Both	Athletes; sedentary; moderate athletes	↑SCFA in athletes	↑ β-diversity in athletes	↑Faecalibacterium, Agathobacter, Blautia, Ruminococcus species in athletes
Iwasaka 2023	Japan	58.7 ± 12.3	General individuals	Both 74% F	Low, moderate-to-vigorous	No significant changes	No significant changes	No significant changes
Jang 2019	South Korea	Bodybuilders: 25 (± 3) Distance Runners: 20 (± 1) Healthy men: 26 (± 2)	Young healthy individuals	M	Bodybuilder; distance runner; healthy men without exercise habits	↓Butyrate in bodybuilder ↓Acetate in bodybuilder ↓Lactate in bodybuilder	No significant changes	↑Faecalibacterium, Sutterella, Clostridium, Haemophilus, Eisenbergiella in bodybuilder ↓Bifidobacterium, parasutterella in bodybuilder
Jie 2021	China	29.6	Volunteers	Both	Varying levels of aerobic and anaerobic fitness scores	↑aldosterone, folic acid with B. cellulosilyticus, B. stercorisoris	↑Diversity with increased fitness scores	↑F. prausnitzii, B. adolescentis, A. shahii with higher vital capacity ↓C. clostridioforme, R. gnavus, E. coli with higher vital capacity ↓E. coli with increased handgrip strength ↑B cellulosilytics, B stercorisoris with increased fitness score
Jung 2020	South Korea	Unknown	Healthy civilians & Korean navy trainees	Unknown	Lifestyle changes to navy trainee group for 8 weeks	No significant changes	No significant changes	No significant changes
Kang 2023	China	Unknown	College student basketball players	Unknown	Control: no changes to routine; Experimental: add on 5 months regular Tai Chi at 70% max HR	↓HDL cholesterol and triglycerides with Tai Chi group ↓Diastolic blood pressure in Tai Chi group	↑A-diversity in Tai Chi group	↑Bacteroidetes, Ruminococcaceae, Lachnospiraceae, Rikenellaceae in Tai Chi group ↓Proteobacteria, Oxalobacteraceae in Tai Chi group

Table 3
Effects of physical activity on gut microbiota part 2

Authors	Country	Age (Years)	Population Demographic	Gender	Level(s) of Fitness	Metabolic Pathways	Microbiota Diversity Outcomes	Microbiota Specific Outcomes
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Table 4
Effects of other lifestyle factors on gut microbiota

Kern 2020	Denmark	-	Physically inactive adults with BMI 25–35	-	Habitual living (control); Active commuting by bike; Moderate exercise; Vigorous exercise	-	↑Beta diversity on the genus level with exercise	↑ Akkermansia and Proteobacteria with exercise
Langsetmo 2019	USA	84 (78–98)	Sedentary, community-dwelling men	M	Self-reported physical activity by step count	↑SCFA ↑Butyrate	↑β-diversity in high step count	↑Cetobacterium, Faecalibacterium, Lachnospira, Prevotella, & Clostridium in high step count ↓Coprobaillus, Adlercreutzia, & Erysipelotrichaceae CC-115 genera in high step count
Martinez-Tellez 2025	Spain	18–25	Sedentary, young, disease-free	Both	Control, moderate, vigorous exercise	↑SCFA	No significant changes	↑Coproccocus in moderate exercise group
Memili 2023	USA	47–61	Randomly selected disease-free adults	Both	Self-reported physical activity	↑SCFA	↑A-diversity	↑Agathobacter, Butyricoccus, GCA-900066575, & Lachnospiraceae NK4A136 Group with exercise
Morita 2019	Japan	70 (66–75)	Healthy elderly women	F	Aerobic exercise (AE); Trunk muscle training (TM)	-	-	↑Bacteroides in AE ↓Clostridium subcluster XIVa in AE, ↓Clostridium cluster IX in TM
Perez-Prieto 2024	Finland	58	Women from Northern Finland Birth Cohort 1966	F	Sedentary behaviour; Leisurely physical activity; MVPA	↑Butyrate in MVPA	No significant changes	↑Agathobacter and Lachnospiraceae CAG56 (butyrate producing bacteria) in MVPA
Peteren 2017	USA	33 (19–49)	Healthy cyclists	Both	Professional to amateur (exercise intensity, time)	↑SCFA, propionate, butanoate & methane ↑Methane	↑Diversity	↑Prevotella with hours of exercise ↑M smithii in professional Akkermansia present in all cyclists
Resende 2021	Brazil	25.1 ± 4.66	Healthy sedentary men	M	10-week moderate aerobic exercise vs control (untrained)	-	↑A-diversity with increased VO2 peak	↑Roseburia, Sutterella & Odoribacter genera with VO2peak ↑Faecalibacterium genera with decreased BMI
Shah 2023	Canada	56.9 ± 6.3	Cancer-free individuals of high & normal BMI	Both, 72% F	Low; moderate; high exercise duration and intensity	↑Butyrate	↑A-diversity with moderate exercise time	↑Faecalibacterium & F. prausnitzii with grip strength ↑Actinobacteria & Proteobacteria phyla; Collinsella & Prevotella genera with exercise in normal BMI
Shi 2022	China	51–89 years	Older urban Chinese individuals	Both	Non-exercise; regular light intensity physical activity (LIPA) exerciser	-	↑B-diversity with regular exercise	↓Ruminococcus with long-term regular exercise ↑Prevotella and Coprococcus with exercise
Urban 2024	Poland	Pro: 26 ± 7 Amateur: 24 ± 6	Healthy individuals	M	Professional (4hr daily) & amateur (1.5hr twice weekly) footballers	↑butyrate, succinate	↑Diversity in professional	↑F:B ratio in professional ↑Clostridiales in professional

Kern 2020	Denmark	-	Physically inactive adults with BMI 25–35	-	Habitual living (control); Active commuting by bike; Moderate exercise; Vigorous exercise	-	↑Beta diversity on the genus level with exercise	↑ Akkermansia and Proteobacteria with exercise
								↓ Firmicutes, Bacteroidetes & Actinobacteria with increased exercise
Whisner 2018	USA	18.4 ± 0.6	Random college students	Both	Self reported MVPA	-	No significant changes	↑Paraprevotellaceae, Lachnospiraceae, and Lachnospira in MVPA ↑Enterobacteriaceae and Enterobacteriales in low activity
Zhong 2021	Ireland	55–74 years; median 69.0	Older adults	Both	LIPA; MVPA	↑Bacteria for butyrate, anti-inflammation and glucose metabolism with increasing PA	No significant changes	↑Prevotella with MVPA ↑Bacteroides with sedentary and sleep time

Author	Country	Age (Years)	Population Demographic	Gender	Factors explored	Key findings
Allen 2018	USA	20–45	Health sedentary adults	Both	BMI	↑Fecal SCFA concentrations in leaner adults Differences in beta diversity between BMI groups
Castro -Mejia 2020	Denmark	70.2 ± 3.9	Healthy older adults	Both	Diet, BMI	↑Bifidobacteriales abundance with increased energy intake, starch and dietary fiber ↑Alpha diversity with reduced BMI, increased energy and starch intake
Clarke 2014	Ireland	29 ± 4	Healthy Irish males	M	Diet, BMI	Improved metabolic markers in lower BMI ↑Overall diversity with protein intake ↑Akkermansia with lower BMI
Cronin 2018	Ireland	33.7	Healthy Caucasian volunteers	Both	Whey protein supplementation	↑Lactic acid bacteria ↑Taxonomic Richness of gut virome
Cui 2021	Denmark	70 ± 5	Healthy adults	Both	BMI	↑Concentrations of amino acids, SCFAs, uracil and xanthine fecal metabolites with higher BMI
Estaki 2016	Canada	24.3 ± 3.7	Healthy young adults	Both	Diet	↑Bacteroides with protein intake
Jang 2019	South Korea	20–26	Young healthy Individuals	M	Diet	↓SCFA with high protein, low carb diet ↓Overall diversity with high protein, poor carb and poor fibre intake ↓SCFA producing bacteria with high protein, low carb diet
Jie 2021	China	29.6	Volunteers	Both	Diet	↑Alpha diversity with increased dairy consumption ↑Streptococcus thermophilus, Veillonella with yoghurt consumption
Jung 2020	South Korea	Unknown	Healthy civilians & Korean navy trainees	Unknown	Smoking, alcohol, sleep, BMI	Smoking had significant impact on alpha diversity Other lifestyle changes (healthy diet, sleep, alcohol abstinence) did not show significant changes to microbiota
Koliada 2017	Ukraine	Unknown	Ukrainian adults	Both	BMI	↑Firmicutes with increased BMI ↓Bacteroides with increased BMI
Memili 2023	USA	47–61	Randomly selected disease-free adults	Both	Diet	↑Lachnospiraceae with increased diet quality ↓Anaerotruncus and Ruminococcaceae with diet quality
Shah 2023	Canada	56.9 ± 6.3	Cancer-free individuals of high & normal BMI	Both, 72% F	BMI	↓Butyrate (Oscillibacter spp.) with BMI ↓A-diversity in overweight with increased exercise time
Whisner 2018	USA	18.4 ± 0.6	Random college students	Both	BMI, screen time, diet	No significant differences between BMI and gut microbiome abundance ↓Clustering differences with low fiber intake
Yu 2018	China	68 ± 1.5	Urban Chinese adults free of cardiovascular diseases, diabetes and cancer	Both	Diet	↑Alpha diversity with better diet quality ↑Firmicutes, Actinobacteria, Tenericutes with better diet quality ↑Bifidobacterium with dairy consumption ↓Roseburia with processed meat consumption

Author	Country	Age (Years)	Population Demographic	Gender	Factors explored	Key findings
Zhang 2021	China	50–75 years	Asymptomatic Chinese individuals	Both	Diet	↑Anaerostipes with lower refined grain intake

Metabolic pathways

Small-chain fatty acid production

Exercise interventions were associated with significant alterations in metabolic pathways related to physical activity and gut microbiome health. A robust body of evidence demonstrates that exercise increases the abundance of gut microbiota with SCFA-producing capacity across diverse populations and study designs [7–18]. Notably, production of butyrate, a primary SCFA produced during carbohydrate fermentation and bacterial cross-feeding, increased with physical activity across a wide range of studies [7, 9, 12, 15, 19–24].

These associations were consistently observed across varying exercise modalities, intensities, and durations, as well as across age and sex groups. RCTs reported increases in SCFA-producing taxa following resistance training in sedentary overweight adults [12], endurance training in lean female adults [7], and moderate-intensity exercise interventions [25]. Observational studies similarly reported higher SCFA-producing capacity in individuals with greater self-reported physical activity [16, 22], higher step counts in older men [15], and increasing exercise intensity [24]. These effects extended to aerobic exercise interventions in previously sedentary adults and to comparisons between elite athletes and non-athletic controls.

However, several studies reported null or inverse associations. No differences in SCFA production were observed across fitness or activity levels in older adults [26, 27] or in young healthy East Asian populations [28, 29]. Reduced SCFA production was also reported in highly fit older adults [30] and bodybuilders [28]. These discrepancies may reflect population-specific dietary, lifestyle, or genetic factors, particularly when comparing East Asian to Western populations. In bodybuilders, a decrease in butyrate, acetate and lactate production was observed [28]. While butyrate serves as a primary energy source for colonocytes exerting anti-inflammatory and anti-tumorigenic effects within the colon, acetate is the most abundant SCFA and exerts systemic metabolic effects [31]. Lower SCFA concentrations do not necessarily indicate adverse microbial changes, as SCFAs may exert context-dependent inflammatory effects, consistent with the “butyrate paradox” [32].

Further metabolic pathway changes due to exercise

Physical exercise also modulated carbohydrate metabolism. Duan et al [33] found that carbohydrate and glycan metabolism pathways were enriched in healthy adults, with starch and sucrose metabolism significantly increased in runners. This increase in carbohydrate metabolism was also observed in professional cyclists due to the increased abundance of *Prevotella* [18], which also enhanced amino acid metabolism. Urban et al [23] describe the increase in succinate-producing bacteria (i.e. *Parabacteroides distasonis*) from increased intensive physical activity. These bacteria activate intestinal gluconeogenesis to assist with carbohydrate metabolism and enhance secondary bile acids that mediate lipid metabolism [34]. A study by Zheng et al [35] demonstrated decreased nitrite-oxidising bacteria (NOB) (i.e. Nitrospirae), nitrogen and carbohydrate metabolism in perimenopausal women with low metabolic equivalents (METs) compared to young, active women, whose increased physical activity assisted their nitrite waste disposal through NOB upregulation.

Pro-inflammatory pathways were also downregulated by physical activity. Inflammatory markers, including CRP, leptin and adiponectin, were reduced when comparing active groups to controls [36, 37]. This trend also existed for elderly adults participating in light and moderate physical activity [24]. These effects may be related to the full-body aerobic capacity of athletic training, allowing for increased oxygen consumption and energy supply that fuels these specific anti-inflammatory changes.

Gut microbiota diversity

In general, physical activity corresponds with greater alpha and beta diversity of the gut microbiome, although findings remain inconsistent. Alpha diversity measures the diversity of microorganisms within an individual sample, considering both the number of species present (richness) and their relative abundance (evenness). In contrast, beta diversity measures how microbial communities differ between samples or populations.

While many studies reported a positive association between exercise and increased alpha diversity [9, 16, 18, 19, 22, 23, 26, 37–41], others observed no significant changes [20, 21, 24, 42, 43]. These discrepancies may relate to intervention duration and intensity, as a systematic review by Oritz-Alvarez et al [44] suggested that alpha diversity is more likely to increase following long-term exercise interventions and in individuals with healthier baseline phenotypes. Baseline fitness may also be influential, given that increases in alpha diversity were more consistently reported in physically active individuals and elite athletes.

Several studies reported higher beta diversity in individuals engaging in regular physical activity, including runners and athletes [7, 9, 14, 15, 18, 23, 33, 42, 43], supporting an association with healthier phenotypes. However, other studies [8, 19, 38] found no consistent relationship between physical exercise and beta diversity. Notably, fewer studies have examined beta diversity compared with alpha diversity, limiting firm conclusions and highlighting the need for further investigation. Across both diversity measures, several studies reported no significant changes in microbial diversity with exercise [12, 25, 27–29, 36, 45, 46].

Changes within specific microbial taxa

Significant changes were observed in Bacteroidetes, Firmicutes, Proteobacteria and Actinobacteria when comparing physically active to sedentary populations, with specific genera implicated in each of these phyla.

Bacteroidetes

Bacteroidetes play diverse roles within the gut microbiome, functioning as commensal organisms that contribute to pathogen resistance and cross-feeding via propionate production, while certain species (e.g. *B. fragilis*) may act as opportunistic pathogens through LPS expression and oncogenic mechanisms [47].

Across multiple studies, Bacteroidetes abundance was lower in physically active individuals and higher in sedentary or control groups, regardless of exercise modality [23, 24, 33, 36, 37]. This pattern was corroborated by several systematic reviews [8, 13, 17].

Trends within Bacteroidetes

Within Bacteroidetes, *Bacteroides* and *Prevotella* genera were most consistently associated with physical activity (Fig. 2). *Bacteroides* abundance increased with higher levels of physical activity across several studies [24, 33, 48]. Members of this genus are commensal gut bacteria that contribute to microbial cross-feeding and immune regulation through the production of metabolites, including SCFA such as butyrate and acetate [49]. These metabolites contribute to gut barrier integrity and modulate immune homeostasis by downregulating pro-inflammatory pathways, including IL-6 and STAT3 signalling [50].

Similarly, *Prevotella* abundance was higher in physically active individuals [18, 22, 24, 43, 46]. *Prevotella* is commonly enriched in high-fibre diets and facilitates the fermentation of complex carbohydrates, thereby enhancing SCFA production. Through these mechanisms, *Prevotella* has been associated with protective effects against obesity, type 2 diabetes mellitus, cardiovascular disease, and inflammatory conditions [51].

Firmicutes

Firmicutes (Bacillota) increased following exercise interventions [37] and in elite athletic populations [17]. Prominent commensal genera within Firmicutes include *Clostridium*, *Faecalibacterium*, *Lachnospiraceae* taxa, and *Ruminococcus*, many of which are major SCFA producers. Their changes, summarised in Fig. 3, are notable and will be explored below.

Clostridium

Within the *Clostridium* genus, several clusters, particularly clusters IV and XIVa, are recognised butyrate producers with anti-inflammatory effects [52]. Others, such as cluster IX, assist in propionate production [53]. Modest increases in *Clostridium* were observed in older adults with higher step counts and in individuals with greater aerobic fitness or endurance training exposure [7, 15, 19, 23], supporting a role for exercise in enriching metabolically beneficial taxa. In contrast, Morita et al [48] reported reduced cluster XIVa and increased cluster IX following a 12-week aerobic intervention in elderly Japanese women, consistent with previously described discrepancies in East Asian cohorts.

Faecalibacterium

The *Faecalibacterium* genus, a member of the *Ruminococcaceae* family, was consistently increased across multiple exercise modalities and populations [7–9, 12, 14, 15, 20, 22, 28, 36, 39, 41]. As a major butyrate producer, this genus is typically depleted in inflammatory bowel disease (IBD), CRC, and other inflammatory conditions, supporting a role for physical activity in promoting anti-inflammatory intestinal homeostasis through butyrate and D-lactate production [54]. *F. prausnitzii*—one of the most abundant butyrate-producing species in the gastrointestinal tract with established anti-inflammatory and barrier-supportive properties [55]—was repeatedly enriched in physically active cohorts [9, 12, 20, 22, 36, 39]. These findings point to the significant beneficial role of the *Faecalibacterium* family in exercise-mediated effects on the gut microbiome, and support their protective role highlighted earlier. A discrepancy was noted in Fiorilli et al [38], whereby a low physical activity program for elderly adults corresponded with the depletion of *F. prausnitzii*—a contradictory relationship which could be explained by the concurrent upregulation of other SCFA-producers that competed for similar substrates.

Ruminococcus

Findings for *Ruminococcus* were heterogeneous, though most studies reported increases with higher physical activity [14, 33, 37, 40]. Species-level analyses suggest differential effects: increases in *R. bromii* (a key degrader of resistant starch) may enhance SCFA production [14], whereas reductions in *R. gnavus* (a mucin-degrading species associated with increased oxidative stress leading to inflammatory states found in IBD [56]) were observed in some cohorts [39]. Collectively, these findings indicate species-specific modulation within *Ruminococcus*, rather than uniform genus-level responses to physical activity.

Lachnospiraceae

Members of the commensal, SCFA-producing, *Lachnospiraceae* family were enriched with physical activity across diverse cohorts and exercise types, including high step counts, aerobic training, Tai Chi, and running [7, 15, 19, 33, 40], with confirmation from systematic reviews [8, 17].

Butyrate-producing genera such as *Agathobacter*, *Coprococcus*, and *Roseburia* were repeatedly increased [14, 16, 21, 33, 43], of which *Roseburia* was the most frequently mentioned [7, 9, 12, 19, 36, 41]. *Agathobacter* contributes to butyrate-mediated gut homeostasis [57]. *Coprococcus* species strengthen epithelial barrier function and may influence metabolic and neurological pathways [58]. *Roseburia* is associated with anti-inflammatory and

immunomodulatory effects that protect against IBD and CRC [59]. These findings suggest that physical exercise modulates anti-inflammatory and homeostatic effects within the gut microbiome through positive *Lachnospiraceae* expression.

Distinct changes occurred in the order *Clostridiales*, with modulation of three key genera (*Faecalibacterium*, *Clostridium*, *Ruminococcus*). The *Lachnospiraceae* family was also notably increased, with *Agathobacter*, *Coprococcus* and *Roseburia* genera being most beneficially affected with increased physical exercise.

Firmicutes-Bacteroidetes ratio

The Firmicutes–Bacteroidetes ratio is a key marker of gut homeostasis and is frequently disrupted in obesity and inflammatory disease, while remaining highly sensitive to lifestyle factors such as physical activity [60]. Although widely used, the Firmicutes–Bacteroidetes ratio remains an imperfect and sometimes inconsistent marker of gut dysbiosis across studies. For example, a reduced ratio has been implicated in IBD through upregulation of pro-inflammatory pathways, including TNF- α , Toll-like receptors, and cytokine expression [61]. In contrast, physically active populations consistently demonstrate an increased ratio—characterised by higher Firmicutes and lower Bacteroidetes—an effect associated with greater cardiorespiratory fitness (VO_{2max}) [36, 37, 62]. Collectively, these findings suggest a protective role of regular physical activity against gut inflammation through Firmicutes–Bacteroidetes modulation. An exception was reported by Urban et al [23] whereby Firmicutes abundance was reduced in professional footballers compared with amateur players. This raises the possibility that extreme training loads may adversely alter gut microbial composition; however, further investigation is required.

Proteobacteria

Proteobacteria, also known as Pseudomonadota, are a phylum of gram-negative bacteria, including genera such as *Salmonella*, *Escherichia*, *Helicobacter*, *Sphingomonas* and *Vibrio*, some of which are implicated in pathogenic processes [63]. Typically a minor component of the gut microbiota, increases in Proteobacteria often indicate microbial dysbiosis, epithelial dysfunction, and hypoxia, contributing to low-grade intestinal inflammation via lipopolysaccharide (LPS) production and chronic inflammatory states [64].

Physical activity has mixed effects on Proteobacteria modulation. Moderate exercise has been associated with small increases in Proteobacteria in healthy adults [22, 42], whereas Tai Chi interventions reported reductions [40]. A systematic review by Aya et al [8] observed slight increases following six weeks of supervised aerobic training in individuals with BMI > 25, highlighting variability in exercise-related effects despite the genus's inflammatory potential. At the genus and species level, trends are similarly inconsistent. *E. coli* was elevated in sedentary middle-aged women [9] but decreased in Chinese participants with greater grip strength or vital capacity [39]. *Sphingomonas* was associated with higher levels of daily moderate-to-vigorous physical activity in young women when compared to perimenopausal women with lesser METs [35]. *Enterobacter* abundance was higher in sedentary college students [46]. These taxa are part of the normal microbiota but have opportunistic pathogenic potential, and their upregulation in sedentary individuals may reflect an elevated inflammatory state. More targeted research is required to obtain discernible trends within Proteobacteria.

Actinobacteria

Actinobacteria, also commonly referred to as Actinomycota, are gram-positive, non-spore-forming anaerobic rods that constitute a functionally important component of the human gut microbiome. Within this phylum, *Bifidobacterium* is one of the most prevalent and metabolically significant genera in healthy individuals [65].

Actinobacteria contribute to gut barrier homeostasis through multiple mechanisms. The intestinal barrier comprises epithelial tight junctions, a mucus layer, immune components and commensal microbiota. Commensals within this phylum enhance tight junction expression, regulate mucin synthesis and turnover, support epithelial proliferation via SCFA production, and modulate mucosal immunity [66]. Metabolically, Actinobacteria ferment carbohydrates to produce acetate, which confers protection against enteropathogens such as *E. coli*. They are also implicated in cholesterol reduction and the metabolism of complex carbohydrates, including resistant starch [22].

Increased Actinobacteria was associated with physically active and aerobically trained individuals, including after structured aerobic interventions [8, 17, 22]. Higher *Bifidobacterium* levels were observed in elderly adults engaging in habitual physical activity [26] and individuals with greater cardiopulmonary fitness [39]. These findings are corroborated by systematic reviews [17, 67].

Role of lifestyle factors in microbiome dysbiosis

Diet and the gut microbiome

Diet is a major modifiable factor influencing gut microbiome composition and function, with implications for CRC risk caused by metabolic changes as previously mentioned. Eleven studies examined dietary effects on the gut microbiome [16, 19, 26, 28, 37, 39, 46, 68–71], highlighting the importance of caloric intake, macronutrient composition, and micronutrients. These studies were completed independent of investigating physical activity in affecting the gut microbiome. A summary of findings is available in Table 4 of the Appendix.

Calorie intake

High-calorie diets have been associated with increases in *Bifidobacteriales* abundance, yet their effects on microbial diversity remain inconsistent. A systematic review by Castro-Mejía et al [26] reported improved alpha diversity with higher energy intake, whereas Shah et al [22] observed decreased

diversity alongside increased *Bifidobacteriales*. Such contradictions may arise from the limited number of studies examining caloric load alone rather than broader dietary composition, which may exert stronger influence on microbial profiles.

Macronutrients

Various macronutrients have been affected by changes in gut microbiota. These changes have been summarised below, particularly with effects on carbohydrate, protein and dairy intake.

A high-carbohydrate, low-protein diet was associated with greater microbial diversity and higher short-chain fatty acid (SCFA) production compared with a high-protein, low-carbohydrate diet, which demonstrated reduced overall diversity and decreased abundance of SCFA-producing taxa [28]. In contrast, other studies [19, 37, 45] observed positive associations between increased protein intake and microbial diversity, including higher proportions of bacteriophages linked to lactic acid bacteria and increased *Bacteroides* abundance. These inconsistencies suggest that the effects of protein on the gut microbiome may depend on unmeasured variables such as protein source, overall dietary composition, and host factors.

Complex carbohydrates such as rice have shown beneficial changes to the gut microbiome. Residues from freshly cooked white rice with high amylose content contained more medium-to-long chains, which significantly enhanced butyrate production and enriched beneficial genera such as *Agathobacter* and *Lachnospiraceae* groups [68]. These modulations are associated with anti-inflammatory effects and metabolic optimism.

Dairy intake has similarly been linked to favourable microbiome modulation. Some studies [39, 70] reported increased alpha diversity and higher *Bifidobacterium* abundance with dairy consumption, while yoghurt specifically increased *Streptococcus thermophilus* and *Veillonella*, indicating source-dependent microbial effects. Calcium and vitamin D are hypothesised to reduce CRC risk by binding secondary bile acids and ionised fatty acids to form insoluble complexes and by attenuating epithelial proliferation; vitamin D may additionally promote epithelial differentiation. However, findings remain inconsistent when systematically reviewing epidemiological data [72].

Fibre

High-fibre diets, particularly those rich in fruits, vegetables, and plant-based foods, are consistently associated with favourable alterations in the gut microbiome. Castro-Mejía et al [26] reported that increased fibre intake was linked to a greater abundance of *Lactobacillus* and *Bifidobacterium*, which consequently increases SCFA production. Another review [69] found that high-fiber diets stimulated SCFA production and enhanced gut microbiome composition. Conversely, low-fibre intake has been associated with reduced microbial diversity and less distinct microbial clustering [28, 46].

Body mass index

Seven studies examined associations between BMI and gut microbiome composition, with lower BMI generally correlating with favourable metabolic markers, greater microbial diversity, and increased abundance of putatively beneficial taxa [7, 22, 26, 29, 30, 37, 46]. However, BMI is an imperfect surrogate for adiposity, as it does not distinguish between lean mass and fat mass or account for fat distribution. Reliance on BMI alone may therefore misclassify cardiometabolic risk; adjunct measures such as waist-to-hip ratio, waist circumference, or waist-to-height ratio have been recommended to improve risk stratification [73].

Most studies compared microbial diversity between higher and lower BMI groups, yet findings regarding alpha and beta diversity remain inconsistent. Several analyses reported no independent association between BMI and diversity metrics, whereas others observed higher alpha diversity in individuals with lower BMI [7, 22, 26, 29, 30, 37, 46]. These discrepancies may reflect confounding by co-examined lifestyle factors, particularly diet and physical activity, which independently shape microbiome structure.

Taxonomically, lower BMI has been associated with increased abundance of *Akkermansia*, *Bacteroides*, and *Oscillibacter*, genera frequently linked to enhanced SCFA production and improved metabolic profiles [7]. In contrast, higher BMI has been correlated with enrichment of taxa such as Proteobacteria, certain Firmicutes members [26], and an increased Firmicutes to *Bacteroides* ratio [74] which is often associated with obesity, dysbiosis and metabolic dysfunction.

Smoking and alcohol consumption

Among modifiable lifestyle factors, smoking cessation appears to exert one of the most rapid effects on gut microbiome composition. In an 8-week longitudinal study assessing multiple lifestyle variables, smoking was identified as a significant determinant of alpha diversity and microbial taxonomic shifts [29]. The most prominently modulated phyla were Firmicutes and Bacteroidetes. Notably, unlike dietary or exercise interventions that typically require sustained implementation to produce measurable microbiome changes, smoking cessation induced substantial alterations within a relatively short timeframe. These findings suggest that tobacco exposure exerts strong selective pressure on microbial ecology, and that cessation may rapidly restore microbial balance.

Alcohol consumption appears to exert an overall negative change on the gut microbiome. Chronic alcohol consumption is associated with gut dysbiosis and evidence suggests that alcohol dependence showed negative correlation with butyrate-producing *Clostridium* species [75]. Furthermore, these correlations appear to selectively modulate certain taxa, affecting the gut microbiome composition rather than overall diversity. Alcohol is further proposed to cause gut dysbiosis through generating acetaldehyde and reactive oxygen species during metabolism, which are toxic to microbial cell function and gut barrier integrity [75]. These changes to the gut microbiome caused by alcohol consumption are commonly linked with pathogenesis of chronic diseases, such as colorectal cancer.

CONCLUSION

This review synthesised current evidence on the interplay between the gut microbiome, colorectal cancer, and modifiable lifestyle factors. Physical activity emerged as a significant modulator of microbial composition and function. Numerous metabolic changes were observed, primarily in upregulating short-chain fatty acid (SCFA) and carbohydrate metabolism, with some influence on decreasing pro-inflammatory pathways. However, changes in alpha and beta diversity were inconsistent across a wide range of studies. Exercise was associated with shifts in major phyla, particularly an increased Firmicutes-Bacteroidetes ratio, influencing metabolic and inflammatory pathways relevant to colorectal cancer pathogenesis. Notably, key SCFA-producing bacteria, especially within Firmicutes, were augmented with increased physical exercise (e.g. *F. prausnitzii*), underscoring the importance of short-chain fatty acid production as a key protective mechanism for human gut health.

Other modifiable lifestyle factors have been studied for their effects on the gut microbiome. Diet appears to also exert a strong influence on microbial architecture, with energy-dense, low-fibre dietary patterns disrupting microbial diversity and intestinal homeostasis. However, the magnitude and durability of these effects remain incompletely defined, particularly across sex-specific and diverse population cohorts, and activity thresholds for clinically meaningful benefit require clarification. While BMI appears to influence gut microbiome diversity and composition, result discrepancies were prominent due to confounding with lifestyle factors and consideration of BMI as an imperfect measure of adiposity and cardiometabolic risk. Smoking cessation exerts substantial positive changes to the gut microbiome in a short timeframe, modulating Firmicutes and Bacteroidetes, and increasing alpha diversity.

Overall, more research is required to quantify dose-dependent relationships between physical exercise and other lifestyle factors on gut microbiota changes, and to focus on specific bacterial species relevant to CRC pathogenesis. Exploration of extreme levels of physical activity, longitudinal effects of physical activity, as well as demographic differences (i.e. age, sex, ethnicity), will assist in addressing discrepancies identified within primary studies and allow for a more nuanced understanding of modulators of the human gut microbiome. This will also assist in determining whether regular physical activity or performance-based exercise goals optimally change gut microbiota composition. Future longitudinal and mechanistic studies are required to establish dose-dependent and population-specific relationships between lifestyle behaviours and microbiome modulation, thereby informing targeted preventive strategies for colorectal cancer and other chronic inflammatory diseases.

Declarations

Author Contribution

All authors conceptualised the study, and all authors offered methodological guidance, performed title and abstract screening, full text screening, and data extraction. JZ and LW interpreted results to write the main manuscript text, completed the Risk of Bias and jointly prepared Table 1. JZ prepared Figure 1, Figure 3, and Tables 2-3. LW prepared Figure 2 and Table 4. VG supervised the study, provided conceptual input, and approved the final manuscript. All authors contributed to the interpretation of results and approved the submitted version.

Data Availability

All data analysed in this systematic qualitative synthesis were derived from publicly available sources, including PubMed, MEDLINE, ScienceDirect, and Scopus. No primary data were generated in this study. The full texts of included studies were accessed through institutional subscriptions or publisher platforms. Synthesised tables and figures of the data extraction generated during the analysis are included within the manuscript and its supplementary information. No datasets were deposited in a public repository.

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Figures

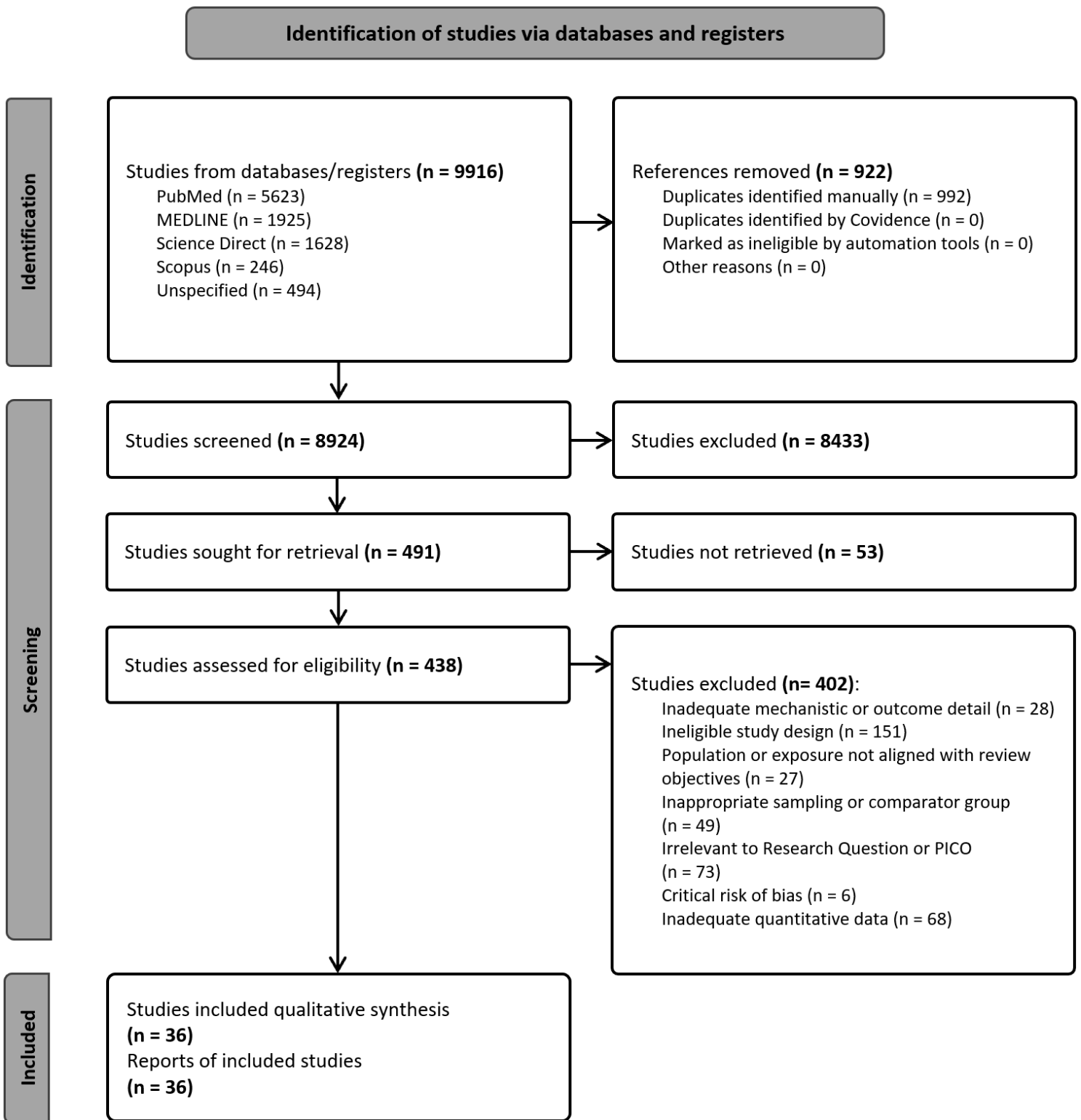


Figure 1
 PRISMA flow diagram of the study identification, screening, eligibility, and inclusion process for the narrative synthesis, indicating the subset of studies excluded from this review for incorporation into the quantitative meta-analysis.

Impacts of increased physical activity on the gut microbiome

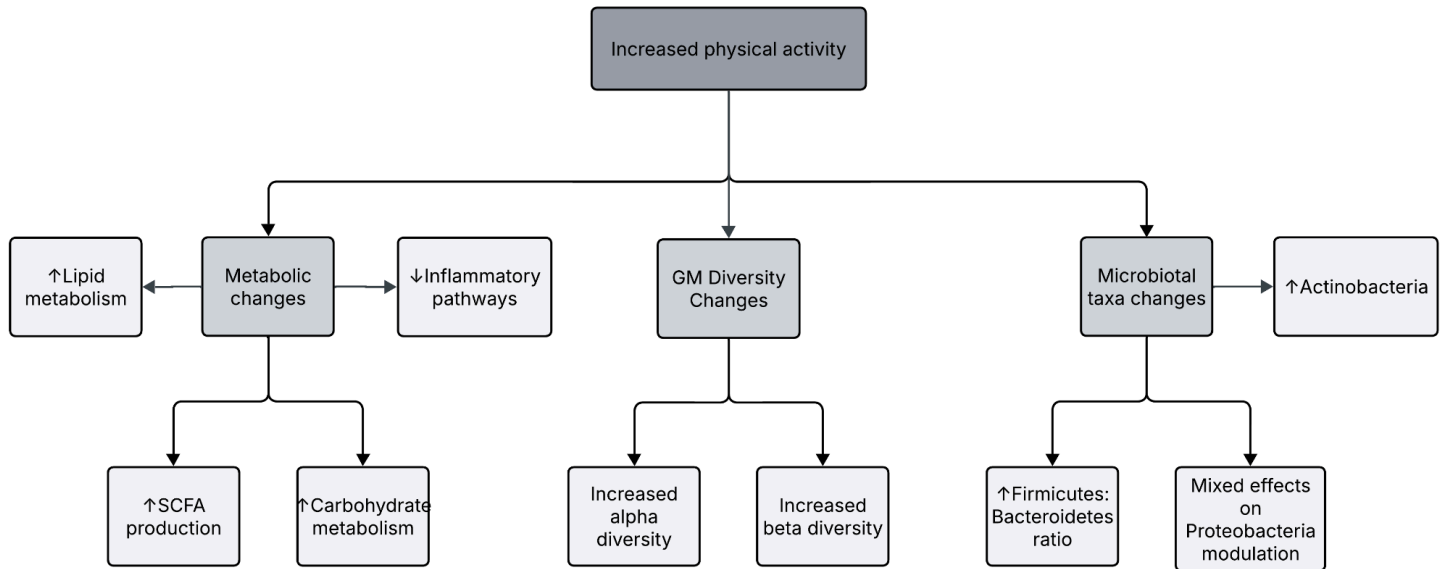


Figure 2

Impacts of increased physical activity on the gut microbiome: a flowchart summarising microbiome changes discussed in this section.

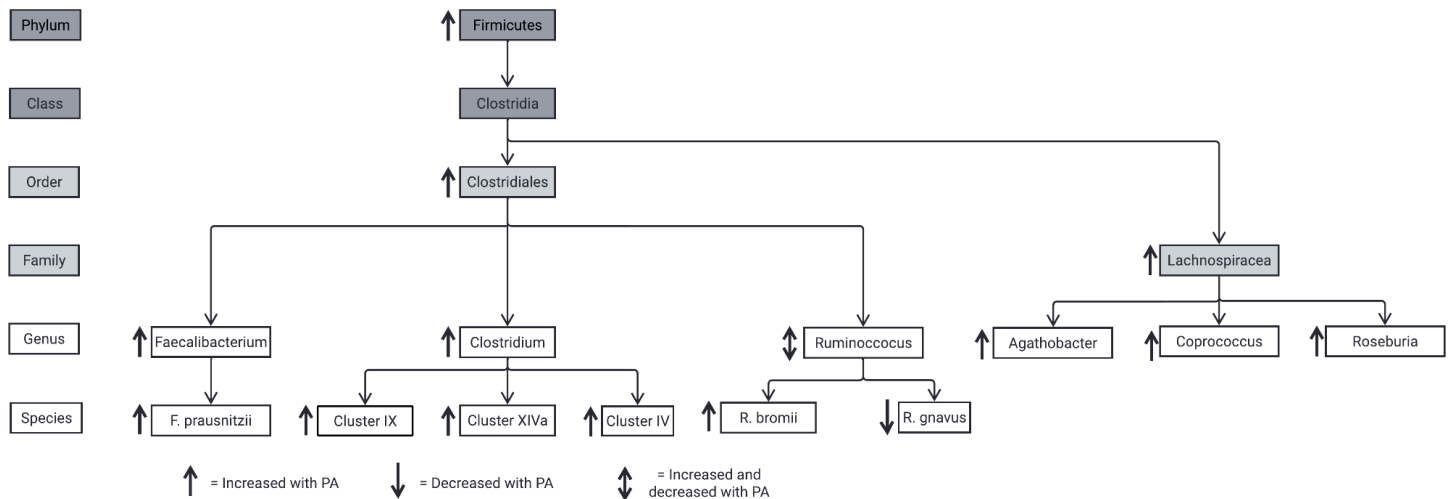


Figure 3

Changes within *Firmicutes* phyla and specific differences in bacterial groups through increased physical exercise observed in cross-sectional studies.