THE IMPACT OF CONGESTED FIXTURES ON THE GUT MICROBIOTA OF ELITE FEMALE FOOTBALL PLAYERS

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A dissertation submitted in partial fulfillment of the requirements for the Degree of Masters in Metabolism and Human Nutrition

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ABBREVIATIONS

FDR	False Discovery Rate
FIFA	Fédération Internationale de Football Association
GPS	Global Positioning System
PCoA	Principal Coordinates Analysis
RPE	Rating of Perceived Exertion
SCFAs	Short-Chain Fatty Acids
SD	Standard Deviation
sRPE	Session-Rating of Perceived Exertion

ABSTRACT

Introduction: Recently, it has been shown that the gut microbiota of athletes changes after periods of intensive acute exercise such as competitive sports events. However, to date, no previous study investigated the impact of a period of fixture congestion on the gut microbiota of male or female football players. As such, and to respond to a scarcity of data regarding the gut microbiota composition of female athletes, this study was conducted to investigate whether the gut microbiota composition of elite female football players is affected by a period of fixture congestion.

Methodology: This study was conducted during the 2019 Algarve Cup and lasted ten days, encompassing three official matches and seven training sessions. The matches were separated by 48-72 hours. Of the 21 elite female football players from the Portuguese women's national football team who agreed to participate, 17 were included in this study. Faecal samples were collected at two time points: at the beginning and end of the tournament. Faecal microbiota was analysed by sequencing the 16S rRNA gene. Throughout the study, the volume (i.e., duration of training sessions and matches) and rating of perceived exertion (RPE) for each player were recorded after training sessions and matches. The internal load was subsequently determined by session-RPE (sRPE).

Results: At the beginning of the tournament, the gut microbiota profiles of players were predominantly composed of bacteria from the genera *Faecalibacterium* (29% of relative abundance), *Collinsella* (16%), and *Prevotella* (13%). Overall, no significant changes were observed from the beginning to the end of the tournament. Also, no relationship was found between any of the exercise parameters assessed and variations in alpha diversity and gut microbiota composition.

Conclusion: To our knowledge, such a considerably high abundance of *Collinsella* is a novelty in research with athletes. Altogether, these findings demonstrate that an eight-day international football tournament with three consecutive matches separated by 48-72 hours does not significantly change the gut microbiota composition of elite female football players. Furthermore, our results support the idea that the gut microbiota of athletes appears resilient to their load and type of training. Future studies are needed to confirm the impact of competing in fixture congestion on the gut microbiota of male football players.

KEY WORDS

Athlete; *Collinsella*; Diet; Exercise; Gut microbiota; Soccer

RESUMO

Introdução: Nos últimos anos, tem vindo a ser demonstrado que a composição do microbiota intestinal de atletas altera-se após períodos de exercício intenso e agudo, tais como eventos desportivos competitivos. No entanto, até à data, nenhum estudo investigou o impacto de um período de calendário congestionado no microbiota intestinal de jogadores ou jogadoras de futebol. Como tal, e para responder à escassez de dados relativos à composição do microbiota intestinal da mulher atleta, este estudo foi conduzido com o objetivo de investigar se a composição do microbiota intestinal de jogadoras de futebol de elite é afetada por um período de calendário congestionado.

Métodos: Este estudo foi realizado durante a Algarve Cup de 2019 e durou dez dias, englobando três jogos oficiais e sete sessões de treino. Os jogos estiveram separados por 48-72 horas. Das 21 jogadoras de futebol de elite da seleção portuguesa de futebol feminino que aceitaram participar, 17 foram incluídas neste estudo. As amostras de fezes foram recolhidas em dois momentos: no início e no final do torneio. o microbiota fecal foi analisada através da sequenciação do gene 16S rRNA. Ao longo do estudo, o volume (ou seja, a duração das sessões de treino e dos jogos) e a perceção subjetiva do esforço (RPE) para cada jogador foram registados após as sessões de treino e os jogos. A carga interna foi subsequentemente determinada por sessão-RPE (sRPE).

Resultados: No início do torneio, o microbiota intestinal das jogadoras era predominantemente composto por bactérias dos géneros *Faecalibacterium* (29%), *Collinsella* (16%) e *Prevotella* (13%). Globalmente, não foram observadas alterações significativas do início para o final do torneio. Também não foi encontrada qualquer relação entre os parâmetros de exercício avaliados e variações na diversidade alfa e na composição do microbiota intestinal.

Conclusão: Para nosso conhecimento, uma abundância relativa tão elevada de *Collinsella* é uma novidade em estudos com atletas. No seu conjunto, estes resultados demonstram que um torneio internacional de futebol com duração de oito dias e três jogos consecutivos separados por 48-72 horas, não altera a composição do microbiota intestinal de jogadoras de futebol de elite. Além disso, os nosso resultados apoiam a ideia de que o microbiota intestinal de atletas aparenta ser resiliente à sua carga e tipo de treino. Assim, são necessários estudos futuros para confirmar o impacto de competir em calendário congestionado no microbiota intestinal de jogadores de futebol.

PALAVRAS-CHAVE

Alimentação; Atleta; *Collinsella*; Exercício; Microbiota intestinal; Futebol

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1 INTRODUCTION

1.1 The Human Gut Microbiota

The human gut harbours a collection of microorganisms that include bacteria, archaea, viruses, fungi, and helminths [1]. The gut microbiota, defined as the assemblage of microorganisms present in the gut, constitutes the largest community in the body, with the highest abundance found in the colon (large intestine) [2, 3]. The gut microbiome comprises the microbiota, structural elements, metabolites, and molecules produced by coexisting hosts and structured by the surrounding environmental conditions [4]. The stability, the resistance to ecological stress, and the ability to recover from a stress-related perturbation (i.e., resilience) are recognised characteristics of health-associated gut microbiota [5, 6]. Besides, another significant property of the gut ecosystem is functional redundancy, which means that species are interchangeable in terms of function [7]. Nevertheless, when the microbial ecosystem is perturbed to the extent that exceeds its resistance and resilience capacities, alterations in its composition and function may occur (i.e., dysbiosis) [8]. The gut microbiota is implicated in several areas that are fundamental to health and, indirectly, to athletic performance, namely energy production [9], immune regulation [10] and defence [11], promotion of the intestinal barrier integrity [12], and reduction of oxidative stress and the exercise-induced inflammation [13].

To date, multiple groups of microbiota-derived metabolites have been identified [14]. Among those, short-chain fatty acids (SCFAs), mainly produced by non-digestible carbohydrates, are the principal end-products [15, 16]. Of all the produced SCFAs, the most abundant are acetate, propionate, and butyrate, accounting for 90-95% of the total [17, 18]. Of the three major SCFAs, butyrate is particularly relevant as it is the preferred energy source for colonocytes [19]. The genus *Faecalibacterium prausnitzii* is one of the butyrate producers found in human faecal samples and uses acetate as the substrate [20]. These metabolites have been associated with various metabolic effects [19], of which the role in energy metabolism is particularly relevant for athletic performance. Suggested essentially by the metabolic link between SCFAs and the skeletal muscle, the existence of a gut-muscle axis has been proposed [13, 21]. Besides, due to this role, SCFAs have been suggested as a possible alternative fuel for endurance exercise, mediated by a direct use in the skeletal muscle [22]. Nevertheless, future research is needed as human research is scarce. In addition to this, another bidirectional crosstalk has been suggested to exist between the gut microbiota and the mitochondria, through which the gut microbiota itself and its by-products, namely SCFAs and secondary bile acids, may regulate energy production [23].

From a different perspective, considering the stress and pressure levels that elite athletes are often subject to, the gut-brain axis can be particularly meaningful. Over the last years, the exercise has been suggested to mediate this connection; nevertheless, the exact causal relationship is still unknown [24]. Notwithstanding, it has been proposed a pathway through which bacteria can influence exercise performance through this crosstalk [24, 25]. Bacterial subproducts can access the brain in various ways, such as the bloodstream [25]. Reversely, stress hormones or sympathetic neurotransmissions during intensive training and competition may influence bacterial gene expression, changing the composition and activity of the gut microbiome [25].

In recent years, due to technical advances, it became possible to study the composition of microbial communities and compare them within and between individuals [26]. Aside from investigating the role of the gut microbiota in human health and disease, literature into gut microbiota and sports have grown exponentially in the last decade. Simultaneously, research with elite athletes emerged, prompting growing public interest in understanding how the gut microbiota could be modulated to enhance athletic performance and recovery.

1.2 The Gut Microbiota of Athletes

The first characterisation of the athletes’ gut microbiota was published in 2014 and was conducted with male rugby players and two control groups – the low and the high body mass index groups [27]. Compared to the low body mass index group, rugby players had lower abundances of the *Bacteroides* and *Lactobacillus* genera. However, compared to the high body mass index group, both the rugby players and the low body mass index group had higher proportions of the genus *Akkermansia*. Later, Barton et al. [28] investigated the metabolic activity of the gut microbiota of the same groups. Results revealed that the athletes had relative increases in diverse pathways, such as carbohydrate metabolism and faecal metabolites, namely the microbial-derived SCFAs. This subsequent study confirmed the results of the former and revealed a greater separation between athletes and controls at the metagenomic and metabolic levels.

Most studies conducted to date are cross-sectional, essentially focusing on characterising athletes’ gut microbiota, comparing them with healthy sedentary individuals. The composition and functionality of the gut microbiome of athletes from diverse sports and nationalities are already known [27-34]. However, despite some significant findings, knowledge in this field is still limited. A frequent outcome is that athletes, compared to healthy sedentary controls, have a higher abundance of health-promoting bacterial species and a greater microbial diversity [27, 31, 33], which is considered beneficial as it seems to be associated with the stability and resilience of the ecosystem [35]. However, increased diversity has also been associated with increased proteolytic fermentation by gut bacteria in athletes [36]. While it is true that low diversity indexes have been linked to disease states [37, 38], in many cases, much context is needed for interpreting such values [39]. Also, technical differences between laboratories may cause significant differences in the observed diversity [40].

Sports nutrition is an evolving area, and more than ever, it is acknowledged that an athlete's diet must supply the nutritional demands of the sport being practised and the athletes' goals [41]. As a result, athletes from different sports may have distinct dietary patterns. For example, Jang et al. [34] showed that athletes' sport (bodybuilding, distance running) was associated with their diet, particularly the proportion of macronutrients. Upon comparing the gut microbiota of these athletes with that of healthy sedentary individuals, the authors observed that certain beneficial bacteria widely used as probiotics and some SCFAs producing bacteria were the lowest in bodybuilders. Besides, distance runners had a negative correlation between protein intake and the Shannon's diversity index. Such findings are of particular interest considering the overall beneficial composition that has been found in the gut microbiota profiles of athletes, as it suggests that the eating patterns of some athletes may not promote a gut microbiota associated with health. Apart from the impact on the gut microbiota, poor nutrition in conjunction with inadequate recovery from training and competition may jeopardise athletes' health and physical performance [42]. Therefore, diet is a critical factor to consider when investigating the athlete's gut microbiota, essentially due to the magnitude of the impact of diet in shaping the gut microbiota [43, 44], but also due to the challenging task of controlling or even changing an athletes' diet for research projects. Recently, Murtaza et al. [30] studied the impact of distinct dietary patterns (*High Carbohydrate* diet; *Periodised Carbohydrate* diet; *Ketogenic Low Carbohydrate High Fat* diet) on the gut microbiota of elite race walkers during a three-week intensified training program. The *Ketogenic Low Carbohydrate High Fat* diet was associated with a decrease in the relative abundance of *Faecalibacterium* and an increase in *Bacteroides* and *Dorea*. Besides, the relative abundance of *Bacteroides* correlated negatively with fat oxidation, whereas the relative abundance of *Dorea* correlated negatively with an economy test. Overall, dietary patterns appear to exert a subtle but meaningful change in an athlete's gut microbiota profile.

1.3 The Impact of Exercise and Competitive Sports Events on the Gut Microbiota

Recently, several studies have evaluated the response of the gut microbiota to competitive sports events. For example, Scheiman et al. [45] studied the gut microbiota of marathon runners before and after the 2015 Boston Marathon. Results showed an increase in the relative abundance of *Veillonella*, a lactate utiliser, in the post-race period. Besides, in an athlete cohort, the same research group observed an increase in the relative abundance of genes encoding enzymes involved in the methylmalonyl-coenzyme A pathway after exercise, which correlated with an increased relative abundance of *Veillonella* species. This pathway is the one through which *Veillonella* converts lactate into propionate [45]. Posteriorly, the same researchers conducted a mouse experiment to assess whether these findings had any benefits on performance. With this experiment, published in the same research paper as the former [45], the authors observed that mice gavaged with *Veillonella atypica* had longer running times. Hence, since its publication, this study by Scheiman et al. [45] has sparked public and scientific interest in this field, as it was the first to suggest a mechanism by which the gut microbiome could enhance exercise performance. More in-depth discussion and comments on this research can be found elsewhere [46-48]. Subsequently, Grosicki et al. [49] examined changes in the gut microbiota of a male world-class ultramarathon runner before and after a 163 km mountain footrace. Alpha diversity oscillated throughout the study, decreasing after 19 weeks of specific race preparation but increasing two hours post-race. Also, two hours post-race, the authors observed a 69% reduction in the relative abundance of Bacteroidetes. In addition, the authors observed increases in the relative abundance of the *Haemophilus*, *Veillonella*, and *Streptococcus* genera. Although it is a case study, this research has shown that the gut microbiota can change rapidly and pronouncedly after acute strenuous exercise. Still concerning runners, but in research with healthy amateurs, Zhao et al. [50], through a combined analysis of the faecal metabolites and microbiome, reported that after a half-marathon, the gut microbes could rapidly respond to the altered faecal metabolites by adjusting some bacterial taxa, which highlights the health-promoting benefits of exercise. Also, Keohane et al. [51] studied the response of the gut microbiota of four well-trained males to a 5000 km transoceanic rowing race. Alpha diversity increased throughout the event. Besides, the authors observed an increase in the abundance of butyrate-producing species (e.g., *Roseburia hominis*) and species associated with improved metabolic health (e.g., *Dorea longicatena*). The authors also reported that many of the observed adaptations persisted after three months. Notwithstanding, the exercise stimulus in this study was beyond the one to which most athletes are exposed.

Aside from the influence of diet and strenuous competitive sports events, the impact of different types of sports on the gut microbiome has also been investigated. O'Donovan et al. [32] recruited athletes from various sports and grouped them based on the dynamic and static components of the sport to assess if the gut microbiome differed across sports classification groups. The main findings of this study were that the differences observed in the gut microbiome and metabolome between groups happened in the absence of significant differences between any nutrients or food groups between sports groups.

Overall, these data suggest that intensive exercise can change the gut microbiota on its own. Furthermore, it appears that an athlete's gut microbiota is conditioned by the characteristics of the sport played. However, many questions remain. For example, which exercise (e.g., type, frequency, mode, intensity, or duration) induces most changes, and the mechanisms by which exercise alters the microbiota [52].

1.4 Sex Differences in Gut Microbiota

Lately, sex-related differences in gut microbiota have been suggested, and although the magnitude of the effect is still unclear, it should not be overlooked [53]. There appear to be several ways in which the sex of the host shapes its gut microbiota, notably through sex hormones which may have an important role [54]. Regarding data from research with the athletic population, little is known about sex-related differences. Lately, many investigations have recruited male and female athletes [29, 31-33, 55, 56]; however, no significant differences have been found, and results are often reported collectively, which can confound the outcomes. To date, very few have exclusively characterised the gut microbiota of healthy active women [57] or female athletes [58]. In a very recent review by Pugh et al. [59], female-specific considerations concerning gastrointestinal function were discussed, such as those related to the gut microbiome.

1.5 Women's Football and Fixture Congestion

Women's football is becoming increasingly popular worldwide, with a growing number of registered players and national teams [60]. Moreover, as women's football continues to develop and grow, new official competitions will emerge, filling and strengthening their competitive calendar [61]. As a result, the likelihood of competing in fixture congestion (i.e., multiple matches played with short rest periods in between) will increase. From the perspective of physical activities and technical performance, research with male football players suggests that competing under such conditions is not likely to impact the total distance covered [62]. Similarly, among elite female football players, Póvoas et al. [63] did not observe considerable alterations in plasma stress markers, physical load, and technical performance after four consecutive football matches separated by 48-72 hours, during a Fédération Internationale de Football Association (FIFA) tournament. As mentioned previously, the gut microbiota has been shown to adapt to periods of intensive exercise and rapidly change its composition seemingly favourably. However, to the best of our knowledge, despite being an increasingly frequent occurrence in football, the impact of a fixture congestion period on the gut microbiota has not been previously assessed. Also, the study of this thematic in female athletes is innovative and needed.

Therefore, the main objective of this study was to investigate whether the gut microbiota composition of elite female football players is affected by a period of fixture congestion. To this end, we analysed the gut microbiota composition of elite female football players before and at the end of the 2019 Algarve Cup, an eight-day international football tournament with three consecutive matches separated by 48-72 hours. Based on previous research, we hypothesised that by the end of the international football tournament, the gut microbiota profiles of these players would change as a response to the intensive exercise stimuli.

2 AIMS

2.1 Main Aims

The present study aimed to investigate if the 2019 Algarve Cup, an eight-day international football tournament with three consecutive matches separated by 48-72 hours, changes the composition of the gut microbiota of elite female football players.

2.2 Secondary Aims

The secondary aims of this study are as follows:

- To review the current literature on the impact of exercise on the gut microbiota;
- To analyse the composition of the gut microbiota of elite female football players at baseline (i.e., ahead of a period of fixture congestion) and end of an eight-day international tournament;
- To assess the volume and load of the training sessions and matches of elite female football players during an eight-day international tournament;
- To compare the gut microbiota composition of elite female football players at the end of an eight-day international tournament with the baseline profiles;
- To evaluate the relationship between variations in the gut microbiota composition of elite female football players and the volume and load of their training sessions and matches during an eight-day international tournament;
- To measure the dietary intake of elite female football players during an eight-day international tournament;
- To conclude if an eight-day international football tournament changes the composition of the gut microbiota of elite female football players.

3 METHODOLOGY

3.1 Study Design and Participants

The present study was conducted during the 26th edition of the Algarve Cup (27th February to 6th March 2019) and the respective preparation period (25th and 26th February 2019) (**Figure 1**). The Algarve Cup is a worldwide women's football tournament that has been held annually in Algarve (Portugal) since 1994. The study encompassed seven training sessions and three official matches. Twelve senior national teams (Canada, China, Denmark, Iceland, Netherlands, Norway, Poland, Portugal, Scotland, Spain, Sweden, Switzerland) participated in the 2019 Algarve Cup. All elite female football players from the Portugal women's national football team (*n* = 22) were invited to participate in the present study. The players were approached by a researcher who provided them with oral and written information about the study.

The exclusion criteria were antibiotic treatment within the previous three months and the presence of gastrointestinal co-morbidities or cardiovascular disease from the time of faecal sample collection. Written informed consent was obtained from all participants. The study was approved by the Ethical Committee of the NOVA Medical School | Faculdade de Ciências Médicas, Universidade NOVA de Lisboa (109/2018/CEFCM).

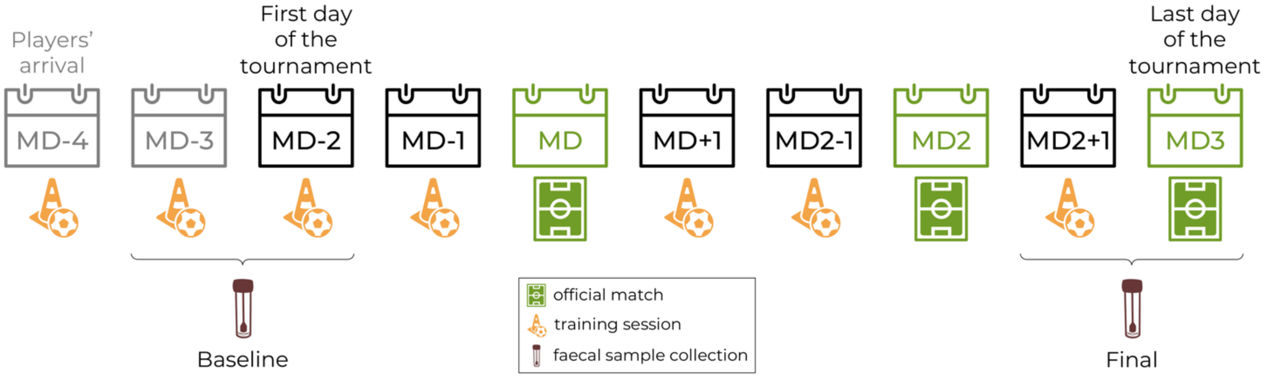

Figure 1. Study design timeline.
The study lasted ten days, the last eight days corresponding to the 2019 Algarve Cup. Overall, the study encompassed seven training sessions and three official matches. The Baseline faecal samples were collected between the 2nd (MD-3) and 3rd (MD-2) day of the study. The Final faecal samples were collected between the 9th (MD2+1) and 10th (MD3) day of the study, before the 3rd match.

3.2 Anthropometric Measurements and Body Composition

Body composition was measured at the beginning of the study using the InBody® 270 (InBody Co., Ltd., Korea) in a fasted state (> 10 hours) and with minimal clothing. The height was measured using a seca® stadiometer (seca GmbH & Co. KG, Germany) according to the protocol of the International Society for the Advancement of Kinanthropometry [64]. At the end of the study, the weight was measured again.

3.3 Training Sessions and Matches

Around 15-30 minutes, after each training and match session, participants were asked to score their rating of perceived exertion (RPE) using the Borg's category ratio-scale (CR-10) [65] modified by Foster et al. [66], as previously performed by Costa et al. [67]. All participants had been familiarised with this scale for rating perceived exertion before the beginning of the study. The session-RPE (sRPE) was subsequently determined by multiplying the RPE by the training or match session duration; the sRPE has been previously shown to be a good indicator of the global internal load of male football training [68] and later of female football players [67].

Training sessions and matches were also analysed with Global Positioning System (GPS) units (Apex, STATSports, Ireland). The variables measured were total distance covered (m), relative distance covered per minute (m/min), and distances in different speed zones (13-15.9 km/h; 16-17.9 km/h; and 18 km/h). Sprints were measured by frequency, the average time interval, and the average distance covered [69]. Due to the reduced data available (less than five out of the ten days) for 29% (n = 5) of the participants, data obtained from the GPS units were exclusively used to characterise the training sessions and matches globally and is available as a supplement to this study (APPENDIX A: GPS Data).

3.4 Dietary Assessment

Dietary intake was assessed using food records. Participants were asked to fill by hand ten 24-hour food records corresponding to the whole period of the study, from arrival (25th February) until the last day of the tournament (6th March). A trained nutritionist gave them detailed oral and written instructions on how to fill out food records, including estimating portion sizes. Participants were instructed to describe the foods, fluids, and dietary supplements consumed, estimate the amount ingested using standardised household measures or record the weight or volume, and annotate the commercial name of packed food. Each morning, participants handed the paper record of the previous day filled and received the next to avoid mixing the days. Data obtained from the food records were transformed into energy and nutrients using ESHA's Food Processor® Nutrition Analysis software, version 11.5 (Salem, OR). Data were subsequently imported into the SPSS® software v26 (IBM SPSS Statistics corporation, Chicago, IL, USA) for analysis. To further explore participants' dietary intake during the study, food groups created were as follows: Fruits and Vegetables, including fresh fruits and raw and cooked vegetables; Legumes; Cheese and Yoghurt; and Red Meat. The recommendations proposed by Rocha-Rodrigues et al. [70], Dobrowolski et al. [71], and Collins et al. [72] were considered for the evaluation of the adequacy of the macronutrient intake of study participants. These recommendations reflect the current evidence on the macronutrient recommendations for female athletes, female football players, and football players in general, respectively.

The dietary assessment was carried out to monitor and assess qualitatively and quantitatively the participants' dietary and nutritional intake during the tournament. However, given the results obtained and the availability of this data, it was considered relevant to assess the existence of relationships between the participants' daily consumption of certain nutrients (protein; carbohydrates; fat; saturated sat; polysaturated fat; monosaturated fat; trans fat; fibre) and food groups (fruits and vegetables; legumes; cheese and yoghurt; red meat) and some bacterial taxa. Due to their relevance in this study, the *Faecalibacterium* and *Collinsella* genera were considered. Thus, the relationship between their relative abundance and every nutrient and food group pointed above was tested. Additionally, based on scientific literature [73], the relationship between the relative abundance of *Prevotella* and the daily consumption of carbohydrates, fibre, and fruits and vegetables was computed. Based on the results obtained in this study (i.e., no significant differences from baseline to the end of the tournament) and the fact that food records were collected daily between the two faecal collections, it was considered the relative abundance at the end of the tournament. No further analysis was carried out as the dietary assessment was not undertaken for this purpose.

3.4.1 Identifying Records of Poor Validity: Under- and Over-Reporting

In this study, to identify under- and over-reporting, the ratio energy intake to basal metabolic rate was used [74]. The energy intake was obtained from the analysis of the food records, whereas the basal metabolic rate was estimated by the InBody® 270

(InBody Co., Ltd., Korea). The under-reporting cut-off was set at 1.1 [75], and the over-reporting cut-off was set at 4. An over-reporting cut-off of 4 corresponds to the upper limit of the physical activity level for professional endurance athletes [76]; as such, it is unreasonable for elite female football players to have such a high energy intake.

3.5 Faecal Sample Collection and Processing

The days of collection of the faecal samples are illustrated in **Figure 1**. Participants were asked to collect their faecal samples with the faecal collection kit (EasySampler®, ALPCO) provided the night before and stored in a tube containing RNAlater® (Sigma-Aldrich). Samples were kept at -20°C until DNA extraction. Genomic DNA was extracted and purified from faecal samples using NZY Tissue gDNA Isolation Kit (NZYTech) as previously described by Marques et al. [77].

All 16S DNA libraries (V3 and V4 regions) were prepared, sequenced, and analysed according to the manufacturer's instructions for each kit and instrument. Briefly, 16S DNA libraries were prepared using the Ion 16S^{TM} Metagenomics Kit (Thermo Fisher Scientific) targeted panel, and each sample was individually identified with the Ion Xpress^{TM} Barcode Adapters Kit (Thermo Fisher Scientific). The amplified fragments were prepared for sequencing using the Ion CHEF^{TM} system (Thermo Fisher Scientific) and loaded into Ion 318^{TM} Chip Kit v2 BC (Thermo Fisher Scientific). Sequencing runs were performed on an Ion Personal Genome Machine® (PGM^{TM}) System (Thermo Fisher Scientific), aiming for a mean sequencing depth coverage of 10000x. The taxonomy of each sample was determined using the software Kraken and further improved using the software Bracken, using a custom 16S database (GutHealth_DB). This database was manually curated by enriching GreenGenes (versions 13_5 and 13_8) with clinically relevant taxa from NCBI RefSeq 16s rRNA sequences (04/2019). The GutHealth_DB currently holds 4765 16S rRNA sequences mapping 1822 species, 1685 genera, 515 families, 404 orders, 248 classes and 89 phyla, and is available upon request.

3.6 Bioinformatic Analysis

The microbiome data analysis was performed using Microbiome Analyst – a web-based tool for comprehensive statistical, visual, and meta-analysis of microbiome data [78]. All features were included in the analysis regardless their prevalence in the samples. Nevertheless, the percentage of features to remove based on low variance was set to 10%, using the interquartile range. The number of features remaining after data filtering were as follows: phyla (n = 79), genera (n = 247), and species (n = 125). No normalisation of the data was performed.

Alpha diversity was measured by Shannon's diversity index. Alpha diversity summarises both the species richness (total number of species) and evenness (abundance distribution across species) within a sample [79].

The *Beta-diversity analysis* function in Microbiome Analyst was used to create the Principal Coordinates Analysis (PCoA) plot based upon Bray-Curtis dissimilarity to evaluate differences in the community of bacterial species according to the experimental factor – Timing (Baseline and Final). The distances (or dissimilarity) between samples of the same group were compared to the distances between groups using the PERMANOVA test [78].

The *Pattern Search* function in Microbiome Analyst, using Spearman's rank correlation as the *Distance measure*, was used to identify the top phyla, genera, and species most correlated with the fixture congestion period [78].

3.7 Statistical Analysis

Statistical analysis was carried out using SPSS® software, v26 (IBM SPSS Statistics corporation, Chicago, IL, USA). Shapiro-Wilk's test indicated that the participant characteristics data were normally distributed ($p \geq 0.05$); thus, descriptive statistics were presented as means and standard deviations (SDs), and the paired samples t-test was used to compare the body mass at baseline with the end of the tournament. Values of $p < 0.05$ were considered statistically significant. The results of the other variables (gut microbiota analysis, exercise outcomes, and nutritional data) were presented as medians (Q_1; Q_3). The Wilcoxon signed-rank test was used to compare the gut microbiota composition at baseline with the end of the tournament (relative abundance of phyla, genera, and species; the Firmicutes to Bacteroidetes ratio; the *Bacteroides* to *Prevotella* ratio; the number of observed genera and species; alpha diversity). Spearman's rank correlation (r_s) was used to assess the relationship between the variation in the gut microbiota composition and the total exercise volume and sRPE. The variation variable was calculated by subtracting the relative abundance of taxa at baseline from the relative abundance at the end of the tournament. Spearman's rank correlation was also used to assess the relationship between the daily consumption of certain nutrients and food groups and the relative abundance of the three most abundant bacterial genus at the end of the tournament. Benjamini and Hochberg's procedure was applied for multiple testing correction, and the false discovery rate (FDR) adjusted *p*-values were reported. FDR-adjusted *p*-values lower than 0.05 were assumed to be statistically significant.

4 RESULTS

4.1 Characteristics of Study Participants

Out of the 22 players approached and potentially eligible, 95% (*n* = 21) agreed to participate; from these, 19% (*n* = 4) were excluded. The reasons for exclusion were as follows: one of the two faecal samples required was not collected (*n* = 2); the player left the tournament due to illness (*n* = 1) or injury (*n* = 1). Thus, the final sample comprised 17 elite female football players. Participant characteristics are presented in **Table 1**. No significant difference in participants' body mass (mean difference = -0.0 ± 0.2 kg; *p* = 0.600) was found between the two time points.

Table 1: Participant Characteristics.

Characteristic	**All Participants (*n* = 17)**
Age (y)	24.1 ± 3.4
Height (cm)	167.0 ± 4.0
Body mass (kg)	59.9 ± 6.4
Body mass index ($kg.m^{-2}$)	21.4 ± 1.7
Total body water (kg)	36.2 ± 2.7
Body fat mass (kg)	10.2 ± 3.7
Body fat (%)	16.7 ± 4.5
Skeletal muscle mass (kg)	27.8 ± 2.3
Basal metabolic rate (kcal)	1442 ± 82

Values are expressed as mean ± SD (Standard Deviation).

4.2 Training Sessions and Matches

During the study, the training and match volume (i.e., duration) and RPE of each training session and match were recorded, and the sRPE was calculated. The training and match volume, RPE, and sRPE are presented in **Table 2**.

Whenever possible, GPS units were used. The variables measured with the GPS units and the respective data are shown in **Supplementary Table 1**.

Table 2: Volume, RPE and sRPE of training sessions and matches.

Day	**Volume** (min)	RPE	sRPE
MD-4	80 (80; 80)	3 (3; 4)	240 (240; 320)
MD-3	80 (80; 80)	4 (3; 4)	320 (240; 320)
MD-2	100 (100; 100)	4 (3; 4)	400 (300; 400)
MD-1	80 (80; 80)	3 (3; 4)	240 (200; 280)
MD	70 (0; 90)	6 (0; 9)	460 (0; 765)
MD+1	60 (60; 80)	2 (1; 4)	120 (75; 300)
MD2-1	60 (45; 60)	3 (2; 3)	180 (90; 180)
MD2	46 (0; 90)	6 (0; 9)	276 (0; 599)
MD2+1	45 (45; 65)	2 (1; 3)	90 (56; 195)
MD3	45 (0; 90)	5 (0; 10)	225 (0; 855)

MD, Match Day; RPE, Rating of Perceived Exertion; sRPE, Session-RPE. Values are expressed as median (Q_1; Q_3). Data were available for all participants (*n* = 17) except for the RPE scores of MD3, in which only data for 76% of participants (*n* = 13) was available. The sRPE was determined by multiplying the volume (i.e., duration) of the training sessions and matches by the respective RPE.

4.3 Nutritional Data

Estimated daily energy and macronutrient intakes in participants during the study and comparison with general recommendations are provided in **Table 3.** The estimated daily consumption of food groups is provided in **Table 4**. For statistical analysis, the first and last food records collected, corresponding to travelling days, were excluded since it does not reflect a typical dietary intake day. Besides, 2 out of 17 players were excluded due to under-reporting (*n* = 1) and incomplete fulfilment (*n* = 1; 2 full days out of 8), which was not representative of their dietary intake during the study.

Table 3: Estimated daily energy and macronutrient intakes in participants during the study and comparison with general recommendations.

Macronutrients	Median (Q_1; Q_3)	General Recommendations	
Energy (kcal)	2416 (1943; 2654)		
Protein (g)	142.8 (116.1; 149.7)		
Protein (g/kg)	2.2 (1.7; 2.7)	1.2-2.0 (1)	
Fat (g)	82.8 (60.7; 96.4)		
Total energy from fat (%)	30.0 (27.8; 34.9)	20-30 (2)	
Saturated fat (g)	26.8 (23.6; 34.3)		
Monosaturated fat (g)	28.4 (21.9; 36.1)		
Polyunsaturated fat (g)	12.7 (9.8; 16.7)		
Carbohydrate (g)	268.4 (213.8; 339.0)		
Sugar (g)	98.8 (84.3; 120.3)		
Carbohydrate (g/kg)	4.2 (3.8; 5.9)	6-8 In-season training (congested fixture periods) (3a)	7-12 (High intensity training program or match preparation) (3b)
Fibre (g)	22.4 (12.4; 34.0)	25 (4)	

Data are presented as median (Q_1; Q_3). Only data for 15 participants was available. Out of the 8 days of the study, the number of food records filled were as follows: 8 (*n* = 11), 7 (*n* = 3), and 5 (*n* = 1) records.

(1) The recommendation for protein (g/kg) was taken from Rocha-Rodrigues et al. [70].

(2) The recommendations for the percentage of energy from fat was taken from Dobrowolski et al. [71].

(3a) The recommendation for carbohydrate (g/kg) was taken from Collins et al. [72].

(3b) The recommendation for carbohydrate (g/kg) was taken from Dobrowolski et al. [71].

(4) The recommendation for fibre was taken from the EFSA Panel on Dietetic Products, Nutrition, and Allergies [80].

Table 4: Estimated daily intake of food groups in study participants.

Food Groups	Median (Q_1; Q_3)
Fruits and Vegetables (g)	524.5 (366.3; 853.0)
Legumes (g)	34.5 (14.7; 77.1)
Cheese and Yoghurt (g)	74.0 (54.0; 188.2)
Red Meat (g)	126.8 (82.8; 161.7)

Data are presented as median (Q_1; Q_3). Only data for 15 participants was available. Out of the 8 days of the study, the number of food records filled were as follows: 8 (*n* = 11), 7 (*n* = 3), and 5 (*n* = 1) records.

4.4 Gut Microbiota Composition

4.4.1 Changes in gut microbiota composition after a period of fixture congestion

4.4.1.1 At the phylum level

When examining the overall composition of the gut microbiota at baseline, the most abundant bacterial phyla were Firmicutes (50%), followed by Bacteroidetes (28%) and Actinobacteria (19%). Similarly, at the end of the tournament, the overall most abundant bacterial phyla were Firmicutes (52%), followed by Bacteroidetes (31%) and Actinobacteria (14%). The graphic representations of the topmost dominant bacterial phyla at baseline and end of the tournament are provided in **Figure 2**. The complete list of phyla relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final) is available in **Supplementary Table 2**.

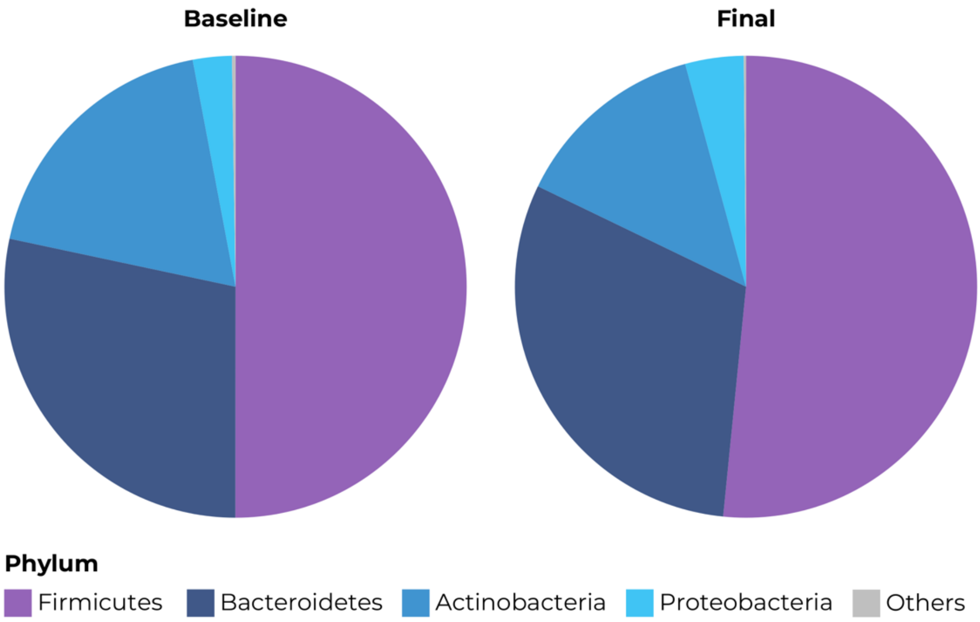

Figure 2. Phyla relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).
Sections represent the average of each phylum relative abundance. Each phylum is represented by a different colour. All phyla with a relative abundance below 1% were grouped into *Others*.

When examining the individual composition of the gut microbiota at baseline, the relative abundance of Firmicutes ranged from ~31% to ~74%, the relative abundance of Bacteroidetes ranged from ~13% to ~61%, and the relative abundance of Actinobacteria ranged from ~4% to ~29%. At the end of the tournament, the relative abundance of Firmicutes ranged from ~26% to ~65%, the relative abundance of Bacteroidetes ranged from ~14% to ~68%, and the relative abundance of Actinobacteria ranged from ~2% to ~29%. The relative abundance of the topmost dominant bacterial phyla per participant at baseline and end of the tournament is illustrated in **Figure 3**.

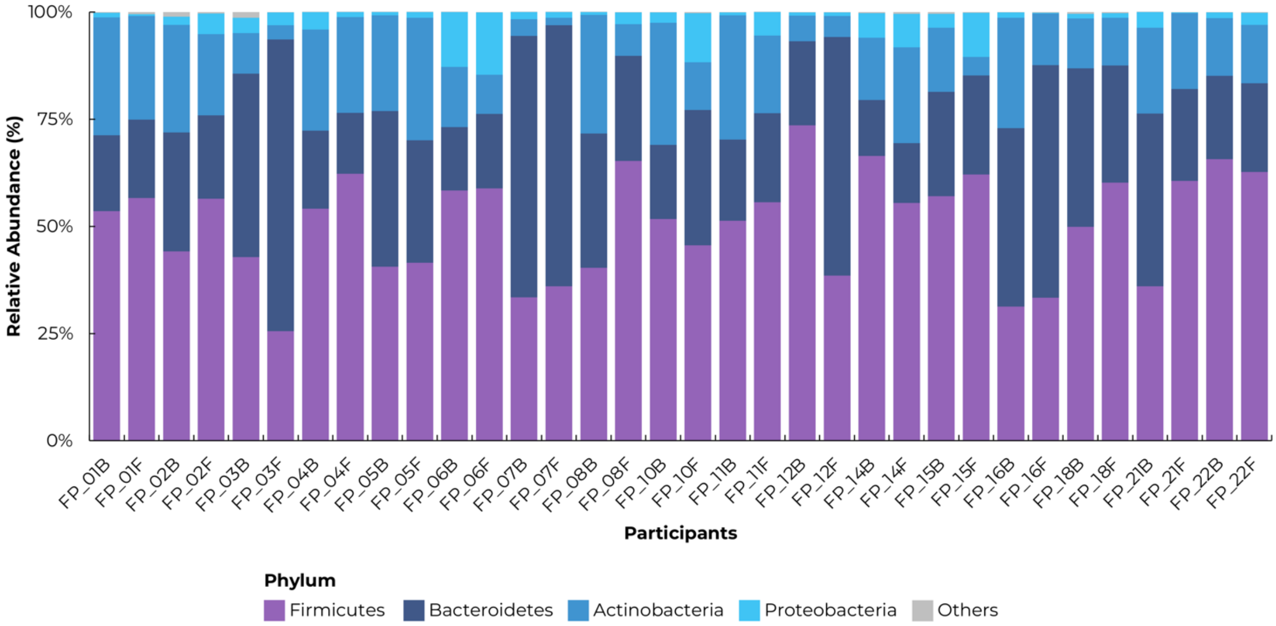

Figure 3. Phyla relative abundances across all participants' samples.
Each sample is represented by one bar. Bars represent each phylum relative abundance. Each phylum is represented by a different colour. Baseline samples are identified with the letter *B* whereas samples from the end of the tournament are identified with the letter *F*. All phyla with a relative abundance below 1% were grouped into *Others*.

The Firmicutes to Bacteroidetes ratio at baseline and end of the tournament are illustrated in **Figure 4**. No significant difference was found between the two time points [Baseline = 2.340 (1.058; 3.200) vs Final = 2.682 (1.069; 3.071); FDR-adjusted *p* = 0.896].

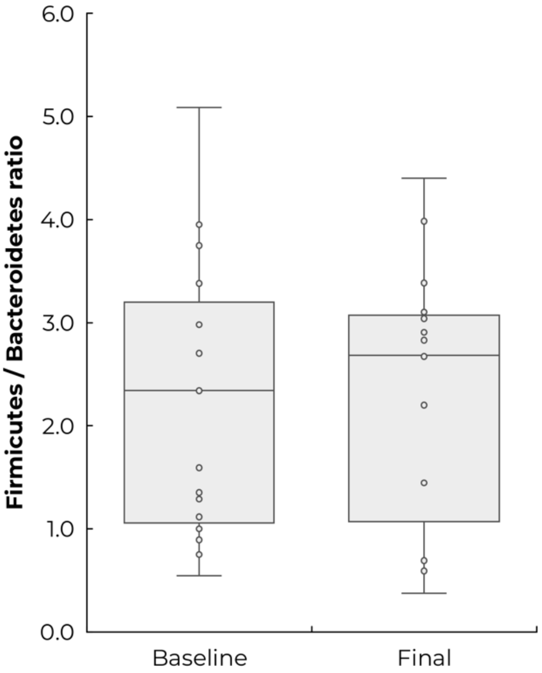

Figure 4. Boxplot of the Firmicutes to Bacteroidetes ratio at baseline (Baseline) and end of the tournament (Final).

The inside line represents the median; the box, the interquartile range; and the whiskers, the highest and lowest values. Each point represents a sample. No significant difference was found between the two time points (FDR-adjusted *p* = 0.896).

After adjusting for multiple comparisons, no significant differences were found between the two time points for any phylum (FDR-adjusted $p \geq 0.05$). Notwithstanding, the results suggest that there is a trend towards a reduction in the relative abundance of Actinobacteria from baseline to the end of the tournament [Baseline = 20% (13%; 27%) vs Final = 12% (6%; 21%); non-adjusted $p = 0.013$; FDR-adjusted $p = 0.575$].The *p*-values obtained by the Wilcoxon signed-rank tests and the respective FDR-adjusted *p*-values are presented in **Supplementary Table 6**. The top 17 phyla correlated with the fixture congestion period are illustrated in **Figure 5**.

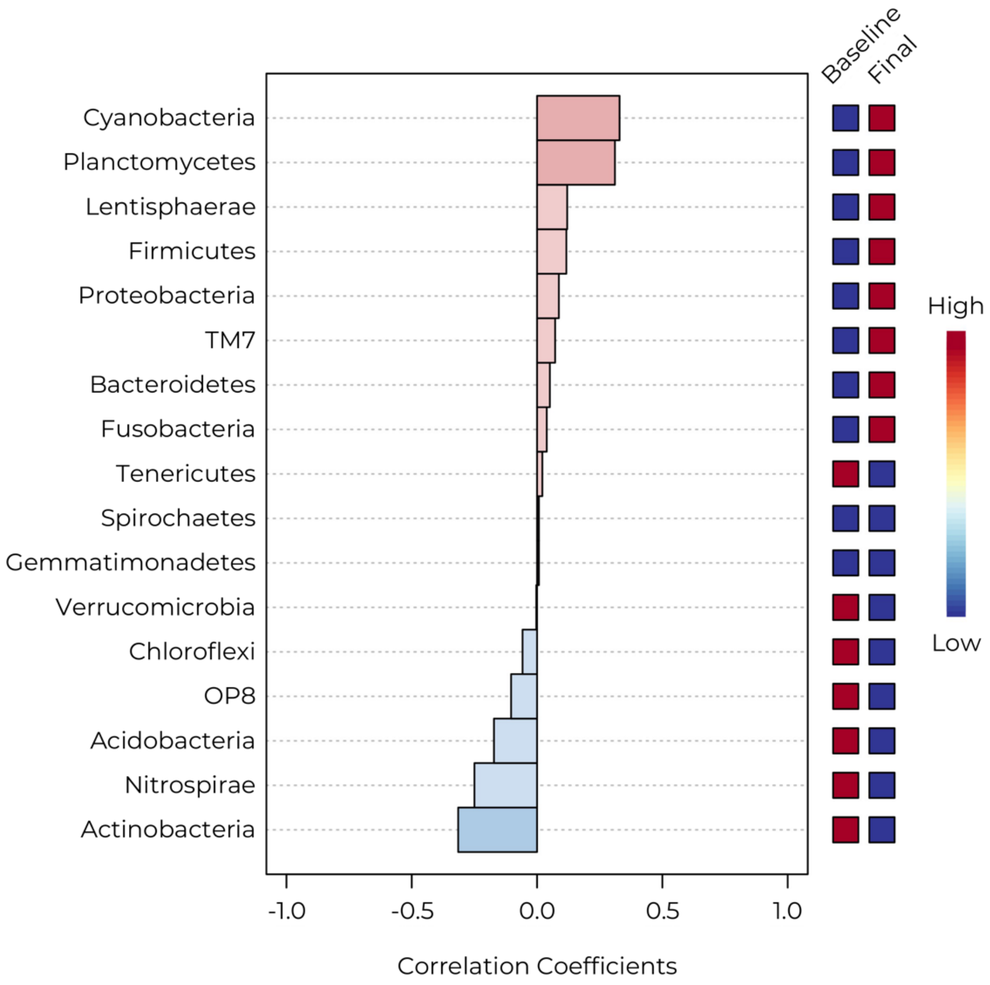

Figure 5. Top 17 phyla correlated with the fixture congestion period.
Phyla are ranked by their correlation. Red and blue denote positive and negative correlations, respectively. The intensity of the colours represents the degree of association between the phyla abundances and the fixture congestion period as measured by Spearman's rank correlation. The heatmap shows whether the phyla abundance is higher (red) or lower (blue) in each time point.

4.4.1.2 At the genus level

The number of observed genera at baseline and end of the tournament are illustrated in **Figure 6**. No significant difference was found between the two time points [Baseline = 123 (103; 164) vs Final = 125 (101; 143); FDR-adjusted *p* = 0.959].

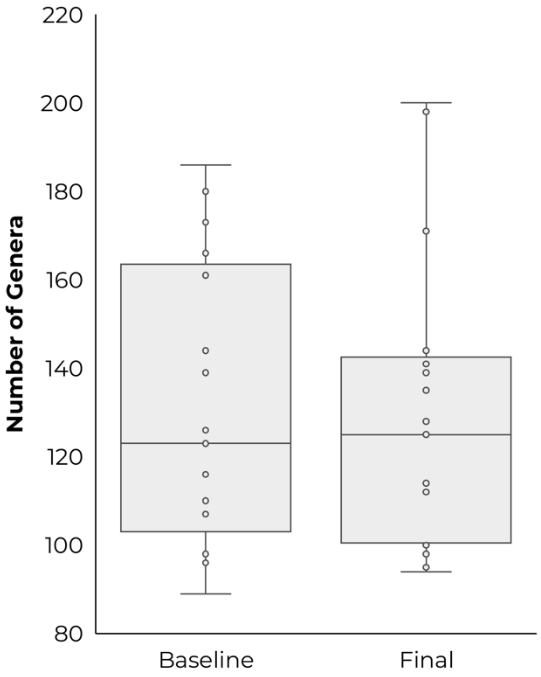

Figure 6. Boxplot of the number of observed genera at baseline (Baseline) and end of the tournament (Final).
The inside line represents the median; the box, the interquartile range; and the whiskers, the highest and lowest values. Each point represents a sample. No significant difference was found between the two time points (FDR-adjusted *p* = 0.959).

At baseline, the overall most abundant bacterial genera were *Faecalibacterium* (29%), followed by *Collinsella* (16%) and *Prevotella* (13%). At the end of the tournament, the overall most abundant bacterial genera were *Faecalibacterium* (29%), followed by *Prevotella* (17%) and *Collinsella* (12%). The graphic representations of the topmost dominant bacterial genera at baseline and end of the tournament are provided in **Figure 7**. The complete list of genera relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final) is available in **Supplementary Table 3**.

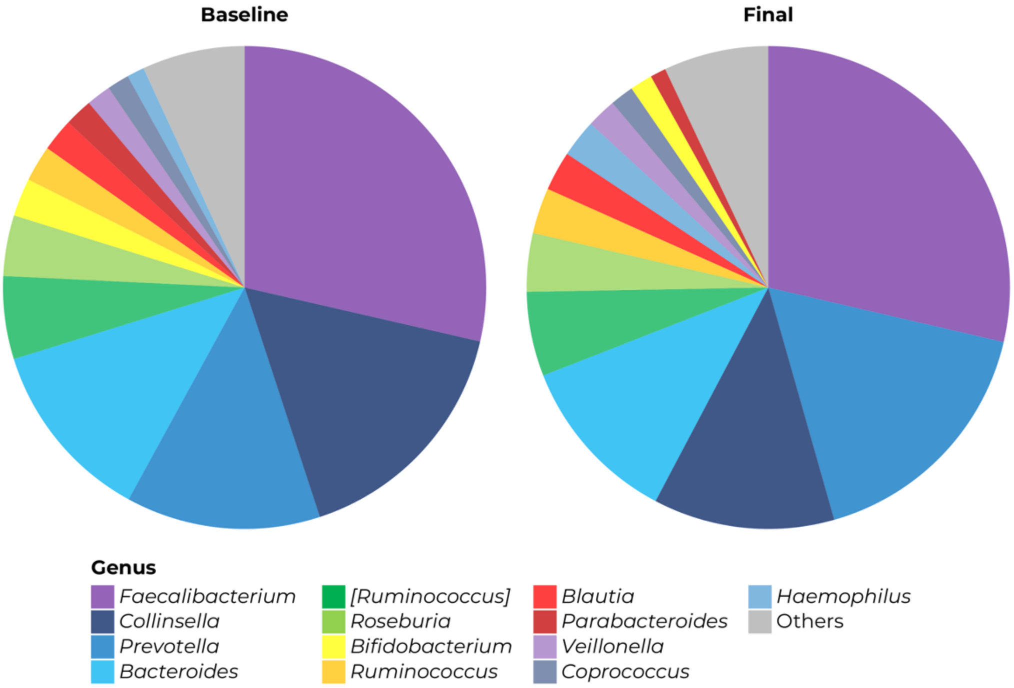

Figure 7: Genera relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).
Sections represent the average of each genus relative abundance. Each genus is represented by a different colour. All genera with a relative abundance below 1% were grouped into *Others*.

At baseline, the relative abundance of *Faecalibacterium* ranged from ~13% to ~50%, the relative abundance of *Collinsella* ranged from ~4% to ~26%, and the relative abundance of *Prevotella* ranged from ~0% to ~46%. At the end of the tournament, the relative abundance of *Faecalibacterium* ranged from ~10% to ~43%, the relative abundance of *Prevotella* ranged from ~0% to ~59%, and the relative abundance of *Collinsella* ranged from ~2% to ~28%. The relative abundance of the topmost dominant bacterial genera per participant at baseline and end of the tournament are illustrated in **Figure 8**.

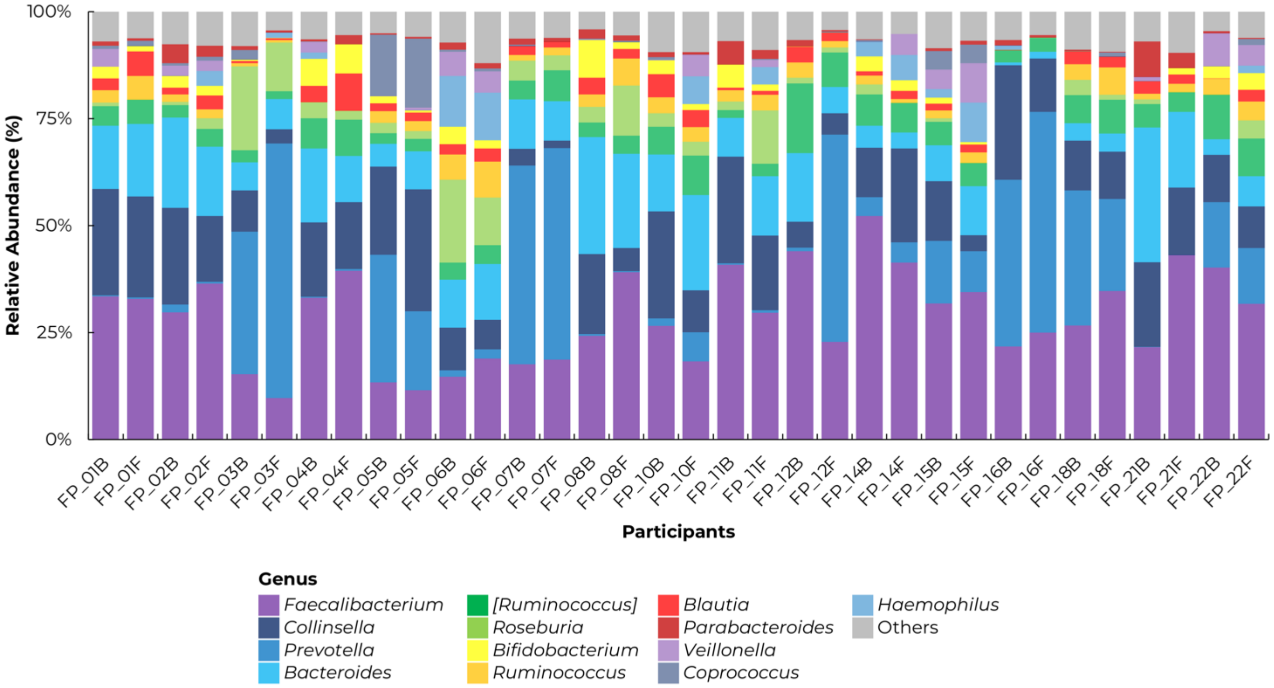

Figure 8. Genera relative abundances across all participants' samples.
Each sample is represented by one bar. Bars represent each genus relative abundance. Each genus is represented by a different colour. Baseline samples are identified with the letter *B* whereas samples from the end of the tournament are identified with the letter *F*. All genera with a relative abundance below 1% were grouped into *Others*.

The *Bacteroides* to *Prevotella* ratio at baseline ranged from ~0 to ~227, while the *Bacteroides* to *Prevotella* ratio at the end of the tournament ranged from ~0 to ~795. The variation in the *Bacteroides* to *Prevotella* ratio (Final – Baseline) ranged from ~-45 to ~570. However, despite the observed changes, no significant difference was found between the two time points [Baseline = 7.45 (0.22; 40.80) vs Final = 1.20 (0.19; 31.24); FDR-adjusted $p = 0.844$].

After adjusting for multiple comparisons, no significant differences were found between the two time points for any genera (FDR-adjusted $p \geq 0.05$). Notwithstanding, the results suggest that there is a trend towards a reduction in the relative abundance of *Collinsella* from baseline to the end of the tournament [Baseline = 17% (10%; 23%) vs Final = 11% (5%; 16%); non-adjusted $p = 0.015$; FDR-adjusted $p = 0.575$]. Thus, to further explore the changes in the second and third most dominant bacterial genera, the abundance of *Collinsella* and *Prevotella* at baseline and end of the tournament was further explored. The **Figure 9** shows a tendency for the reduction in the abundance of *Collinsella* from baseline to the end of the tournament, whereas the abundance of *Prevotella* appears to have remained relatively stable. The *p*-values obtained by the

Wilcoxon signed-rank tests and the respective FDR-adjusted *p*-values are presented in **Supplementary Table 7**. The top 25 genus correlated with the fixture congestion period are illustrated in **Figure 10**.

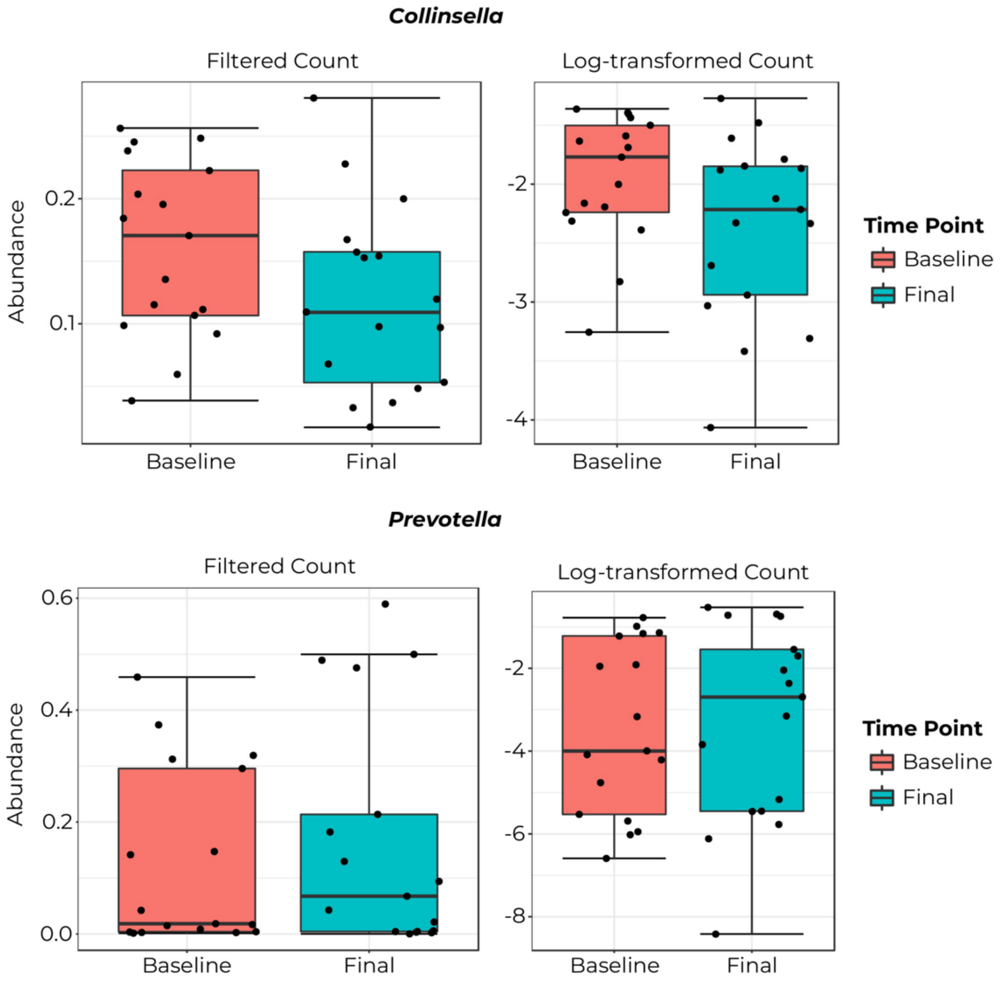

Figure 9. Abundance of bacterial *Collinsella* and *Prevotella* at baseline (Baseline, coral bars) and end of the tournament (Final, blue bars).
Absolute abundance is displayed in the left panels, and log-transformed abundance is displayed in the right panels. Each point represents a sample.

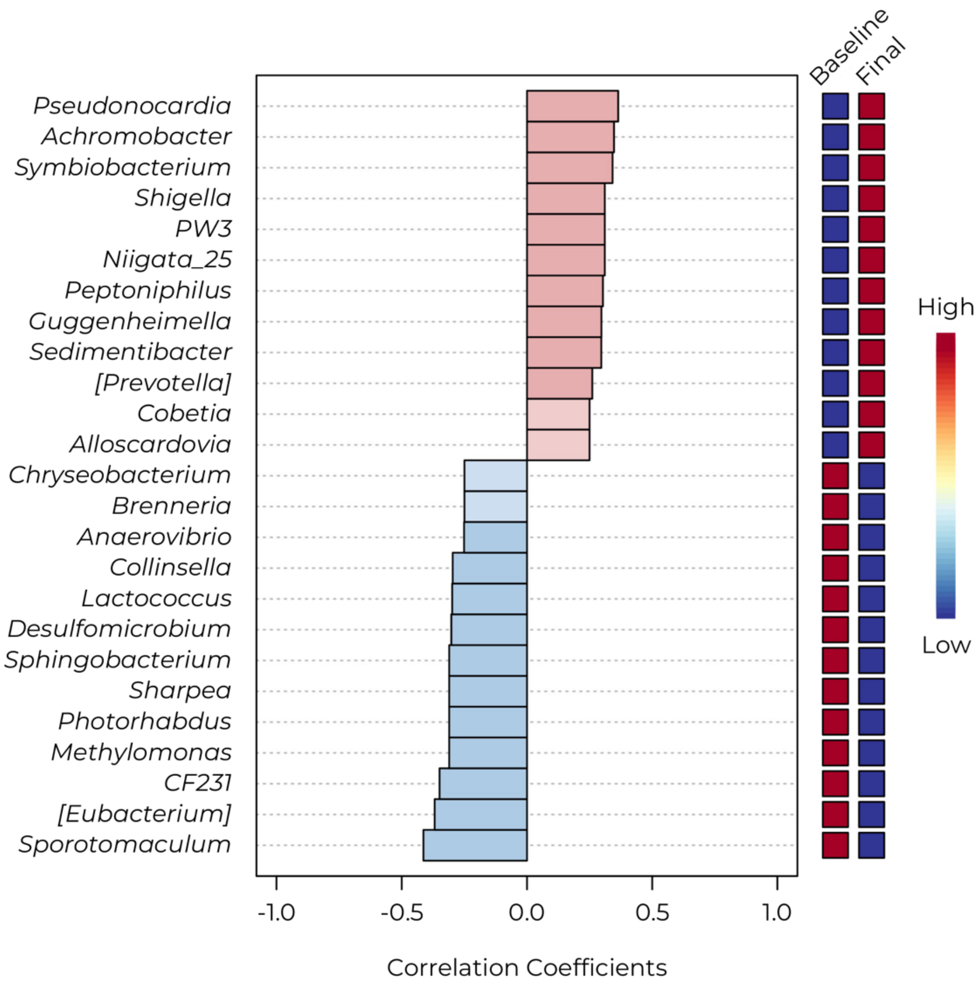

Figure 10. Top 25 genera correlated with the fixture congestion period.
Genera are ranked by their correlation. Red and blue denote positive and negative correlations, respectively. The intensity of the colours represents the degree of association between the genera abundances and the fixture congestion period as measured by Spearman's rank correlation. The heatmap shows whether the phyla abundance is higher (red) or lower (blue) in each time point.

4.4.1.3 At the species level

The number of species detected at baseline and end of the tournament is illustrated in **Figure 11a**. No significant difference was found between the two time points [Baseline = 143 (125; 192) vs Final = 151 (122; 169); FDR-adjusted $p = 0.991$]. The alpha diversity (Shannon's diversity index) at baseline and end of the tournament is illustrated in **Figure 11b**. The alpha diversity of the two time points did not differ significantly from each other [Baseline = 2.48 (2.29; 2.61) vs Final = 2.41 (2.32; 2.68); FDR-adjusted $p > 0.999$]. A PCoA plot of Bray-Curtis index distance was applied for the visualization of the complex relationships of gut microbiota composition at each time point (baseline and end of the tournament) (**Figure 11c**). No differences were observed, suggesting similarity among the groups clustered together ($p < 0.669$).

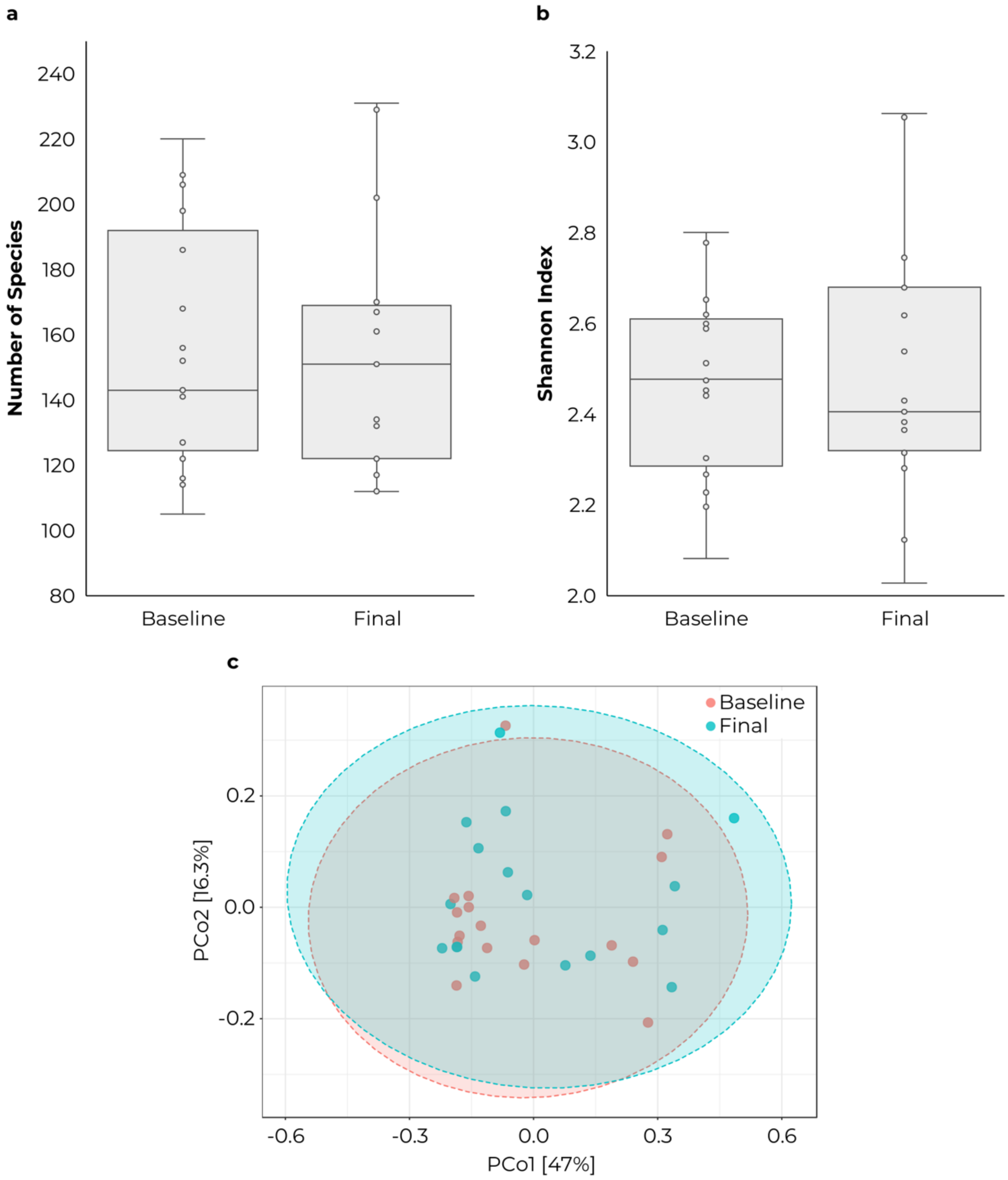

Figure 11. Measures of diversity, comparing baseline samples (Baseline) with end of the tournament samples (Final).

a. Boxplot of number of observed species (richness) at baseline and end of the tournament. The inside line represents the median; the box, the interquartile range; and the whiskers, the highest and lowest values. Each point represents a sample. No significant difference was found between the two time points (FDR-adjusted *p* = 0.991). **b.** Boxplot of bacterial diversity (Shannon's diversity index) at baseline and end of the tournament. The inside line represents the median; the box, the interquartile range; and the whiskers, the highest and lowest values. Each point represents one sample. The alpha diversity of the two time points did not differ significantly from each other (*p* > 0.999). **c.** Clustering of bacterial genera communities by principal coordinates analysis (PCoA). Data are plotted according to the first two components, which explain 47% (PCo1) and 16.3% (PCo2) of gut microbiota variation at baseline and end of the tournament. Each point represents one sample. The points are coloured by time point.

At baseline, the overall most abundant bacterial species were *Faecalibacterium prausnitzii* (30%), followed by *Collinsella aerofaciens* (17%) and *Prevotella copri* (9%). At the end of the tournament, the overall most abundant bacterial species were *Faecalibacterium prausnitzii* (30%), followed by *Collinsella aerofaciens* (13%) and *Prevotella copri* (12%). The graphic representations of the topmost dominant bacterial species at baseline and end of the tournament are provided in **Figure 12**. The complete list of species relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final) is available in **Supplementary Table 4**.

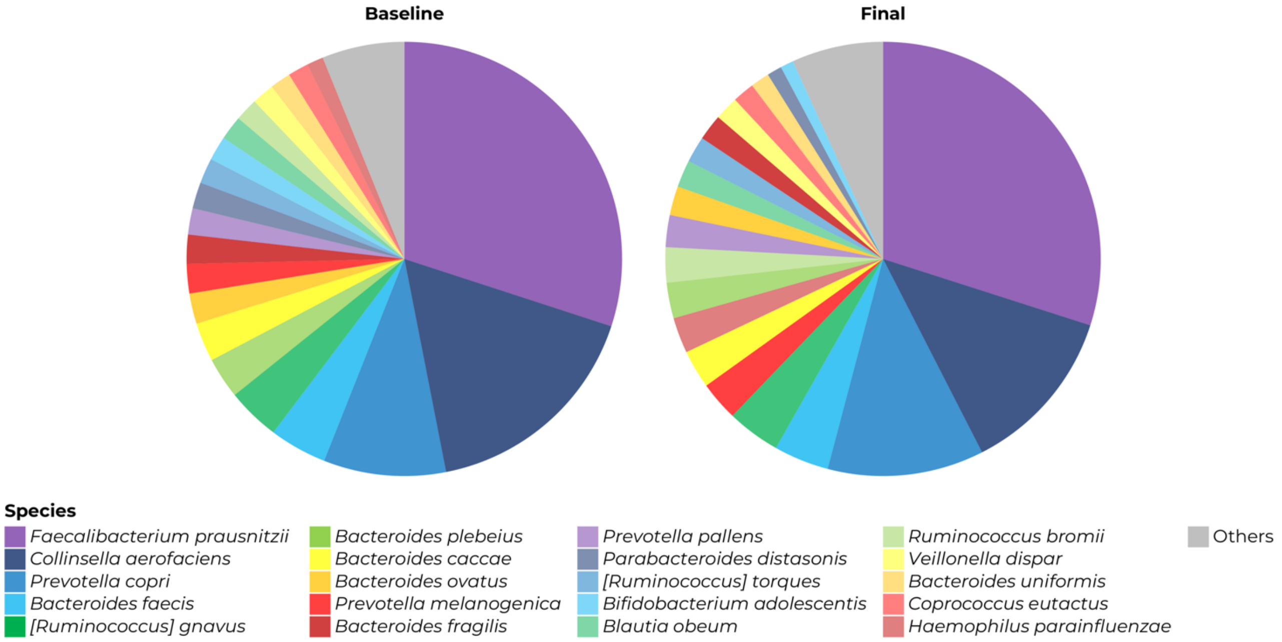

Figure 12. Species relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).
Sections represent the average of each species relative abundance. Each species is represented by a different colour. All species with a relative abundance below 1% were grouped into *Others*

At baseline, the relative abundance of *Faecalibacterium prausnitzii* ranged from ~13% to ~50%, the relative abundance of *Collinsella aerofaciens* ranged from ~4% to ~25%, and the relative abundance of *Prevotella copri* ranged from ~0% to ~29%. At the end of the tournament, the relative abundance of *Faecalibacterium prausnitzii* ranged from ~10% to ~43%, the relative abundance of *Collinsella aerofaciens* ranged from ~2% to ~28%, and the relative abundance of *Prevotella copri* ranged from ~0% to ~37%. The relative abundance of the topmost dominant bacterial species per participant at baseline and end of the tournament is illustrated in **Figure 13**.

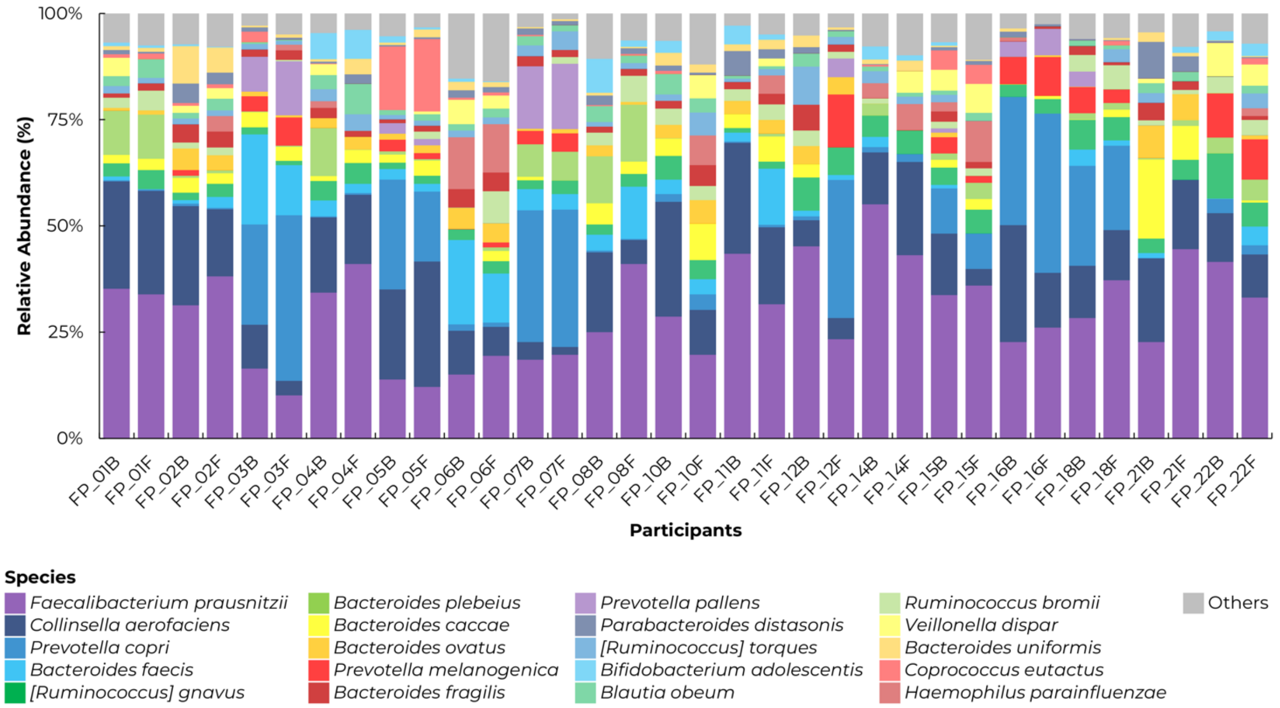

Figure 13. Species relative abundances across all participants' samples.
Each sample is represented by one bar. Bars represent each species relative abundance. Each species is represented by a different colour. Baseline samples are identified with the letter *B* whereas samples from the end of the tournament are identified with the letter *F*. All species with a relative abundance below 1% were grouped into *Others*.

After adjusting for multiple comparisons, no significant differences were found between the two time points for any species (FDR-adjusted $p \geq 0.05$). Notwithstanding, similar to the results observed for the *Collinsella* genus, there seems to be a trend towards a reduction in the relative abundance of *Collinsella aerofaciens* from baseline to the end of the tournament [Baseline = 17% (10%; 23%) vs Final = 11% (5%; 16%); non-adjusted $p = 0.015$; FDR-adjusted $p = 0.575$]. The *p*-values obtained by the Wilcoxon signed-rank tests and the respective FDR-adjusted *p*-values are presented in **Supplementary Table 8**. The top 25 species correlated with the fixture congestion period are illustrated in **Figure 14**.

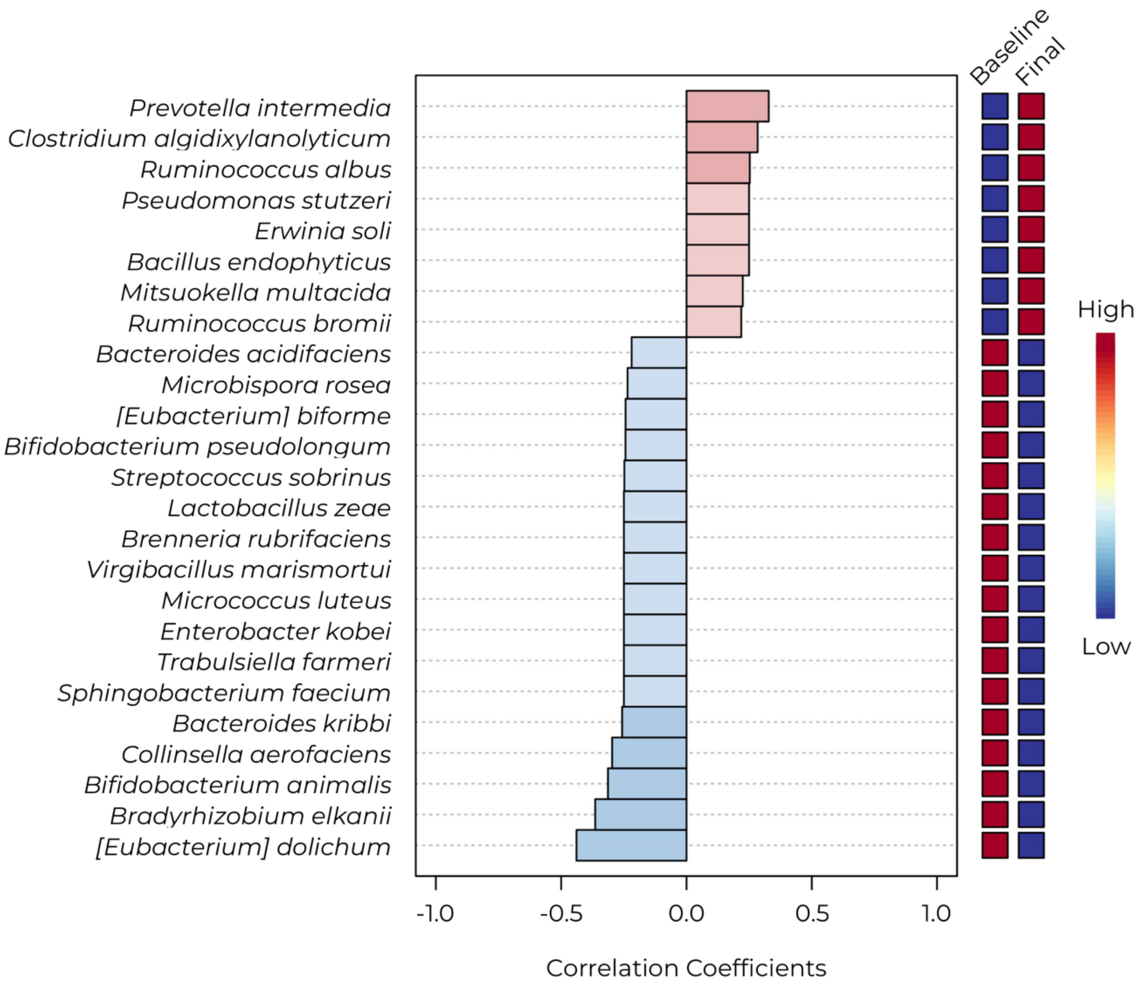

Figure 14. Top 25 species correlated with the fixture congestion period.
Species are ranked by their correlation. Red and blue denote positive and negative correlations, respectively. The intensity of the colours represents the degree of association between the species abundances and the fixture congestion period as measured by Spearman's rank correlation. The heatmap shows whether the phyla abundance is higher (red) or lower (blue) in each time point.

4.4.2 Relationships between variation in gut microbiota composition and exercise outcomes

No relationship was found between the total volume of training sessions and matches and the variation in the gut microbiota composition (FDR-adjusted $p \geq 0.05$). The variables analysed were as follows: relative abundance of phyla, genera, and species; the Firmicutes to Bacteroidetes ratio; the *Bacteroides* to *Prevotella* ratio; the number of observed genera and species; alpha diversity. Similarly, no relationship was found between the total sRPE of training sessions and matches and the variation in the gut microbiota composition (FDR-adjusted $p \geq 0.05$). The variables analysed were the same as previously mentioned for the total volume of training sessions and matches. The complete list of Spearman's rank correlation coefficients, the *p*-values obtained, and the respective FDR-adjusted *p*-values are in APPENDIX D: Spearman's rank correlations.

4.4.3 Relationships between gut microbiota composition and dietary intake

Since no significant differences were found between the gut microbiota composition of the players at baseline and end of the football tournament and, to explore possible relationships between the three most abundant bacterial genera and players reported dietary intake, further analysis was performed. The relationships tested between certain nutrients and food groups and the relative abundance of the three most abundant bacterial genera at the end of the tournament are provided in **Table 5**.

Table 5: Spearman's rank correlation between nutrients and food groups and the three most abundant bacterial genera.

Nutrient or Food Group	**Genus**								
	Faecalibacterium			***Collinsella***			***Prevotella***		
		p-values			*p*-values			*p*-values	
	r_s	non-adjusted	FDR-adjusted	r_s	non-adjusted	FDR-adjusted	r_s	non-adjusted	FDR-adjusted
Protein	-0.650	0.009	0.059	-0.186	0.508	0.721			
Fat	-0.725	0.002	0.027	-0.271	0.328	0.576			
Saturated fat	-0.714	0.003	0.027	-0.461	0.084	0.283			
Monosaturated fat	-0.504	0.056	0.215	-0.107	0.704	0.864			
Polyunsaturated fat	-0.264	0.341	0.576	-0.018	0.950	0.990			
Trans Fat	-0.586	0.022	0.107	-0.579	0.024	0.107			
Carbohydrates	0.025	0.930	0.990	-0.025	0.930	0.990	-0.129	0.648	0.833
Fibre	0.143	0.612	0.826	0.361	0.187	0.452	-0.186	0.508	0.721
Fruits and Vegetables	0.221	0.428	0.679	0.436	0.104	0.291	-0.350	0.201	0.452
Legumes	0.004	0.990	0.990	0.432	0.108	0.291			
Cheese and Yoghurt	-0.315	0.253	0.526	-0.016	0.955	0.990			
Red Meat	-0.711	0.003	0.027	-0.264	0.341	0.576			

FDR, False Discovery Rate. All nutrients and food groups were considered in grams per day. For genera, the relative abundance at the end of the tournament was considered. Based on scientific literature [73], only the relationship between the relative abundance of *Prevotella* and the daily consumption of carbohydrates, fibre, and fruits and vegetables was computed. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

5 DISCUSSION

In recent years, factors related to the impact of exercise on the human gut microbiota, such as different exercise modalities [81], changes in training volume [56], and competitive sports events [45, 49, 51], have been the focus of several studies. The scientific evidence suggests that the athletes' gut microbiota can respond favourably to periods of intensive exercise [45, 49, 51]; however, to date, no previous study investigated the impact of a period of fixture congestion on the gut microbiota of male or female football players.

Altogether, the findings presented in this study demonstrate that an eight-day international football tournament with three consecutive matches separated by 48-72 hours did not significantly change the gut microbiota of a women's national football team.

5.1 Gut Microbiota Composition: Ahead of a Fixture Congestion Period

The faecal samples collected at baseline provided valuable insight into the gut microbiota profiles of elite female football players when consuming their usual diet ahead of a period of fixture congestion.

5.1.1 At the phylum level

At the phylum level, collectively, the gut microbiota of players in this study was dominated by Firmicutes, followed by lower relative abundances of Bacteroidetes and Actinobacteria. Our findings contrast with results from Bressa et al. [57] that showed that the gut microbiota of women with an active lifestyle consisted mainly of Bacteroidetes (~49.5%) with a very low abundance of Actinobacteria (~0.1%). However, our results are in line with other data from our research group that, using the same methodology and bioinformatic analysis, analysed the gut microbiota of 26 healthy male Portuguese adults (unpublished data). Similar to the current investigation, this study found a dominance of Firmicutes (48%), followed by lower relative abundances of Bacteroidetes (33%) and Actinobacteria (14%). These results will be discussed further throughout this chapter and in chapter 5.2.

5.1.2 At the genus and species level

5.1.2.1 Faecalibacterium and Faecalibacterium prausnitzii

At the genus level, the gut microbiota of players in this study was predominantly composed of bacteria from the genus *Faecalibacterium*, from the Firmicutes phylum. Likewise, *Faecalibacterium* was one of the dominant bacteria found in elite female rowing athletes [58]. Within this genus, *Faecalibacterium prausnitzii* was the species with higher relative abundance. Similarly, *Faecalibacterium prausnitzii* has been previously found to be in greater relative abundance in women with an active lifestyle when compared to sedentary women [57]. Recently, to determine if the gut microbiome differed across sports classification groups, O'Donovan et al. [32] recruited international level athletes and grouped them based on the dynamic and static components of the sport, a classification proposed by Mitchel et al. [82]. According to this classification, football falls into class IC [i.e., a group characterised by high dynamic (I) and low static components (C)] [82]. Although O'Donovan et al. [32] did not recruit football players in their research, results showed that the relative abundance of *Faecalibacterium prausnitzii* was associated with the class IC, which agrees with our observation. Also, among collegiate swimmers, the genus *Faecalibacterium* responded to changes in training volume, with a decrease in its abundance observed following a reduction in training volume [56]. Collectively, these results suggest a possible positive association between *Faecalibacterium*, namely *Faecalibacterium prausnitzii*, and exercise. The species *Faecalibacterium prausnitzii* has been reported as one of the principal butyrate producers in the human gut [83, 84]. Besides, this species has been demonstrated to have anti-inflammatory effects and is suggested to be depleted in many gut disorders [85]. In recent research, *Faecalibacterium prausnitzii* was one of the bacterial species most affected by diet, correlating positively with the consumption of foods such as fruit, oily fish, legumes, and nuts, but negatively with high-sugar foods [86]. Among elite race walkers, the relative abundance of *Faecalibacterium* was reduced after a Ketogenic Low Carbohydrate High Fat diet [30]. In this study, the relative abundance of *Faecalibacterium* correlated negatively with the daily intake of total fat, saturated fat, and red meat. In addition, we observed a trend towards an inverse relationship between the relative abundance of *Faecalibacterium* and the daily intake of protein and trans fat. Hence, such a high prevalence of this species as we found in this study seems beneficial for athletes, particularly given the potential role of SCFA in health [87] and endurance exercise performance [22]. Also, these data suggests that the overall quality of these female players' dietary patterns is adequate and promoter of a favourable composition of the gut microbiota.

5.1.2.2 Collinsella and Collinsella aerofaciens

The genus *Collinsella*, from the Actinobacteria phylum, was the second most prevalent in our study, with a relative abundance of 16% at baseline. To the best of our knowledge, such a considerably high abundance is a novelty in research with athletes. Data from our research group that analysed the gut microbiota of 26 healthy male Portuguese adults (unpublished data) revealed a relative abundance of 10% for this genus. Notwithstanding, our finding was surprising considering that *Collinsella* has been previously found to be increased in patients with several diseases, such as type 2 diabetes [88, 89], symptomatic atherosclerosis [90], rheumatoid arthritis [91], and non-alcoholic steatohepatitis [37]. Moreover, the abundance of *Collinsella* has been shown to correlate negatively with a low dietary fibre intake [92]. In our study, such a relationship was not observed. In opposition to what is often reported in the literature, a very recent study with Portuguese COVID-19 patients observed that moderate and severe COVID-19 patients had lower relative abundances of the Actinobacteria phylum and the *Collinsella* genus than mild COVID-19 patients [93]. Together with our results, this study suggests that a higher abundance of *Collinsella* might not be as detrimental as has been thought. Supporting this, is the trend towards an inverse relationship between the relative abundance of *Collinsella* and the daily intake of trans fat that we observed here.

Within the genus *Collinsella*, *Collinsella aerofaciens* was the most abundant species identified here. Among the same group of healthy male Portuguese adults (unpublished data), the relative abundance of *Collinsella aerofaciens* found was 9%, almost half of the relative abundance we observed here (17%). The species *Collinsella aerofaciens* can ferment a wide range of carbohydrates, such as glucose, mannose, galactose, fructose, maltose, and lactose, and the fermentation products of glucose are H_2, ethanol, formate, and lactate [94]. As mentioned above, data from the scientific literature currently available [37, 88-92] have been mainly associating *Collinsella* to various disease states. Conversely, results from studies conducted by our research group have found consistent opposite outcomes, namely higher relative abundances of *Collinsella* and *Collinsella aerofaciens* associated with better health outcomes. That said, the critical issue of combining data from different studies that used distinct methods must be acknowledged. It is widely recognised that each step, namely sample collection, sample storage, DNA extraction, polymerase chain reaction or library construction, sequencing, and bioinformatics analysis, can affect the results obtained [95]. Thus, this may help explain the discrepancies in the outcomes regarding the abundance of the *Collinsella* genus. Nevertheless, it may also be a characteristic of the Portuguese population.

5.2 Gut Microbiota Composition: At the End of a Fixture Congestion Period

Upon comparing the gut microbiota composition of the elite female football players before the tournament with the samples collected at the end, we observed that the congested fixture period did not cause significant changes. Nevertheless, despite these results, we noted shifts in the relative abundance of some bacterial taxa, which are worth discussing. Due to the compositional nature of microbiome data [96], it is not possible to identify with certainty which bacterial taxa whose absolute abundance has changed; thus, the following results should be interpreted with caution. While the relative abundance of *Faecalibacterium* appears to have remained relatively stable, there was a shift in the overall relative abundance of the genera *Collinsella* and *Prevotella*. When comparing the abundance of both genera between the time points, it is somewhat noticeable that the abundance of *Collinsella* tended to decrease from baseline to the end of the tournament. Besides, Actinobacteria, *Collinsella* and *Collinsella aerofaciens*, although weakly and non-significantly, correlated negatively with the fixture congestion period. The opposite was not observed for *Prevotella* or *Prevotella copri*, the species of the *Prevotella* genus found in higher abundance. In previous research, the genus *Collinsella* has been shown to be increased in the gut microbiota of amateur runners after a half-marathon [50], which contrasts with the results of this study. Still, despite the conflicting results with Zhao et al. [50] and the absence of significant differences, we suggest the following hypothesis to explain our findings. As mentioned earlier, *Collinsella aerofaciens* species can produce lactate, among other end products [94]. Besides, during a game, intermittent exercise in football augments blood lactate levels [97]. In this study, carried out during a football tournament, we observed a trend toward a reduction in the abundance of the Actinobacteria phylum, the *Collinsella* genus and the *Collinsella aerofaciens* species from baseline to the end. From an opposing perspective, the relative abundance of the genus *Veillonella*, a lactate utiliser, was shown to be increased in marathon runners after a marathon [45]. Posteriorly, a case study with an ultramarathon runner also observed an increase in the relative abundance of *Veillonella* in the post-race period [49]. Thus, based on these data, we hypothesise that the changes observed in our study (decreased abundance of *Collinsella* and *Collinsella aerofaciens* at the end of the tournament) may be induced by a gut microbiota response and adaptation to an exercise-induced increase in circulating lactate levels. Nevertheless, since we did not collect any other biological samples in this investigation that would allow us to explore or test this hypothesis, future studies are needed. The measurement of faecal lactate concentration was not a viable approach as it would not provide interpretable results for our question. The faecal lactate concentration depends on the balance between bacterial production and host absorption, as well as microbial utilisation [98].

Beyond the comparative analysis, to investigate the relationship between variations in the gut microbiota composition and exercise parameters, we used the total exercise volume (i.e., time spent in training sessions and matches during the study) and load (sRPE). None of these parameters showed any relationship to the variation in the gut microbiota composition. Conversely, among cyclists, a higher abundance of the genus *Prevotella* has been previously shown to be correlated with the time reported exercising during the week [29]. Also, among martial arts athletes, the abundance of the genus *Parabacteroides* correlated with the time participants exercised during the week [31].

5.3 Impact of a Fixture Congestion Period: 2019 Algarve Cup

Fixture congestion is a contemporary issue, and its impact on elite female football players' physical performance has yet to be understood. It was beyond the scope of this study to evaluate the effect of a period of fixture congestion in elite female football players' physical performance; however, given the rise in the number of amateur and professional female football players and competitive tournaments [60], we support the view of Julian et al. [62] that more research in this matter is necessary. In the context of this study, it would be pertinent to interpret the results obtained here considering the changes that occur in sport physical performance parameters. Póvoas et al. [63] did not observe considerable alterations in plasma stress markers, physical load, and technical performance in elite female football players from distinct rank levels after four consecutive football matches separated by 48-72 hours during a FIFA tournament. Concerning male players, results of a very recent meta-analysis suggest that the total distance covered is not impacted by fixture congestion; however, given the scarcity of data and the high variability between studies, other physical performance variables may be negatively affected [62]. Thus, from what is currently known, we hypothesise that if football players are used to playing in fixture congestion to the extent that their physical performance is not compromised, their gut microbiota profiles may also be adapted, yet further research is necessary.

The 26th edition of the Algarve Cup lasted eight days in which each team played a total of three matches. If it is assumed that fixture congestion corresponds to a minimum of two successive bouts of match-play with an inter-match recovery period of less than 96 hours [62], then 59% of players (*n* = 10) recruited for this study competed in fixture congestion. Besides, 45% of players (*n* = 8) played in every match. Overall, our results revealed that a fixture congestion period did not provoke significant changes in the gut microbiota of elite female football players. These results do not conform with previous research that reported changes in the gut microbiota of athletes after periods of prolonged intensive exercise, such as a marathon [45], an ultramarathon [49], and a transoceanic rowing race [51]. Several factors may have contributed to our results. Firstly, just over half of the players competed in fixture congestion, and as such, the squad rotation during the tournament may have contributed to the results observed here by allowing players to rest. While the recruitment of a Women's national football team enabled us to investigate the impact of a period of fixture congestion in the gut microbiota of a football team, avoid geographic bias and reduce the confounding effect of players' competitive level, it also conditioned the sample size. Secondly, this study recruited high-level female football players, which might be more or less used to playing in fixture congestion, depending on the league and club they play. As a result, the gut microbiota profiles of these female players may reflect years of optimised nutrition and high degrees of physical conditioning from an early age [99]. In the current investigation, the training volume and load of players prior to this tournament were not assessed. From a different perspective, stability, resistance, and resilience are generally associated with a health-associated gut microbiota [5]. For these reasons and given the characteristics of the sporting event in which the study took place, compared to others in which differences were observed, the results we found here are justifiable.

Another aspect worth mentioning is that Portugal (i.e., players' country of origin) was the host of the tournament; hence, although some players were playing abroad and had to travel back, it was still a known environment (e.g., climate, food, food preparation, and cooking methods) for them. Recently, O'Donovan et al. demonstrated that travelling periods could negatively impact the gut microbiota [55]. Therefore, the design of this study allowed us to control for this factor.

5.4 Players' Food Intake During the Tournament

During this study, players were asked to fulfil food records daily. The food records allowed to monitor and assess qualitatively and quantitatively the players' dietary and nutritional intake. The nutritionist of the team designed the meal plan. In the current investigation, players' dietary habits before the tournament were not evaluated. However, attending to the fact that players could choose the foods they wished from the daily meal plan and the respective quantities, we consider that the results presented here reflect a decent estimation of their usual dietary habits.

In football, an adequate intake of carbohydrate-rich foods during a period of match preparation is essential for the maintenance and restoration of muscle glycogen stores and, consequently, to delay the onset of muscle fatigue and improve performance [71, 72, 100]. Our results showed that, overall, players did not meet the daily recommendation for carbohydrates. These findings are in line with previous research with female football players of a similar age. For example, Martin et al. [101] observed an intake of 4.1 ± 1.0 g/kg among international female football players. More recently, Dobrowolski et al. [102] found even lower intakes of 3.28 ± 1.2 g/kg among professional female football players. Concerning dietary fibre, for most players, the estimated consumption was below the recommendations. That said, given that an adequate intake of dietary fibre is essential for a healthy gut microbiota [103], increase consumption should be promoted. In this study, we did not observe any relationship between the relative abundance of *Prevotella* and the daily intake of dietary fibre, carbohydrates, and fruits and vegetables, frequently reported in the literature [73]. For at least 50% of players, the daily requirements for protein and fat were met. For the remaining players, the estimated intake was above the recommendations. Given these results, it would be highly relevant to investigate why female football players have a generally suboptimal intake of carbohydrates compared to the dietary recommendations. Additionally, the general nutrition and the nutrition for sports knowledge of female football players should be evaluated to understand if these players are aware of the nutritional demands of the sport they play. Regardless of these results, having the meals planned by a registered dietitian or nutritionist is essential to ensure players have access to nutritionally adequate and diverse meals optimised to their competitive schedule [104].

As mentioned earlier, the food records collected also allowed us to assess the relationship between the daily consumption of certain nutrients and food groups and the top three most abundant bacterial genera. Of the results obtained, the significant inverse correlations between the relative abundance of *Faecalibacterium* and daily consumption of fat, saturated fat and red meat stand out, as they confirm and highlight the beneficial effects that have been associated with this genus.

6 LIMITATIONS

The present study has some limitations that should be acknowledged. In the current investigation, no comprehensive data on players' habitual diet and lifestyle (i.e., before baseline, ahead of a period of fixture congestion) were collected. Nevertheless, the baseline faecal samples collected provide valuable insight into the gut microbiota profiles of elite female football players when consuming their usual diet ahead of a period of fixture congestion. Due to logistical constraints, all final samples were collected before the last match; thus, the additional impact of the third match was not considered. Besides, due to the nature of an international football tournament, the simultaneous recruitment of a matching non-football player control group was inviable; however, the repeated-measures design is a strength of our study. To frame the results obtained in this study, we referenced other data from our research group that, using the same methodology and bioinformatic analysis, analysed the gut microbiota of 26 healthy male Portuguese adults (unpublished data) when considered relevant.

During this study, players could choose whatever they wished from the daily meal plan; however, certain foods and cooking methods, despite being typical Portuguese food, may have differed from their recent dietary habits, particularly players living abroad. Other limitations are related to the food records. Although we were aware of the disadvantages of this method for assessing dietary intake [105], it was chosen as it allowed us to characterise the players' food intake during the tournament period in greater detail. Nevertheless, despite the initial guidance from a trained nutritionist and the written instructions, food records were often incomplete, possibly due to the competitive environment in which the study took place. Also, some players may have felt peer pressure while writing down the foods and the respective quantities. Finally, the lack of metabolomics analysis can also be seen as a limitation since it would allow a more in-depth understanding of the observed changes.

7 CONCLUSION

To the best of our knowledge, this is the first study to provide insights into the gut microbiota profile of elite female football players. Beyond that, it contributed to the growth of scientific research with female athletes. Despite the recognised interest, research on the gut microbiota of elite athletes is still in its infancy and, similarly to other research fields, there is a lack of studies with female athletes exclusively.

Overall, the results of this study add to the body of knowledge that elite athletes have a gut microbiota profile enriched in bacterial taxa generally associated with health, such as bacteria from the *Faecalibacterium* genus, namely *Faecalibacterium prausnitzii*. Also, our results support the finding that athletes from sports with high dynamic and low static components have gut microbiota profiles enriched in this bacterial genus. Another relevant result is the relatively high abundance of *Collinsella* and *Collinsella aerofaciens* in the gut microbiota of elite female football players. Most of the scientific literature published to date has reported that this bacterial genus is associated with various disease states and is pro-inflammatory. However, studies from our research group have been observing opposite results. While this discrepancy of results may be most likely due to distinct methodologies, we cannot dismiss the possibility of it being a characteristic of the Portuguese population. Therefore, the potential role of bacteria from the *Collinsella* genus and particularly from the *Collinsella aerofaciens* species in the gut microbiota requires further investigation.

Our main results demonstrate that a period of fixture congestion, specifically an eight-day international football tournament with three consecutive matches separated by 48-72 hours, did not induce significant changes in the composition of the gut microbiota of a women's national football team. Furthermore, our results support the idea that the gut microbiota of athletes appears resilient and adapted to their load and type of training. These results are particularly relevant considering that competing in fixture congestion is increasingly common for elite female football players. Limiting participants to females removed the potential confounding effect of sex. However, future studies are needed to confirm the impact of competing in fixture congestion on the gut microbiota of male football players.

Based on the results obtained and attending to the fact that players could choose the foods they wished from the daily meal plan and the respective quantities, we conclude that the results presented reflect a decent estimation of their usual dietary habits. However, had they not been provided with nutritionally adequate and diverse meals optimised for their competitive schedule, the results might have differed. To conclude, while the scientific evidence is still far from allowing dietary recommendations based on athletes' baseline gut microbiota profile, nutritional monitoring by a registered nutritionist is essential to ensure that an athlete's diet does not compromise its gut microbiota, either daily or in competition.

8 FUTURE DIRECTIONS

The study of the gut microbiota profiles of athletes is still in its infancy, and despite the progress made over the last years, several issues remain. As such, and based on the current literature and our results, some future directions can be pointed out.

Firstly, future studies aiming to assess the impact of exercise on the gut microbiota in athletes should study beyond the compositional level, also measuring functionality. It has already been demonstrated that the differences between the gut microbiota of athletes and sedentary controls are higher at the metagenomic and metabolic level [28], and it has been suggested that most host-microbiome connections arise from the metabolites produced by bacteria [106].

Secondly, in studies comparing the gut microbiota profiles of athletes with that of sedentary controls, much attention should be placed on the control group recruited. For example, the body mass index has been used to control for physical size [27]; however, the limitations for its use in athletes are widely recognized, and the likelihood of there being differences in body composition that could confound the outcomes are high. Besides, the dietary patterns must be very well controlled. The athletes' dietary intake frequently differs from that of the control group, both in quantity and in the types of foods consumed, which is a confounding factor.

Beyond food intake, another factor worth considering when studying the athlete's gut microbiome is their usage of dietary supplements. We have recently shown that the prevalence of dietary supplements usage is high among elite female football players [107]. In addition, the discrepancy between the number of dietary supplements reported was large, with athletes using between one to eleven or more. Recently, the interactions between some of the most commonly used dietary supplements and the gut microbiota have been reviewed [108]; notwithstanding, much remains unknown, namely the impact of the combined usage of dietary supplements on the gut microbiota. In the current investigation, alongside the intake of food and fluids, we assessed the usage of dietary supplements and considered them when transforming the food records' data into energy and nutrients. However, few were reported in this context, and it was beyond the scope of this study to investigate possible relationships to bacterial taxa.

Finally, concerning microbiome analysis, the future in this research field may require more complex bioinformatical approaches, such as those suggested by Mancin et al. [106].

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APPENDIX A: GPS Data

Supplementary Table 1: Variables measured with the GPS units during training sessions and matches.

Day	***n***	**Session Time** (min)	**Total Distance Covered** (m)	**Distance per minute** (m.min^{-1})	**High-Speed Running** (m)	**Dynamic Stress Load**	**Sprint Count**	**Sprint Distance** (m)
MD-4	4	114 (114; 117)	6091 (4736; 6299)	53 (40; 55)	312 (125; 437)	162 (66; 229)	0	0
MD-3	15	93 (93; 96)	6217 (5753; 6542)	67 (61; 68)	298 (130; 490)	161 (91; 235)	4 (0; 8)	51 (0; 122)
MD-2	17	101 (101; 103)	4691 (3364; 5111)	47 (39; 50)	111 (38; 223)	121 (83; 171)	1 (0; 6)	13 (0; 76)
MD-1	17	79 (78; 80)	3682 (3217; 3780)	45 (42; 48)	169 (83; 272)	74 (52; 134)	3 (1; 6)	30 (12; 93)
MD	12	185 (185; 187)	8993 (4686; 12305)	52 (26; 66)	754 (79; 1416)	185 (64; 408)	16 (1; 25)	250 (16; 596)
MD+1	12	92 (92; 92)	2961 (2609; 4417)	32 (28; 48)	55 (21; 94)	67 (39; 89)	0 (0; 1)	0 (0; 10)
MD2-1	12	82 (80; 84)	2976 (2644; 3879)	36 (32; 48)	94 (48; 136)	70 (50; 92)	2 (0; 3)	15 (0; 44)
MD2	12	187 (179; 188)	8799 (5526; 12810)	55 (31; 70)	657 (141; 972)	227 (82; 262)	12 (2; 22)	245 (98; 393)
MD2+1	11	81 (80; 82)	2765 (2346; 3538)	33 (29; 43)	83 (57; 112)	50 (34; 73)	1 (1; 2)	12 (9; 21)
MD3	11	177 (162; 179)	8845 (2485; 12723)	71 (19; 75)	693 (37; 888)	135 (29; 264)	9 (1; 18)	162 (18; 271)

GPS, Global Positioning System; MD, Match Day. Values are expressed as median (Q_1; Q_3).

APPENDIX B: Gut Microbiota Composition

Supplementary Table 2: Phyla relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).

Phylum	**Baseline** (%)	**Final** (%)
Acidobacteria	0.005	0.004
Actinobacteria	18.687	13.596
Bacteroidetes	28.325	30.579
Chloroflexi	0.001	0.001
Cyanobacteria	0.011	0.010
Firmicutes	50.014	51.581
Fusobacteria	0.001	0.001
Lentisphaerae	0.011	0.011
Planctomycetes	0.000	0.001
Proteobacteria	2.725	4.086
Tenericutes	0.209	0.127
TM7	0.001	0.001
Verrucomicrobia	0.009	0.002

Only phyla with an average relative abundance above or equal to 0.001% in at least one time point are shown.

Supplementary Table 3: Genera relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).

Genus	**Baseline** (%)	**Final** (%)
[Clostridium]	0.001	0.000
[Eubacterium]	0.370	0.264
[Prevotella]	0.063	0.056
[Ruminococcus]	5.429	5.533
02d06	0.001	0.001
1-68	0.017	0.007
5-7N15	0.001	0.001
Acetobacterium	0.001	0.001
Achromobacter	0.001	0.002
Acidaminobacter	0.005	0.006
Acidaminococcus	0.012	0.014
Actinobacillus	0.001	0.010
Actinomadura	0.001	0.000
Actinomyces	0.004	0.004
Adlercreutzia	0.025	0.022

Genus	**Baseline** (%)	**Final** (%)
AF12	0.001	0.002
Aggregatibacter	0.003	0.003
Akkermansia	0.006	0.001
Alcaligenes	0.072	0.013
Alicyclobacillus	0.001	0.001
Alkalibacter	0.002	0.002
Alkaliphilus	0.001	0.001
Allobaculum	0.021	0.027
Alteromonas	0.001	0.001
Anaerococcus	0.015	0.014
Anaerofilum	0.002	0.004
Anaerofustis	0.004	0.002
Anaerophaga	0.001	0.000
Anaerostipes	0.046	0.033
Anaerotruncus	0.010	0.006
Anaerovibrio	0.003	0.002
Anaerovorax	0.004	0.003
Aquabacterium	0.001	0.000
Arcobacter	0.001	0.000
Atopobium	0.003	0.002
Bacillus	0.003	0.002
Bacteroides	11.978	11.103
Bifidobacterium	2.487	1.472
Bilophila	0.239	0.202
Blautia	2.152	2.584
Blvii28	0.001	0.000
Bradyrhizobium	0.001	0.001
BSV43	0.001	0.000
Bulleidia	0.001	0.003
Burkholderia	0.004	0.003
Butyricimonas	0.114	0.090
Butyrivibrio	0.062	0.063
Caldicoprobacter	0.004	0.004
Caloramator	0.001	0.001
Candidatus Ancillula	0.001	0.001
Candidatus Azobacteroides	0.001	0.001
Candidatus Portiera	0.001	0.001
Catenibacterium	0.463	0.111
Catonella	0.003	0.002
cc_115	0.039	0.009

Genus	**Baseline** (%)	**Final** (%)
CF231	0.003	0.001
Christensenella	0.003	0.002
Citrobacter	0.001	0.000
Clostridiisalibacter	0.002	0.000
Clostridium (Clostridiaceae)	0.505	0.595
Clostridium (Lachnospiraceae)	0.038	0.106
Collinsella	16.012	11.877
Coprobacillus	0.003	0.003
Coprococcus	1.437	1.549
Corynebacterium	0.003	0.003
Cronobacter	0.001	0.000
Defluviitalea	0.000	0.001
Dehalobacter_Syntrophobotulus	0.001	0.001
Dehalobacterium	0.026	0.018
Delftia	0.000	0.001
Desulfomicrobium	0.001	0.000
Desulfosporosinus	0.019	0.038
Desulfotomaculum	0.003	0.004
Desulfotomaculum_Desulfovirgula	0.001	0.002
Desulfovibrio	0.042	0.080
Desulfurispora	0.001	0.004
Dethiosulfatibacter	0.001	0.001
Dialister	0.539	0.505
Dorea	0.560	0.752
Dysgonomonas	0.001	0.002
ecb11	0.000	0.001
Eggerthella	0.004	0.001
Enterobacter	0.001	0.001
Enterococcus	0.005	0.004
Epulopiscium	0.009	0.011
Erwinia	0.009	0.003
Ethanoligenens	0.002	0.003
Faecalibacterium	27.967	28.035
Finegoldia	0.010	0.010
Flavobacterium	0.004	0.003
Fusibacter	0.007	0.008
Fusobacterium	0.001	0.001
Gallicola	0.001	0.001
Gardnerella	0.000	0.002
Gemella	0.000	0.001

Genus	**Baseline** (%)	**Final** (%)
Gordonia	0.001	0.000
Gracilibacter	0.001	0.002
Granulicatella	0.001	0.000
Guggenheimella	0.000	0.001
GW-34	0.002	0.002
Haemophilus	1.144	2.486
Halomonas	0.001	0.000
Helcococcus	0.001	0.001
Holdemania	0.008	0.010
Janthinobacterium	0.001	0.005
Klebsiella	0.003	0.002
Lachnobacterium	0.003	0.004
Lachnospira	0.316	0.454
Lactobacillus	0.003	0.002
Lactococcus	0.003	0.001
Lautropia	0.001	0.001
Lawsonia	0.001	0.001
Leuconostoc	0.001	0.000
Megamonas	0.002	0.001
Megasphaera	0.034	0.029
Methylomonas	0.001	0.000
Methylotenera	0.001	0.000
Microbispora	0.075	0.034
Mitsuokella	0.012	0.007
Mogibacterium	0.004	0.006
Moryella	0.004	0.004
NP25	0.002	0.003
Odoribacter	0.154	0.142
Oribacterium	0.004	0.004
Oscillospira	0.416	0.467
Oxalobacter	0.004	0.079
Oxobacter	0.001	0.002
Paenibacillus	0.000	0.001
Paludibacter	0.004	0.003
Pantoea	0.001	0.001
Parabacteroides	1.819	1.035
Paraprevotella	0.222	0.243
Parvimonas	0.003	0.003
Pasteurella	0.001	0.001
Pedobacter	0.001	0.004

Genus	**Baseline** (%)	**Final** (%)
Pelotomaculum	0.002	0.002
Peptococcus	0.002	0.011
Peptoniphilus	0.004	0.007
Peptostreptococcus	0.001	0.001
ph2	0.002	0.002
Phascolarctobacterium	0.652	0.643
Photorhabdus	0.001	0.000
Polynucleobacter	0.000	0.001
Porphyromonas	0.008	0.005
Prevotella	12.723	16.617
Propionibacterium	0.002	0.080
Proteiniclasticum	0.002	0.001
Pseudobutyrivibrio	0.006	0.011
Pseudomonas	0.003	0.003
Pseudonocardia	0.000	0.001
Pseudoramibacter_Eubacterium	0.004	0.002
Psychrobacter	0.001	0.000
Psychromonas	0.003	0.004
PW3	0.000	0.001
Ralstonia	0.001	0.000
rc4-4	0.001	0.000
RFN20	0.007	0.003
Rheinheimera	0.001	0.001
Rhodoferax	0.001	0.000
Rikenella	0.000	0.001
Roseburia	3.980	3.836
Rothia	0.001	0.001
Ruminococcus	2.363	2.995
Salinispora	0.000	0.001
Salmonella	0.001	0.111
Sarcina	0.004	0.006
Sedimentibacter	0.013	0.019
Selenomonas	0.003	0.003
Serratia	0.169	0.078
Sharpea	0.001	0.000
Shigella	0.000	0.020
Shuttleworthia	0.004	0.003
Slackia	0.051	0.085
Sporomusa	0.001	0.001
Sporotomaculum	0.001	0.000

Genus	**Baseline** (%)	**Final** (%)
Staphylococcus	0.002	0.002
Streptococcus	0.179	0.290
Streptomyces	0.009	0.007
Succiniclasticum	0.009	0.007
Sulfurimonas	0.001	0.000
Sutterella	0.776	0.713
Symbiobacterium	0.002	0.004
Syntrophomonas	0.002	0.003
Thauera	0.003	0.001
Thermoanaerobacterium	0.001	0.000
Thermosinus	0.001	0.000
Thiomicrospira	0.001	0.000
Tissierella_Soehngenia	0.008	0.013
Trabulsiella	0.001	0.000
Turicibacter	0.005	0.008
vadinHB04	0.001	0.001
Veillonella	1.606	1.935
Vibrio	0.001	0.001
WAL_1855D	0.002	0.001
WH1-8	0.001	0.001
Xanthomonas	0.001	0.000
Yersinia	0.001	0.000
YRC22	0.003	0.006

Only genera with an average relative abundance above or equal to 0.001% in at least one time point are shown.

Supplementary Table 4: Species relative abundances across all participants' samples at baseline (Baseline) and end of the tournament (Final).

Species	**Baseline** (%)	**Final** (%)
[Eubacterium] biforme	0.339	0.263
[Eubacterium] dolichum	0.030	0.001
[Prevotella] tannerae	0.002	0.004
[Ruminococcus] gnavus	3.674	3.712
[Ruminococcus] torques	1.755	1.821
Achromobacter xylosoxidans	0.001	0.001
Actinobacillus parahaemolyticus	0.001	0.010
Actinomadura vinacea	0.001	0.000
Aggregatibacter pneumotropica	0.001	0.000
Akkermansia muciniphila	0.006	0.001

Species	**Baseline** (%)	**Final** (%)
Alcaligenes faecalis	0.072	0.013
Anaerophaga thermohalophila	0.001	0.000
Bacillus endophyticus	0.000	0.001
Bacteroides acidifaciens	0.023	0.015
Bacteroides barnesiae	0.037	0.027
Bacteroides caccae	2.696	2.675
Bacteroides coprophilus	0.087	0.071
Bacteroides coprosuis	0.001	0.000
Bacteroides eggerthii	0.721	0.683
Bacteroides fragilis	2.009	1.815
Bacteroides kribbi	0.001	0.001
Bacteroides ovatus	2.112	2.024
Bacteroides plebeius	2.855	2.481
Bacteroides uniformis	1.435	1.312
Bifidobacterium adolescentis	1.699	0.915
Bifidobacterium animalis	0.005	0.002
Bifidobacterium bifidum	0.049	0.025
Bifidobacterium breve	0.103	0.061
Bifidobacterium longum	0.584	0.416
Bifidobacterium pseudolongum	0.025	0.008
Bifidobacterium thermacidophilum	0.023	0.045
Bilophila sp.	0.001	0.005
Blautia obeum	1.670	1.900
Blautia producta	0.482	0.684
Bradyrhizobium elkanii	0.001	0.000
Clostridium acetobutylicum	0.000	0.001
Clostridium algidixylanolyticum	0.000	0.001
Clostridium bowmanii	0.000	0.001
Clostridium celerecrescens	0.001	0.000
Clostridium clostridioforme	0.002	0.002
Clostridium hiranonis	0.354	0.378
Clostridium perfringens	0.150	0.214
Clostridium piliforme	0.035	0.103
Clostridium sartagoforme	0.000	0.001
Collinsella aerofaciens	15.751	11.740
Collinsella stercoris	0.262	0.136
Coprobacillus cateniformis	0.001	0.000
Coprococcus catus	0.001	0.001
Coprococcus eutactus	1.429	1.524
Cronobacter sakazakii	0.001	0.000

Species	**Baseline** (%)	**Final** (%)
Defluviitalea saccharophila	0.000	0.001
Desulfosporosinus meridiei	0.019	0.037
Desulfovibrio aminophilus	0.018	0.066
Desulfovibrio C21_c20	0.001	0.001
Desulfovibrio D168	0.022	0.012
Dorea formicigenerans	0.560	0.752
Eggerthella lenta	0.004	0.001
Faecalibacterium prausnitzii	27.967	28.035
Haemophilus parainfluenzae	1.144	2.486
Halomonas anticariensis	0.001	0.000
Janthinobacterium lividum	0.001	0.004
Lactobacillus zeae	0.001	0.000
Methylotenera mobilis	0.001	0.000
Microbispora rosea	0.075	0.034
Mitsuokella multacida	0.000	0.001
Oxalobacter formigenes	0.004	0.079
Parabacteroides distasonis	1.816	1.024
Parabacteroides gordonii	0.003	0.011
Pedobacter cryoconitis	0.001	0.004
Porphyromonas endodontalis	0.003	0.001
Prevotella copri	8.457	10.865
Prevotella intermedia	0.001	0.007
Prevotella melaninogenica	2.044	2.739
Prevotella nanceiensis	0.007	0.019
Prevotella nigrescens	0.154	0.235
Prevotella pallens	1.827	2.230
Prevotella stercorea	0.233	0.522
Propionibacterium acnes	0.002	0.080
Pseudobutyrivibrio xylanivorans	0.000	0.004
Pseudomonas veronii	0.001	0.001
Roseburia faecis	3.980	3.834
Rothia dentocariosa	0.001	0.001
Ruminococcus albus	0.001	0.002
Ruminococcus bromii	1.590	2.455
Ruminococcus callidus	0.015	0.002
Ruminococcus flavefaciens	0.757	0.537
Salmonella enterica	0.001	0.111
Selenomonas noxia	0.001	0.001
Serratia marcescens	0.167	0.076
Serratia symbiotica	0.002	0.002

Species	**Baseline** (%)	**Final** (%)
Shigella flexneri	0.000	0.020
Streptococcus infantis	0.000	0.001
Streptococcus luteciae	0.171	0.285
Streptococcus sobrinus	0.001	0.000
Trabulsiella farmeri	0.001	0.000
Veillonella dispar	1.555	1.665
Veillonella parvula	0.048	0.269
Xanthomonas campestris	0.001	0.000

Only species with an average relative abundance above or equal to 0.001% in at least one time point are shown.

APPENDIX C: Wilcoxon signed rank tests

Supplementary Table 5: List of *p*-values and FDR-adjusted *p*-values of the Wilcoxon signed-rank test of the diversity metrics.

Diversity Metrics	*p*-value	FDR-adjusted *p*-value
Number of Genus	.877	.959
Number of Species	.943	.991
Shannon's Diversity Index	.981	1.000

FDR, False Discovery Rate. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 6: List of *p*-values and FDR-adjusted *p*-values of the Wilcoxon signed-rank test of phyla.

Phylum	*p*-value	FDR-adjusted *p*-value
Acidobacteria	.496	.769
Actinobacteria	.013	.575
Aquificae	.317	.575
Armatimonadetes	.109	.575
Bacteroidetes	.795	.896
Chloroflexi	.929	.983
Cyanobacteria	.173	.575
Firmicutes	.356	.624
Fusobacteria	.695	.838
Gemmatimonadetes	.655	.807
Lentisphaerae	.814	.908
Nitrospirae	.180	.575
OP8	.593	.807
OP9	.317	.575
Planctomycetes	.109	.575
Proteobacteria	.163	.575
Spirochaetes	.285	.575
Synergistetes	.317	.575
Tenericutes	.605	.807
TM7	.686	.830
Verrucomicrobia	.477	.761
WS3	.317	.575
Firmicutes/Bacteroidetes Ratio	.795	.896

FDR, False Discovery Rate. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 7: List of *p*-values and FDR-adjusted *p*-values of the Wilcoxon signed-rank test of genera.

Genus	***p*-value**	**FDR-adjusted *p*-value**
[Clostridium]	.398	.676
[Eubacterium]	.028	.575
[Prevotella]	.136	.575
[Ruminococcus]	.210	.575
02d06	.208	.575
1-68	.650	.807
5-7N15	.937	.990
Acetobacterium	.889	.962
Achromobacter	.023	.575
Acidaminobacter	.109	.575
Acidaminococcus	.756	.866
Acinetobacter	1.000	1.000
Actinobacillus	.208	.575
Actinomadura	.655	.807
Actinomyces	.875	.959
Adlercreutzia	.831	.922
Aerococcus	.655	.807
Aeromicrobium	.317	.575
AF12	.203	.575
Afifella	.317	.575
Aggregatibacter	.445	.741
Akkermansia	.173	.575
Alcaligenes	.091	.575
Alcanivorax	.317	.575
Alicyclobacillus	.686	.830
Alkalibacter	.959	.998
Alkaliphilus	1.000	1.000
Allobaculum	.496	.769
Alloiococcus	.317	.575
Alloscardovia	.180	.575
Alteromonas	.441	.737
Anaerococcus	.795	.896
Anaerofilum	.088	.575
Anaerofustis	.285	.575
Anaerophaga	.655	.807
Anaerostipes	.356	.624
Anaerotruncus	.136	.575
Anaerovibrio	.173	.575
Anaerovorax	.255	.575
Aneurinibacillus	.317	.575
Aquabacterium	.285	.575

Genus	***p*-value**	**FDR-adjusted *p*-value**
Arcobacter	.273	.575
Arthrobacter	1.000	1.000
Asteroleplasma	.655	.807
Atopobium	.470	.752
Bacillus	.594	.807
Bacteriovorax	.317	.575
Bacteroides	.758	.867
Baumannia	.317	.575
BF311	1.000	1.000
Bifidobacterium	.028	.575
Bilophila	.943	.991
Blattabacterium	.317	.575
Blautia	.554	.807
Blvii28	.500	.769
Bradyrhizobium	.272	.575
Brenneria	.180	.575
Brevibacillus	.317	.575
Brevibacterium	.593	.807
Brevundimonas	.317	.575
BSV43	.715	.844
Bulleidia	.484	.763
Burkholderia	.255	.575
Butyricimonas	.163	.575
Butyrivibrio	.723	.844
Caldicoprobacter	.363	.632
Caloramator	.678	.830
Campylobacter	.593	.807
Candidatus Accumulibacter	.317	.575
Candidatus Ancillula	.484	.763
Candidatus Aquiluna	.655	.807
Candidatus Arthromitus	.317	.575
Candidatus Azobacteroides	1.000	1.000
Candidatus Phytoplasma	.317	.575
Candidatus Portiera	.735	.857
Candidatus Tremblaya	.317	.575
Candidatus Xiphinematobacter	.317	.575
Capnocytophaga	.655	.807
Carboxydocella	.180	.575
Cardiobacterium	.317	.575
Catenibacterium	.055	.575
Catonella	.959	.998
cc_115	.124	.575
Cellulosimicrobium	.317	.575

Genus	***p*-value**	**FDR-adjusted *p*-value**
CF231	.019	.575
Christensenella	.110	.575
Chryseobacterium	.180	.575
Chthonomonas	.317	.575
Citrobacter	.144	.575
Clostridiisalibacter	.225	.575
Clostridium (Clostridiaceae)	.795	.896
Clostridium (Lachnospiraceae)	.196	.575
Clostridium (Peptostreptococcaceae)	.317	.575
Clostridium (Ruminococcaceae)	.317	.575
Cobetia	.180	.575
Collimonas	.317	.575
Collinsella	.015	.575
Conchiformibius	.317	.575
Coprobacillus	.917	.978
Coprococcus	.435	.732
Corynebacterium	.925	.983
Cronobacter	.715	.844
Cryobacterium	.317	.575
Cupriavidus	.317	.575
Cylindrospermopsis	.317	.575
Dechloromonas	.180	.575
Defluviitalea	.499	.769
Dehalobacter_Syntrophobotulus	.249	.575
Dehalobacterium	.079	.575
Delftia	.593	.807
Dermabacter	.317	.575
Desulfitobacter	.317	.575
Desulfococcus	.715	.844
Desulfomicrobium	.173	.575
Desulfosporosinus	.363	.632
Desulfotomaculum	.609	.807
Desulfotomaculum_Desulfovirgula	.214	.575
Desulfovermiculus	.317	.575
Desulfovibrio	.510	.778
Desulfurispora	.048	.575
Dethiosulfatibacter	.674	.830
Dialister	.463	.746
Dickeya	.317	.575
Dietzia	.317	.575
Dok59	.317	.575
Dorea	.523	.787

Genus	***p*-value**	**FDR-adjusted *p*-value**
Dysgonomonas	.859	.949
ecb11	.075	.575
Edwardsiella	.317	.575
Eggerthella	.917	.978
Enterobacter	.465	.746
Enterococcus	.570	.807
Epulopiscium	.379	.653
Erwinia	.255	.575
Erysipelothrix	.317	.575
Escherichia	.655	.807
Ethanoligenens	.308	.575
Exiguobacterium	.686	.830
Facklamia	.180	.575
Faecalibacterium	.981	1.000
Filifactor	.593	.807
Fimbriimonas	.180	.575
Finegoldia	.943	.991
Flavisolibacter	.317	.575
Flavobacterium	.233	.575
Frigoribacterium	.317	.575
Fusibacter	.586	.807
Fusobacterium	.799	.896
Gallicola	.799	.896
Gallionella	.180	.575
Garciella	.317	.575
Gardnerella	.715	.844
Gemella	.225	.575
Gemmiger	.655	.807
Geobacter	.317	.575
Geosporobacter_Thermotalea	.655	.807
Gluconacetobacter	.317	.575
Gordonia	.180	.575
Gracilibacter	.441	.737
Granulicatella	.465	.746
Guggenheimella	.314	.575
GW-34	.575	.807
Haemophilus	.102	.575
Halomonas	1.000	1.000
Helcococcus	1.000	1.000
Herbaspirillum	.317	.575
Holdemania	.179	.575
HTCC	.317	.575
HTCC2207	.180	.575

Genus	***p*-value**	**FDR-adjusted *p*-value**
Hydrogenophaga	.317	.575
Hymenobacter	.655	.807
Janthinobacterium	.214	.575
Kitasatospora	.655	.807
Klebsiella	.953	.998
Kocuria	.317	.575
L7A_E11	.317	.575
Lachnobacterium	.600	.807
Lachnospira	.010	.575
Lactobacillus	.397	.676
Lactococcus	.074	.575
Lautropia	.612	.807
Lawsonia	.499	.769
LCP-6	.317	.575
Leclercia	.317	.575
Leptolyngbya	.317	.575
Leptospira	.317	.575
Leptotrichia	.655	.807
Leucobacter	.593	.807
Leuconostoc	.263	.575
Limnobacter	.317	.575
Limnohabitans	.317	.575
Luteolibacter	.317	.575
Lutispora	.180	.575
Lysinibacillus	.317	.575
Lysobacter	.317	.575
Mannheimia	.317	.575
Maribacter	.317	.575
Marinobacter	.715	.844
Megamonas	.889	.962
Megasphaera	.173	.575
Methylobacillus	.655	.807
Methylomonas	.109	.575
Methylophaga	.317	.575
Methylotenera	.465	.746
Microbacterium	.593	.807
Microbispora	.140	.575
Micrococcus	.180	.575
Mitsuokella	.501	.769
Mobiluncus	.655	.807
Mogibacterium	.363	.632
Moorella	.317	.575
Moraxella	.655	.807

Genus	***p*-value**	**FDR-adjusted *p*-value**
Morganella	.317	.575
Moritella	.317	.575
Moryella	.435	.732
Mycoplasma	.273	.575
Natronincola_Anaerovirgula	.715	.844
Neisseria	1.000	1.000
Niigata-25	.109	.575
Nocardia	.655	.807
Nocardiopsis	.317	.575
NP25	.552	.807
Oceanicaulis	1.000	1.000
Oceanimonas	.317	.575
Odoribacter	.523	.787
Oleispira	.655	.807
Oribacterium	.865	.954
Oscillospira	.356	.624
Oxalobacter	.753	.866
Oxobacter	.953	.998
p-75-a5	1.000	1.000
Paenibacillus	.463	.746
Paenisporosarcina	.317	.575
Paludibacter	.326	.589
Pandoraea	.285	.575
Pantoea	.878	.959
Parabacteroides	.006	.575
Paracoccus	.715	.844
Paraprevotella	.379	.653
Parvimonas	.256	.575
Pasteurella	.779	.888
Pectinatus	.317	.575
Pediococcus	.317	.575
Pedobacter	.328	.589
Pelosinus	.655	.807
Pelotomaculum	.570	.807
Peptococcus	.028	.575
Peptoniphilus	.062	.575
Peptostreptococcus	.441	.737
Perlucidibaca	.317	.575
ph2	.374	.648
Phascolarctobacterium	.492	.769
Photobacterium	.285	.575
Photorhabdus	.109	.575
Planomicrobium	.655	.807

Genus	***p*-value**	**FDR-adjusted *p*-value**
Plesiomonas	.593	.807
Polynucleobacter	.893	.962
Porphyromonas	.463	.746
Prevotella	.492	.769
Propionibacterium	.814	.908
Proteiniclasticum	.594	.807
Proteus	.180	.575
Providencia	.180	.575
Pseudoalteromonas	.600	.807
Pseudobutyrivibrio	.278	.575
Pseudochrobactrum	.317	.575
Pseudomonas	.918	.978
Pseudonocardia	.068	.575
Pseudoramibacter_Eubacterium	.078	.575
Psychrobacter	.046	.575
Psychromonas	.820	.913
PW3	.109	.575
Ralstonia	.144	.575
Ramlibacter	.317	.575
Rathayibacter	.317	.575
rc4-4	.109	.575
RFN20	.593	.807
Rheinheimera	.721	.844
Rhizobium	.317	.575
Rhodococcus	.715	.844
Rhodoferax	.285	.575
Rhodothermus	.317	.575
Rikenella	.285	.575
Roseburia	.381	.653
Rothia	.499	.769
Rubrivivax	.593	.807
Ruminococcus	.084	.575
Salinibacter	.655	.807
Salinibacterium	.317	.575
Salinispora	.465	.746
Salmonella	.753	.866
Sarcina	.609	.807
Scardovia	.225	.575
Schwartzia	.273	.575
Sedimentibacter	.039	.575
Selenomonas	.679	.830
Serratia	.642	.807
SGUS912	.317	.575

Genus	*p*-value	FDR-adjusted *p*-value
Sharpea	.109	.575
Shewanella	.655	.807
Shigella	.109	.575
Shuttleworthia	.814	.908
Slackia	.394	.674
SMB53	.317	.575
Sorangium	.655	.807
Sphingobacterium	.109	.575
Sphingobium	.317	.575
Sphingomonas	.655	.807
Sporanaerobacter	.917	.978
Sporomusa	.484	.763
Sporotomaculum	.043	.575
Staphylococcus	.552	.807
Stenotrophomonas	.655	.807
Streptococcus	.093	.575
Streptomyces	.381	.653
Succiniclasticum	.642	.807
Succinivibrio	.180	.575
Sulfobacillus	.285	.575
Sulfurimonas	.465	.746
Sulfuritalea	.180	.575
Sutterella	.831	.922
Symbiobacterium	.096	.575
Syntrophobacter	.317	.575
Syntrophomonas	.756	.866
Syntrophus	.317	.575
T78	.317	.575
Tannerella	1.000	1.000
Telmatospirillum	.317	.575
Tepidibacter	.593	.807
Tepidimicrobium	.345	.613
Tepidimonas	.180	.575
Terracoccus	.655	.807
TG5	.317	.575
Thauera	.139	.575
Thermicanus	.317	.575
Thermoanaerobacter	.317	.575
Thermoanaerobacterium	1.000	1.000
Thermosinus	.686	.830
Thiobacillus	.317	.575
Thiomicrospira	.317	.575
Thiomonas	.317	.575

Genus	***p*-value**	**FDR-adjusted *p*-value**
Tindallia_Anoxynatronum	.593	.807
Tissierella_Soehngenia	.124	.575
Tolumonas	.317	.575
Trabulsiella	.109	.575
Treponema	.317	.575
Trichococcus	.180	.575
Turicibacter	.778	.887
vadinHB04	1.000	1.000
Vagococcus	.317	.575
Varibaculum	.317	.575
Variovorax	.317	.575
Veillonella	.523	.787
Vestibaculum	.317	.575
Vibrio (Pseudoalteromonadacea)	.593	.807
Vibrio (Vibrionaceae)	.594	.807
Virgibacillus	.180	.575
WAL_1855D	.260	.575
WH1-8	.484	.763
Wohlfahrtiimonas	.317	.575
Xanthomonas	.463	.746
Xenorhabdus	.317	.575
Yaniella	.317	.575
Yersinia	.116	.575
YRC22	.182	.575
Bacteroides/Prevotella Ratio	.723	.844

FDR, False Discovery Rate. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 8: List of *p*-values and FDR-adjusted *p*-values of the Wilcoxon signed-rank test of species.

Species	***p*-value**	**FDR-adjusted *p*-values**
[Clostridium] bifermentans	.180	.575
[Clostridium] sordellii	.893	.962
[Eubacterium] biforme	.063	.575
[Eubacterium] dolichum	.002	.575
[Prevotella] tannerae	.799	.896
[Ruminococcus] gnavus	.435	.732
[Ruminococcus] torques	.723	.844
Achromobacter xylosoxidans	.612	.807
Acinetobacter johnsonii	.317	.575
Acinetobacter venetianus	.317	.575
Actinobacillus parahaemolyticus	.249	.575

Species	***p*-value**	**FDR-adjusted *p*-values**
Actinomadura vinacea	.655	.807
Aggregatibacter pneumotropica	.655	.807
Aggregatibacter segnis	.655	.807
Akkermansia muciniphila	.173	.575
Alcaligenes faecalis	.091	.575
Alkaliphilus transvaalensis	.285	.575
Anaerophaga thermohalophila	.655	.807
Aneurinibacillus migulanus	.317	.575
Arthrobacter scleromae	.317	.575
Atopobium rimae	.317	.575
Bacillus badius	.317	.575
Bacillus cereus	.655	.807
Bacillus endophyticus	.180	.575
Bacillus flexus	.285	.575
Bacteroides acidifaciens	.233	.575
Bacteroides barnesiae	.619	.807
Bacteroides caccae	.492	.769
Bacteroides coprophilus	.959	.998
Bacteroides coprosuis	.753	.866
Bacteroides eggerthii	.345	.613
Bacteroides fragilis	.795	.896
Bacteroides kribbi	.018	.575
Bacteroides ovatus	.723	.844
Bacteroides plebeius	.523	.787
Bacteroides uniformis	.653	.807
Baumannia cicadellinicola	.317	.575
Bifidobacterium adolescentis	.056	.575
Bifidobacterium animalis	.136	.575
Bifidobacterium bifidum	.091	.575
Bifidobacterium breve	.331	.592
Bifidobacterium eulemuris	.317	.575
Bifidobacterium longum	.140	.575
Bifidobacterium pseudolongum	.131	.575
Bifidobacterium thermacidophilum	.754	.866
Bilophila sp.	.180	.575
Blautia obeum	.687	.830
Blautia producta	.136	.575
Bradyrhizobium elkanii	.068	.575
Brenneria rubrifaciens	.180	.575
Brevibacillus invocatus	.317	.575
Brevibacillus reuszeri	.317	.575
Brevibacterium casei	.180	.575
Brevibacterium paucivorans	.317	.575

Species	***p*-value**	**FDR-adjusted *p*-values**
Brevundimonas diminuta	.317	.575
Bulleidia moorei	.593	.807
Bulleidia p-1630-c5	.593	.807
Burkholderia bryophila	.317	.575
Burkholderia gladioli	.317	.575
Campylobacter ureolyticus	.317	.575
Candidatus Aquiluna rubra	.655	.807
Capnocytophaga ochracea	.317	.575
Clostridium acetobutylicum	.715	.844
Clostridium algidixylanolyticum	.345	.613
Clostridium bowmanii	.051	.575
Clostridium butyricum	.317	.575
Clostridium celerecrescens	.686	.830
Clostridium clostridioforme	.929	.983
Clostridium colinum	.317	.575
Clostridium hiranonis	.877	.959
Clostridium intestinale	.317	.575
Clostridium islandicum	.317	.575
Clostridium metallolevans	.317	.575
Clostridium neonatale	.317	.575
Clostridium perfringens	.266	.575
Clostridium piliforme	.196	.575
Clostridium purinilyticum	.317	.575
Clostridium sartagoforme	.225	.575
Clostridium sphenoides	1.000	1.000
Collinsella aerofaciens	.015	.575
Collinsella stercoris	.179	.575
Coprobacillus cateniformis	.655	.807
Coprococcus catus	.893	.962
Coprococcus eutactus	.586	.807
Corynebacterium durum	.317	.575
Corynebacterium stationis	.317	.575
Corynebacterium variabile	.317	.575
Cronobacter sakazakii	.715	.844
Cryobacterium psychrophilum	.317	.575
Defluviitalea saccharophila	.499	.769
Desulfosporosinus meridiei	.507	.775
Desulfovibrio aminophilus	.465	.746
Desulfovibrio C21_c20	1.000	1.000
Desulfovibrio D168	.109	.575
Desulfovibrio dechloracetivorans	.180	.575
Dickeya zeae	.317	.575
Dorea formicigenerans	.523	.787

Species	***p*-value**	**FDR-adjusted *p*-values**
Eggerthella lenta	.917	.978
Enterobacter aerogenes	1.000	1.000
Enterobacter cloacae	.317	.575
Enterobacter kobei	.180	.575
Enterobacter ludwigii	.317	.575
Enterococcus haemoperoxidus	.317	.575
Erwinia soli	.180	.575
Escherichia coli	.655	.807
Faecalibacterium prausnitzii	.981	1.000
Gemmiger formicilis	.655	.807
Haemophilus influenzae	.593	.807
Haemophilus parainfluenzae	.102	.575
Halomonas anticariensis	1.000	1.000
Janthinobacterium lividum	.612	.807
Kitasatospora pitsanulaokmensis	.317	.575
Klebsiella oxytoca	.273	.575
Kocuria rhizophila	.317	.575
Lactobacillus delbrueckii	.285	.575
Lactobacillus mucosae	.317	.575
Lactobacillus zeae	.180	.575
Lactococcus garvieae	.317	.575
Leclercia adecarboxylata	.317	.575
Lysinibacillus boronitolerans	.317	.575
Marinobacter hydrocarbonoclasticus	.317	.575
Megamonas hypermegale	1.000	1.000
Methylotenera mobilis	.465	.746
Microbispora rosea	.140	.575
Micrococcus luteus	.180	.575
Mitsuokella multacida	.116	.575
Morganella morganii	.317	.575
Nocardiopsis exhalans	.317	.575
Oscillospira guilliermondii	.593	.807
Oxalobacter formigenes	.753	.866
Pantoea agglomerans	.600	.807
Pantoea ananatis	.317	.575
Pantoea dispersa	.893	.962
Parabacteroides distasonis	.006	.575
Parabacteroides gordonii	.068	.575
Paracoccus aminovorans	1.000	1.000
Paracoccus marcusii	.317	.575
Pasteurella multocida	.317	.575
Pedobacter cryoconitis	.328	.589
Photorhabdus temperata	.180	.575

Species	***p*-value**	**FDR-adjusted *p*-values**
Plesiomonas shigelloides	.593	.807
Porphyromonas endodontalis	.285	.575
Prevotella copri	.619	.807
Prevotella intermedia	.025	.575
Prevotella melaninogenica	.679	.830
Prevotella nanceiensis	.249	.575
Prevotella nigrescens	.619	.807
Prevotella pallens	.721	.844
Prevotella stercorea	.256	.575
Propionibacterium acnes	.875	.959
Propionibacterium granulosum	.317	.575
Pseudoalteromonas piscicida	.655	.807
Pseudobutyrivibrio xylanivorans	.285	.575
Pseudomonas fragi	.317	.575
Pseudomonas stutzeri	.180	.575
Pseudomonas veronii	.929	.983
Rathayibacter caricis	.317	.575
Rhizobium leguminosarum	.317	.575
Rhodococcus fascians	.317	.575
Rhodococcus ruber	.317	.575
Roseburia faecis	.356	.624
Rothia dentocariosa	.753	.866
Rothia mucilaginosa	.180	.575
Ruminococcus albus	.139	.575
Ruminococcus bromii	.076	.575
Ruminococcus callidus	.959	.998
Ruminococcus flavefaciens	.463	.746
Salinispora tropica	.593	.807
Salmonella enterica	.753	.866
Selenomonas noxia	1.000	1.000
Selenomonas ruminantium	.655	.807
Serratia marcescens	.859	.949
Serratia proteamaculans	.465	.746
Serratia symbiotica	.878	.959
Shewanella benthica	.317	.575
Shigella flexneri	.109	.575
Sorangium cellulosum	.655	.807
Sphingobacterium faecium	.180	.575
Sphingobacterium multivorum	.317	.575
Sphingobium yanoikuyae	.317	.575
Sporomusa polytropa	.317	.575
Staphylococcus epidermidis	.655	.807
Stenotrophomonas geniculata	.317	.575

Species	***p*-value**	**FDR-adjusted *p*-values**
Stenotrophomonas retroflexus	.317	.575
Streptococcus alactolyticus	.317	.575
Streptococcus anginosus	.317	.575
Streptococcus infantis	.917	.978
Streptococcus luteciae	.075	.575
Streptococcus sobrinus	.068	.575
Streptomyces ahygroscopicus	.317	.575
Thermoanaerobacter uzonensis	.317	.575
Thermoanaerobacterium saccharolyticum	.893	.962
Trabulsiella farmeri	.180	.575
Vagococcus salmoninarum	.317	.575
Variovorax paradoxus	.317	.575
Veillonella dispar	.554	.807
Veillonella parvula	.600	.807
Vestibaculum illigatum	.317	.575
Vibrio atlanticus	.317	.575
Vibrio cholerae	.317	.575
Vibrio fortis	.317	.575
Vibrio harveyi	.655	.807
Vibrio rumoiensis	.317	.575
Virgibacillus marismortui	.180	.575
Xanthomonas campestris	.463	.746
Xenorhabdus nematophila	.317	.575

FDR, False Discovery Rate. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

APPENDIX D: Spearman's rank correlations

Supplementary Table 9: Spearman's rank correlation between the volume and sRPE of training sessions and matches and the variation in diversity metrics.

Diversity Metrics	r_s	*p*-value	FDR-adjusted *p*-value
Volume			
Number of Genus	-0.037	.888	.962
Number of Species	-0.002	.994	1.000
Shannon's diversity index	-0.198	.445	.838
sRPE			
Number of Genus	-0.047	.859	.951
Number of Species	-0.085	.747	.928
Shannon's diversity index	-0.172	.510	.868

FDR, False Discovery Rate; sRPE, Session-Rating of Perceived Exertion. The variation variable was calculated by subtracting the relative abundance of taxa at baseline from the relative abundance at the end of the tournament. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 10: Spearman's rank correlation between the volume and sRPE of training sessions and matches and the variation in phyla.

Phylum	r_s	*p*-value	FDR-adjusted *p*-value
Volume			
Acidobacteria	-0.239	.355	.829
Actinobacteria	0.120	.648	.907
Aquificae	-0.334	.191	.798
Armatimonadetes	-0.187	.472	.864
Bacteroidetes	-0.159	.542	.872
Chloroflexi	0.060	.820	.943
Cyanobacteria	0.281	.275	.829
Firmicutes	0.174	.505	.868
Fusobacteria	0.445	.073	.798
Gemmatimonadetes	-0.352	.166	.798
Lentisphaerae	-0.066	.801	.943
Nitrospirae	0.088	.737	.928
OP8	0.165	.527	.872
OP9	-0.257	.320	.829
Planctomycetes	0.173	.506	.868
Proteobacteria	-0.260	.314	.829
Spirochaetes	0.344	.177	.798
Synergistetes	-0.205	.429	.832
Tenericutes	-0.149	.568	.879
TM7	-0.051	.845	.943

Phylum	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Verrucomicrobia	0.499	.042	.798
WS3	-0.257	.320	.829
Firmicutes/Bacteroidetes Ratio	0.160	.539	.872
sRPE			
Acidobacteria	-0.281	.275	.829
Actinobacteria	-0.216	.406	.832
Aquificae	-0.357	.159	.798
Armatimonadetes	-0.022	.933	.981
Bacteroidetes	-0.059	.823	.943
Chloroflexi	0.019	.943	.987
Cyanobacteria	0.315	.218	.829
Firmicutes	0.279	.277	.829
Fusobacteria	0.256	.322	.829
Gemmatimonadetes	-0.105	.688	.907
Lentisphaerae	0.035	.895	.962
Nitrospirae	-0.070	.789	.943
OP8	0.026	.922	.976
OP9	-0.255	.323	.829
Planctomycetes	0.241	.351	.829
Proteobacteria	-0.083	.751	.929
Spirochaetes	0.440	.077	.798
Synergistetes	-0.408	.104	.798
Tenericutes	0.015	.955	.993
TM7	-0.470	.057	.798
Verrucomicrobia	0.301	.241	.829
WS3	-0.255	.323	.829
Firmicutes/Bacteroidetes Ratio	0.191	.462	.858

FDR, False Discovery Rate; sRPE, Session-Rating of Perceived Exertion. The variation variable was calculated by subtracting the relative abundance of taxa at baseline from the relative abundance at the end of the tournament. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 11: Spearman's rank correlation between the volume and sRPE of training sessions and matches and the variation in genera.

Genus	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Volume			
[Clostridium]	0.026	.920	.976
[Eubacterium]	0.081	.756	.934
[Prevotella]	-0.012	.963	.996
[Ruminococcus]	-0.037	.888	.962
02d06	0.009	.972	.999
1-68	-0.457	.065	.798
5-7N15	-0.326	.202	.803

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Acetobacterium	0.131	.617	.905
Achromobacter	0.413	.099	.798
Acidaminobacter	0.256	.321	.829
Acidaminococcus	-0.218	.400	.832
Acinetobacter	0.104	.690	.907
Actinobacillus	0.394	.118	.798
Actinomadura	0.370	.144	.798
Actinomyces	0.425	.089	.798
Adlercreutzia	-0.075	.774	.943
Aerococcus	0.475	.054	.798
Aeromicrobium	0.334	.191	.798
AF12	-0.292	.255	.829
Afifella	0.000	1.000	1.000
Aggregatibacter	0.019	.942	.987
Akkermansia	0.177	.496	.867
Alcaligenes	-0.412	.100	.798
Alcanivorax	0.359	.157	.798
Alicyclobacillus	0.131	.617	.905
Alkalibacter	0.084	.748	.929
Alkaliphilus	-0.057	.827	.943
Allobaculum	0.028	.914	.975
Alloiococcus	-0.205	.429	.832
Alloscardovia	0.176	.499	.867
Alteromonas	-0.129	.620	.906
Anaerococcus	0.085	.746	.928
Anaerofilum	0.544	.024	.798
Anaerofustis	-0.020	.938	.985
Anaerophaga	0.370	.144	.798
Anaerostipes	0.297	.247	.829
Anaerotruncus	-0.282	.272	.829
Anaerovibrio	0.087	.740	.928
Anaerovorax	-0.100	.703	.908
Aneurinibacillus	-0.257	.320	.829
Aquabacterium	-0.038	.885	.962
Arcobacter	0.200	.441	.835
Arthrobacter	0.375	.138	.798
Asteroleplasma	0.475	.054	.798
Atopobium	0.017	.947	.988
Bacillus	0.117	.654	.907
Bacteriovorax	0.334	.191	.798
Bacteroides	-0.085	.746	.928
Baumannia	-0.103	.695	.907

Genus	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
BF311	-0.087	.740	.928
Bifidobacterium	-0.160	.539	.872
Bilophila	-0.189	.469	.864
Blattabacterium	-0.103	.695	.907
Blautia	0.235	.363	.832
Blvii28	0.173	.507	.868
Bradyrhizobium	-0.225	.386	.832
Brenneria	-0.158	.544	.872
Brevibacillus	-0.334	.191	.798
Brevibacterium	0.056	.832	.943
Brevundimonas	0.000	1.000	1.000
BSV43	-0.242	.350	.829
Bulleidia	-0.087	.741	.928
Burkholderia	-0.408	.104	.798
Butyricimonas	0.092	.724	.925
Butyrivibrio	0.096	.714	.918
Caldicoprobacter	-0.120	.647	.907
Caloramator	-0.121	.644	.907
Campylobacter	0.187	.472	.864
Candidatus Accumulibacter	-0.103	.695	.907
Candidatus Ancillula	0.179	.492	.867
Candidatus Aquiluna	-0.070	.788	.943
Candidatus Arthromitus	-0.205	.429	.832
Candidatus Azobacteroides	-0.290	.259	.829
Candidatus Phytoplasma	0.359	.157	.798
Candidatus Portiera	0.408	.104	.798
Candidatus Tremblaya	0.205	.429	.832
Candidatus Xiphinematobacter	0.257	.320	.829
Capnocytophaga	-0.176	.499	.867
Carboxydocella	-0.004	.987	1.000
Cardiobacterium	-0.103	.695	.907
Catenibacterium	0.164	.530	.872
Catonella	-0.179	.492	.867
cc_115	0.096	.713	.918
Cellulosimicrobium	0.359	.157	.798
CF231	0.445	.074	.798
Christensenella	0.219	.399	.832
Chryseobacterium	0.246	.340	.829
Chthonomonas	-0.359	.157	.798
Citrobacter	0.025	.925	.979
Clostridiisalibacter	0.253	.327	.829
Clostridium (Clostridiaceae)	-0.068	.796	.943

Genus	r_s	*p*-value	FDR-adjusted *p*-value
Clostridium (Lachnospiraceae)	0.159	.542	.872
Clostridium (Peptostreptococcaceae)	-0.205	.429	.832
Clostridium (Ruminococcaceae)	-0.411	.102	.798
Cobetia	-0.141	.590	.889
Collimonas	0.257	.320	.829
Collinsella	0.244	.345	.829
Conchiformibius	-0.359	.157	.798
Coprobacillus	-0.544	.024	.798
Coprococcus	-0.023	.929	.980
Corynebacterium	0.284	.269	.829
Cronobacter	0.127	.626	.907
Cryobacterium	0.103	.695	.907
Cupriavidus	-0.257	.320	.829
Cylindrospermopsis	0.359	.157	.798
Dechloromonas	0.070	.788	.943
Defluviitalea	-0.228	.378	.832
Dehalobacter_Syntrophobotulus	0.476	.054	.798
Dehalobacterium	0.129	.621	.906
Delftia	-0.498	.042	.798
Dermabacter	-0.205	.429	.832
Desulfitobacter	-0.154	.555	.872
Desulfococcus	0.430	.085	.798
Desulfomicrobium	0.407	.105	.798
Desulfosporosinus	-0.100	.701	.907
Desulfotomaculum	0.127	.627	.907
Desulfotomaculum_Desulfovirgula	-0.111	.673	.907
Desulfovermiculus	0.359	.157	.798
Desulfovibrio	-0.245	.344	.829
Desulfurispora	0.346	.174	.798
Dethiosulfatibacter	0.256	.321	.829
Dialister	-0.086	.742	.928
Dickeya	0.103	.695	.907
Dietzia	0.000	1.000	1.000
Dok59	0.359	.157	.798
Dorea	0.177	.496	.867
Dysgonomonas	-0.039	.882	.962
ecb11	-0.412	.100	.798
Edwardsiella	0.334	.191	.798
Eggerthella	-0.097	.712	.918
Enterobacter	0.185	.476	.866
Enterococcus	0.397	.115	.798
Epulopiscium	-0.036	.892	.962

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Erwinia	0.467	.059	.798
Erysipelothrix	0.359	.157	.798
Escherichia	0.475	.054	.798
Ethanoligenens	0.069	.794	.943
Exiguobacterium	0.022	.933	.981
Facklamia	0.427	.088	.798
Faecalibacterium	0.296	.249	.829
Filifactor	-0.278	.280	.829
Fimbriimonas	0.009	.973	.999
Finegoldia	0.340	.182	.798
Flavisolibacter	0.154	.555	.872
Flavobacterium	0.010	.968	.999
Frigoribacterium	0.205	.429	.832
Fusibacter	0.152	.561	.875
Fusobacterium	0.444	.074	.798
Gallicola	-0.360	.156	.798
Gallionella	-0.444	.074	.798
Garciella	-0.103	.695	.907
Gardnerella	-0.245	.343	.829
Gemella	0.015	.956	.993
Gemmiger	0.246	.340	.829
Geobacter	0.359	.157	.798
Geosporobacter_Thermotalea	-0.422	.091	.798
Gluconacetobacter	0.257	.320	.829
Gordonia	0.018	.947	.988
Gracilibacter	0.120	.645	.907
Granulicatella	0.311	.224	.829
Guggenheimella	-0.238	.357	.832
GW-34	0.267	.300	.829
Haemophilus	-0.308	.229	.829
Halomonas	0.141	.590	.889
Helcococcus	-0.053	.839	.943
Herbaspirillum	0.103	.695	.907
Holdemania	-0.180	.490	.867
HTCC	0.103	.695	.907
HTCC2207	0.198	.446	.838
Hydrogenophaga	-0.359	.157	.798
Hymenobacter	-0.176	.499	.867
Janthinobacterium	-0.080	.760	.937
Kitasatospora	-0.387	.125	.798
Klebsiella	0.444	.074	.798
Kocuria	0.334	.191	.798

Genus	r_s	*p*-value	FDR-adjusted *p*-value
L7A_E11	-0.103	.695	.907
Lachnobacterium	0.048	.856	.951
Lachnospira	0.299	.243	.829
Lactobacillus	0.474	.054	.798
Lactococcus	-0.027	.918	.976
Lautropia	-0.129	.622	.906
Lawsonia	0.003	.992	1.000
LCP-6	0.359	.157	.798
Leclercia	0.334	.191	.798
Leptolyngbya	0.359	.157	.798
Leptospira	0.334	.191	.798
Leptotrichia	0.000	1.000	1.000
Leucobacter	-0.250	.333	.829
Leuconostoc	0.460	.063	.798
Limnobacter	0.103	.695	.907
Limnohabitans	-0.154	.555	.872
Luteolibacter	0.359	.157	.798
Lutispora	0.167	.521	.872
Lysinibacillus	-0.103	.695	.907
Lysobacter	0.000	1.000	1.000
Mannheimia	0.154	.555	.872
Maribacter	-0.154	.555	.872
Marinobacter	-0.045	.865	.954
Megamonas	0.290	.260	.829
Megasphaera	-0.089	.735	.928
Methylobacillus	-0.352	.166	.798
Methylomonas	0.265	.304	.829
Methylophaga	-0.205	.429	.832
Methylotenera	0.477	.053	.798
Microbacterium	-0.376	.137	.798
Microbispora	0.200	.441	.835
Micrococcus	-0.141	.590	.889
Mitsuokella	0.175	.502	.867
Mobiluncus	0.176	.499	.867
Mogibacterium	-0.385	.127	.798
Moorella	-0.359	.157	.798
Moraxella	0.229	.377	.832
Morganella	0.334	.191	.798
Moritella	-0.257	.320	.829
Moryella	0.150	.565	.877
Mycoplasma	-0.248	.336	.829
Natronincola_Anaerovirgula	0.146	.577	.886

Genus	r_s	*p*-value	FDR-adjusted *p*-value
Neisseria	0.281	.275	.829
Niigata-25	-0.315	.218	.829
Nocardia	-0.211	.416	.832
Nocardiopsis	-0.334	.191	.798
NP25	0.449	.071	.798
Oceanicaulis	0.083	.750	.929
Oceanimonas	-0.154	.555	.872
Odoribacter	-0.143	.584	.889
Oleispira	-0.246	.340	.829
Oribacterium	-0.023	.929	.980
Oscillospira	-0.165	.527	.872
Oxalobacter	-0.205	.431	.832
Oxobacter	0.037	.888	.962
p-75-a5	0.149	.568	.879
Paenibacillus	0.065	.805	.943
Paenisporosarcina	0.257	.320	.829
Paludibacter	0.094	.721	.924
Pandoraea	-0.057	.827	.943
Pantoea	-0.130	.618	.905
Parabacteroides	0.314	.219	.829
Paracoccus	0.361	.155	.798
Paraprevotella	-0.352	.165	.798
Parvimonas	-0.290	.258	.829
Pasteurella	0.043	.871	.957
Pectinatus	-0.359	.157	.798
Pediococcus	0.103	.695	.907
Pedobacter	0.174	.503	.867
Pelosinus	-0.141	.590	.889
Pelotomaculum	-0.178	.495	.867
Peptococcus	-0.020	.939	.985
Peptoniphilus	0.022	.933	.981
Peptostreptococcus	-0.201	.439	.835
Perlucidibaca	-0.154	.555	.872
ph2	-0.003	.992	1.000
Phascolarctobacterium	-0.441	.076	.798
Photobacterium	0.157	.546	.872
Photorhabdus	-0.434	.082	.798
Planomicrobium	-0.053	.840	.943
Plesiomonas	0.274	.287	.829
Polynucleobacter	-0.428	.086	.798
Porphyromonas	0.028	.914	.975
Prevotella	-0.142	.587	.889

Genus	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Propionibacterium	-0.085	.746	.928
Proteiniclasticum	-0.065	.804	.943
Proteus	-0.187	.472	.864
Providencia	-0.187	.472	.864
Pseudoalteromonas	0.003	.991	1.000
Pseudobutyrivibrio	-0.027	.918	.976
Pseudochrobactrum	0.205	.429	.832
Pseudomonas	-0.251	.330	.829
Pseudonocardia	0.053	.840	.943
Pseudoramibacter_Eubacterium	0.014	.957	.993
Psychrobacter	-0.208	.424	.832
Psychromonas	-0.378	.135	.798
PW3	0.231	.373	.832
Ralstonia	0.126	.630	.907
Ramlibacter	-0.411	.102	.798
Rathayibacter	-0.103	.695	.907
rc4-4	-0.205	.431	.832
RFN20	-0.066	.802	.943
Rheinheimera	0.022	.934	.982
Rhizobium	-0.103	.695	.907
Rhodococcus	0.056	.830	.943
Rhodoferax	0.269	.297	.829
Rhodothermus	-0.205	.429	.832
Rikenella	-0.471	.057	.798
Roseburia	-0.561	.019	.798
Rothia	0.292	.255	.829
Rubrivivax	0.121	.643	.907
Ruminococcus	0.471	.057	.798
Salinibacter	-0.141	.590	.889
Salinibacterium	-0.103	.695	.907
Salinispora	-0.180	.488	.867
Salmonella	0.173	.507	.868
Sarcina	0.329	.197	.798
Scardovia	0.279	.278	.829
Schwartzia	0.136	.603	.896
Sedimentibacter	0.140	.591	.889
Selenomonas	0.264	.306	.829
Serratia	0.150	.565	.877
SGUS912	0.334	.191	.798
Sharpea	0.163	.532	.872
Shewanella	0.299	.243	.829
Shigella	0.239	.356	.829

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Shuttleworthia	0.044	.868	.957
Slackia	0.147	.574	.884
SMB53	-0.154	.555	.872
Sorangium	0.246	.340	.829
Sphingobacterium	0.434	.082	.798
Sphingobium	-0.103	.695	.907
Sphingomonas	0.211	.416	.832
Sporanaerobacter	-0.242	.349	.829
Sporomusa	-0.270	.295	.829
Sporotomaculum	-0.038	.884	.962
Staphylococcus	0.241	.352	.829
Stenotrophomonas	0.475	.054	.798
Streptococcus	0.295	.251	.829
Streptomyces	0.018	.944	.987
Succiniclasticum	-0.211	.417	.832
Succinivibrio	-0.328	.199	.803
Sulfobacillus	0.083	.750	.929
Sulfurimonas	0.199	.445	.838
Sulfuritalea	0.207	.426	.832
Sutterella	-0.330	.195	.798
Symbiobacterium	0.232	.370	.832
Syntrophobacter	0.205	.429	.832
Syntrophomonas	-0.450	.070	.798
Syntrophus	0.000	1.000	1.000
T78	0.154	.555	.872
Tannerella	0.225	.385	.832
Telmatospirillum	0.103	.695	.907
Tepidibacter	0.030	.910	.973
Tepidimicrobium	-0.213	.413	.832
Tepidimonas	0.172	.510	.868
Terracoccus	-0.387	.125	.798
TG5	-0.205	.429	.832
Thauera	0.130	.618	.905
Thermicanus	0.000	1.000	1.000
Thermoanaerobacter	-0.257	.320	.829
Thermoanaerobacterium	0.184	.479	.867
Thermosinus	0.089	.735	.928
Thiobacillus	0.000	1.000	1.000
Thiomicrospira	0.205	.429	.832
Thiomonas	-0.359	.157	.798
Tindallia_Anoxynatronum	-0.306	.233	.829
Tissierella_Soehngenia	0.116	.658	.907

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Tolumonas	0.334	.191	.798
Trabulsiella	0.170	.513	.872
Treponema	0.359	.157	.798
Trichococcus	0.018	.947	.988
Turicibacter	0.263	.308	.829
vadinHB04	-0.123	.637	.907
Vagococcus	0.334	.191	.798
Varibaculum	-0.154	.555	.872
Variovorax	-0.359	.157	.798
Veillonella	-0.249	.335	.829
Vestibaculum	-0.154	.555	.872
Vibrio (Pseudoalteromonadacea)	0.066	.802	.943
Vibrio (Vibrionaceae)	-0.206	.429	.832
Virgibacillus	0.009	.973	.999
WAL_1855D	0.126	.629	.907
WH1-8	-0.117	.654	.907
Wohlfahrtiimonas	0.000	1.000	1.000
Xanthomonas	-0.252	.329	.829
Xenorhabdus	0.103	.695	.907
Yaniella	-0.103	.695	.907
Yersinia	0.288	.262	.829
YRC22	0.064	.808	.943
Bacteroides/Prevotella Ratio	-0.046	.862	.953
sRPE			
[Clostridium]	-0.106	.687	.907
[Eubacterium]	0.304	.236	.829
[Prevotella]	-0.194	.456	.854
[Ruminococcus]	0.086	.743	.928
02d06	0.260	.313	.829
1-68	-0.287	.264	.829
5-7N15	-0.134	.608	.899
Acetobacterium	0.096	.715	.918
Achromobacter	0.437	.080	.798
Acidaminobacter	0.338	.184	.798
Acidaminococcus	-0.103	.694	.907
Acinetobacter	0.148	.570	.880
Actinobacillus	0.178	.495	.867
Actinomadura	0.350	.168	.798
Actinomyces	0.201	.438	.835
Adlercreutzia	-0.243	.348	.829
Aerococcus	0.420	.093	.798
Aeromicrobium	0.357	.159	.798

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
AF12	-0.348	.171	.798
Afifella	0.051	.846	.943
Aggregatibacter	-0.254	.325	.829
Akkermansia	0.089	.734	.928
Alcaligenes	-0.218	.400	.832
Alcanivorax	0.357	.159	.798
Alicyclobacillus	0.047	.857	.951
Alkalibacter	0.284	.269	.829
Alkaliphilus	0.053	.840	.943
Allobaculum	0.153	.557	.872
Alloiococcus	-0.408	.104	.798
Alloscardovia	0.136	.604	.896
Alteromonas	-0.229	.377	.832
Anaerococcus	0.154	.554	.872
Anaerofilum	0.484	.049	.798
Anaerofustis	0.140	.593	.889
Anaerophaga	0.385	.127	.798
Anaerostipes	0.375	.138	.798
Anaerotruncus	-0.243	.348	.829
Anaerovibrio	-0.007	.978	1.000
Anaerovorax	-0.125	.633	.907
Aneurinibacillus	-0.255	.323	.829
Aquabacterium	-0.077	.768	.943
Arcobacter	0.178	.495	.867
Arthrobacter	0.300	.242	.829
Asteroleplasma	0.420	.093	.798
Atopobium	0.106	.687	.907
Bacillus	0.206	.427	.832
Bacteriovorax	0.306	.232	.829
Bacteroides	-0.042	.874	.958
Baumannia	-0.204	.432	.832
BF311	-0.057	.828	.943
Bifidobacterium	-0.350	.168	.798
Bilophila	-0.267	.300	.829
Blattabacterium	-0.204	.432	.832
Blautia	0.279	.277	.829
Blvii28	-0.032	.903	.969
Bradyrhizobium	-0.047	.857	.951
Brenneria	-0.385	.127	.798
Brevibacillus	-0.357	.159	.798
Brevibacterium	0.142	.587	.889
Brevundimonas	0.051	.846	.943

Genus	***r*** r_s	***p*-value**	**FDR-adjusted *p*-value**
BSL43	-0.257	.320	.829
Bulleidia	-0.058	.824	.943
Burkholderia	-0.167	.523	.872
Butyricimonas	0.201	.439	.835
Butyrivibrio	0.164	.529	.872
Caldicoprobacter	-0.359	.157	.798
Caloramator	-0.170	.515	.872
Campylobacter	0.335	.188	.798
Candidatus Accumulibacter	-0.204	.432	.832
Candidatus Ancillula	0.183	.482	.867
Candidatus Aquiluna	-0.035	.894	.962
Candidatus Arthromitus	-0.204	.432	.832
Candidatus Azobacteroides	-0.499	.041	.798
Candidatus Phytoplasma	0.357	.159	.798
Candidatus Portiera	0.521	.032	.798
Candidatus Tremblaya	0.408	.104	.798
Candidatus Xiphinematobacter	0.255	.323	.829
Capnocytophaga	-0.210	.418	.832
Carboxydocella	0.197	.449	.841
Cardiobacterium	-0.204	.432	.832
Catenibacterium	0.162	.535	.872
Catonella	-0.086	.742	.928
cc_115	0.209	.421	.832
Cellulosimicrobium	0.408	.104	.798
CF231	0.356	.160	.798
Christensenella	0.220	.395	.832
Chryseobacterium	0.127	.627	.907
Chthonomonas	-0.357	.159	.798
Citrobacter	0.010	.970	.999
Clostridiisalibacter	0.366	.148	.798
Clostridium (Clostridiaceae)	-0.301	.240	.829
Clostridium (Lachnospiraceae)	0.096	.715	.918
Clostridium (Peptostreptococcaceae)	-0.204	.432	.832
Clostridium (Ruminococcaceae)	0.000	1.000	1.000
Cobetia	-0.179	.491	.867
Collimonas	0.255	.323	.829
Collinsella	-0.105	.687	.907
Conchiformibius	-0.255	.323	.829
Coprobacillus	-0.372	.141	.798
Coprococcus	-0.186	.474	.864
Corynebacterium	0.233	.367	.832
Cronobacter	0.217	.402	.832

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Cryobacterium	-0.051	.846	.943
Cupriavidus	-0.255	.323	.829
Cylindrospermopsis	0.408	.104	.798
Dechloromonas	-0.114	.664	.907
Defluviitalea	-0.110	.675	.907
Dehalobacter_Syntrophobotulus	0.327	.200	.803
Dehalobacterium	0.265	.305	.829
Delftia	-0.295	.251	.829
Dermabacter	-0.408	.104	.798
Desulfitobacter	-0.306	.232	.829
Desulfococcus	0.514	.035	.798
Desulfomicrobium	0.367	.147	.798
Desulfosporosinus	-0.327	.200	.803
Desulfotomaculum	0.081	.757	.935
Desulfotomaculum_Desulfovirgula	0.101	.700	.907
Desulfovermiculus	0.408	.104	.798
Desulfovibrio	-0.069	.793	.943
Desulfurispora	0.285	.268	.829
Dethiosulfatibacter	0.236	.361	.832
Dialister	-0.066	.801	.943
Dickeya	-0.051	.846	.943
Dietzia	-0.051	.846	.943
Dok59	0.408	.104	.798
Dorea	0.137	.599	.894
Dysgonomonas	-0.253	.327	.829
ecb11	-0.396	.116	.798
Edwardsiella	0.357	.159	.798
Eggerthella	-0.186	.474	.864
Enterobacter	0.191	.463	.858
Enterococcus	0.088	.736	.928
Epulopiscium	0.059	.823	.943
Erwinia	0.346	.174	.798
Erysipelothrix	0.255	.323	.829
Escherichia	0.490	.046	.798
Ethanoligenens	0.104	.691	.907
Exiguobacterium	0.149	.568	.879
Facklamia	0.442	.076	.798
Faecalibacterium	0.297	.248	.829
Filifactor	-0.076	.773	.943
Fimbriimonas	0.193	.459	.855
Finegoldia	0.358	.158	.798
Flavisolibacter	0.306	.232	.829

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Flavobacterium	0.152	.560	.875
Frigoribacterium	0.408	.104	.798
Fusibacter	0.164	.529	.872
Fusobacterium	0.226	.383	.832
Gallicola	-0.267	.301	.829
Gallionella	-0.363	.152	.798
Garciella	-0.204	.432	.832
Gardnerella	-0.422	.092	.798
Gemella	0.026	.922	.976
Gemmiger	0.350	.168	.798
Geobacter	0.408	.104	.798
Geosporobacter_Thermotalea	-0.140	.592	.889
Gluconacetobacter	0.153	.557	.872
Gordonia	-0.123	.639	.907
Gracilibacter	0.167	.522	.872
Granulicatella	0.000	1.000	1.000
Guggenheimella	-0.013	.961	.996
GW-34	0.069	.794	.943
Haemophilus	-0.272	.291	.829
Halomonas	0.283	.271	.829
Helcococcus	-0.080	.761	.938
Herbaspirillum	0.204	.432	.832
Holdemania	0.066	.801	.943
HTCC	-0.051	.846	.943
HTCC2207	0.048	.854	.951
Hydrogenophaga	-0.255	.323	.829
Hymenobacter	-0.280	.276	.829
Janthinobacterium	0.193	.458	.855
Kitasatospora	-0.455	.066	.798
Klebsiella	0.391	.121	.798
Kocuria	0.357	.159	.798
L7A_E11	-0.204	.432	.832
Lachnobacterium	0.068	.796	.943
Lachnospira	0.103	.694	.907
Lactobacillus	0.319	.211	.826
Lactococcus	-0.079	.764	.940
Lautropia	-0.405	.107	.798
Lawsonia	0.325	.203	.803
LCP-6	0.357	.159	.798
Leclercia	0.357	.159	.798
Leptolyngbya	0.357	.159	.798
Leptospira	0.357	.159	.798

Genus	***r_s***	***p*-value**	**FDR-adjusted *p*-value**
Leptotrichia	-0.035	.894	.962
Leucobacter	-0.273	.290	.829
Leuconostoc	0.364	.151	.798
Limnobacter	0.204	.432	.832
Limnohabitans	0.102	.697	.907
Luteolibacter	0.357	.159	.798
Lutispora	0.088	.738	.928
Lysinibacillus	0.051	.846	.943
Lysobacter	0.051	.846	.943
Mannheimia	-0.102	.697	.907
Maribacter	0.102	.697	.907
Marinobacter	-0.043	.870	.957
Megamonas	0.149	.569	.880
Megasphaera	-0.052	.844	.943
Methylobacillus	-0.105	.688	.907
Methylomonas	0.190	.466	.862
Methylophaga	-0.408	.104	.798
Methylotenera	0.362	.153	.798
Microbacterium	-0.555	.021	.798
Microbispora	0.314	.219	.829
Micrococcus	-0.241	.352	.829
Mitsuokella	0.135	.606	.898
Mobiluncus	0.210	.418	.832
Mogibacterium	-0.381	.131	.798
Moorella	-0.357	.159	.798
Moraxella	0.280	.276	.829
Morganella	0.306	.232	.829
Moritella	-0.255	.323	.829
Moryella	0.213	.411	.832
Mycoplasma	-0.072	.782	.943
Natronincola_Anaerovirgula	0.168	.519	.872
Neisseria	0.394	.117	.798
Niigata-25	-0.118	.652	.907
Nocardia	-0.140	.592	.889
Nocardiopsis	-0.306	.232	.829
NP25	0.358	.159	.798
Oceanicaulis	0.059	.822	.943
Oceanimonas	0.102	.697	.907
Odoribacter	-0.123	.639	.907
Oleispira	-0.210	.418	.832
Oribacterium	0.076	.772	.943
Oscillospira	-0.147	.573	.884

Genus	r_s	*p*-value	FDR-adjusted *p*-value
Oxalobacter	-0.186	.474	.864
Oxobacter	0.101	.700	.907
p-75-a5	0.164	.529	.872
Paenibacillus	0.155	.553	.872
Paenisporosarcina	0.255	.323	.829
Paludibacter	0.145	.580	.888
Pandoraea	0.018	.944	.987
Pantoea	-0.257	.320	.829
Parabacteroides	0.172	.510	.868
Paracoccus	0.329	.197	.798
Paraprevotella	-0.042	.874	.958
Parvimonas	0.040	.877	.960
Pasteurella	-0.114	.663	.907
Pectinatus	-0.357	.159	.798
Pediococcus	-0.051	.846	.943
Pedobacter	0.400	.112	.798
Pelosinus	-0.105	.688	.907
Pelotomaculum	-0.146	.576	.886
Peptococcus	-0.060	.818	.943
Peptoniphilus	0.238	.358	.832
Peptostreptococcus	-0.397	.114	.798
Perlucidibaca	-0.306	.232	.829
ph2	-0.040	.879	.961
Phascolarctobacterium	-0.100	.701	.907
Photobacterium	0.011	.966	.998
Photorhabdus	-0.405	.106	.798
Planomicrobium	0.245	.343	.829
Plesiomonas	0.160	.539	.872
Polynucleobacter	-0.012	.963	.996
Porphyromonas	0.257	.319	.829
Prevotella	-0.012	.963	.996
Propionibacterium	-0.176	.499	.867
Proteiniclasticum	-0.135	.607	.898
Proteus	-0.311	.225	.829
Providencia	-0.271	.292	.829
Pseudoalteromonas	0.063	.810	.943
Pseudobutyrivibrio	-0.154	.554	.872
Pseudochrobactrum	0.408	.104	.798
Pseudomonas	-0.162	.535	.872
Pseudonocardia	0.092	.725	.925
Pseudoramibacter_Eubacterium	-0.307	.231	.829
Psychrobacter	-0.350	.169	.798

Genus	r_s	*p*-value	FDR-adjusted *p*-value
Psychromonas	-0.216	.405	.832
PW3	-0.041	.877	.960
Ralstonia	-0.046	.861	.952
Ramlibacter	0.000	1.000	1.000
Rathayibacter	0.051	.846	.943
rc4-4	-0.166	.525	.872
RFN20	0.061	.817	.943
Rheinheimera	0.201	.440	.835
Rhizobium	-0.204	.432	.832
Rhodococcus	-0.132	.614	.904
Rhodoferax	0.343	.178	.798
Rhodothermus	-0.204	.432	.832
Rikenella	-0.461	.063	.798
Roseburia	-0.250	.333	.829
Rothia	0.273	.289	.829
Rubrivivax	0.298	.245	.829
Ruminococcus	0.502	.040	.798
Salinibacter	-0.035	.894	.962
Salinibacterium	-0.204	.432	.832
Salinispora	0.086	.744	.928
Salmonella	0.241	.352	.829
Sarcina	0.255	.323	.829
Scardovia	0.292	.256	.829
Schwartzia	0.333	.192	.798
Sedimentibacter	0.071	.786	.943
Selenomonas	0.382	.130	.798
Serratia	0.331	.195	.798
SGUS912	0.357	.159	.798
Sharpea	0.262	.310	.829
Shewanella	0.210	.418	.832
Shigella	0.240	.354	.829
Shuttleworthia	0.270	.294	.829
Slackia	-0.105	.687	.907
SMB53	-0.306	.232	.829
Sorangium	0.350	.168	.798
Sphingobacterium	0.267	.300	.829
Sphingobium	-0.204	.432	.832
Sphingomonas	0.245	.343	.829
Sporanaerobacter	-0.206	.427	.832
Sporomusa	-0.138	.597	.893
Sporotomaculum	0.003	.991	1.000
Staphylococcus	0.030	.910	.973

Genus	r_s	*p*-value	FDR-adjusted *p*-value
Stenotrophomonas	0.490	.046	.798
Streptococcus	0.221	.395	.832
Streptomyces	-0.154	.554	.872
Succiniclasticum	-0.118	.653	.907
Succinivibrio	-0.376	.137	.798
Sulfobacillus	0.177	.497	.867
Sulfurimonas	0.214	.409	.832
Sulfuritalea	0.057	.828	.943
Sutterella	-0.199	.445	.838
Symbiobacterium	0.241	.352	.829
Syntrophobacter	0.408	.104	.798
Syntrophomonas	-0.360	.155	.798
Syntrophus	0.051	.846	.943
T78	-0.102	.697	.907
Tannerella	0.088	.736	.928
Telmatospirillum	-0.051	.846	.943
Tepidibacter	-0.332	.193	.798
Tepidimicrobium	-0.172	.510	.868
Tepidimonas	0.267	.300	.829
Terracoccus	-0.525	.030	.798
TG5	-0.408	.104	.798
Thauera	0.432	.084	.798
Thermicanus	0.102	.697	.907
Thermoanaerobacter	-0.153	.557	.872
Thermoanaerobacterium	0.111	.671	.907
Thermosinus	0.161	.537	.872
Thiobacillus	0.051	.846	.943
Thiomicrospira	0.204	.432	.832
Thiomonas	-0.255	.323	.829
Tindallia_Anoxynatronum	-0.321	.210	.822
Tissierella_Soehngenia	0.260	.314	.829
Tolumonas	0.357	.159	.798
Trabulsiella	0.221	.394	.832
Treponema	0.357	.159	.798
Trichococcus	-0.210	.418	.832
Turicibacter	0.101	.700	.907
vadinHB04	-0.047	.859	.951
Vagococcus	0.357	.159	.798
Varibaculum	-0.306	.232	.829
Variovorax	-0.255	.323	.829
Veillonella	-0.255	.323	.829
Vestibaculum	0.102	.697	.907

Genus	r_s	***p*-value**	**FDR-adjusted *p*-value**
Vibrio (Pseudoalteromonadacea)	-0.033	.899	.966
Vibrio (Vibrionaceae)	-0.116	.656	.907
Virgibacillus	-0.179	.491	.867
WAL_1855D	0.072	.782	.943
WH1-8	-0.180	.488	.867
Wohlfahrtiimonas	0.051	.846	.943
Xanthomonas	-0.347	.172	.798
Xenorhabdus	-0.051	.846	.943
Yaniella	-0.204	.432	.832
Yersinia	0.376	.137	.798
YRC22	-0.077	.769	.943
Bacteroides/Prevotella Ratio	-0.074	.779	.943

FDR, False Discovery Rate; sRPE, Session-Rating of Perceived Exertion. The variation variable was calculated by subtracting the relative abundance of taxa at baseline from the relative abundance at the end of the tournament. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.

Supplementary Table 12: Spearman's rank correlation between the volume and sRPE of training sessions and matches and the variation in species.

Species	r_s	***p*-value**	**FDR-adjusted *p*-value**
Volume			
[Clostridium] bifermentans	-0.141	.590	.889
[Clostridium] sordellii	0.109	.678	.907
[Eubacterium] biforme	0.052	.844	.943
[Eubacterium] dolichum	0.349	.169	.798
[Prevotella] tannerae	-0.246	.340	.829
[Ruminococcus] gnavus	-0.004	.989	1.000
[Ruminococcus] torques	-0.117	.655	.907
Achromobacter xylosoxidans	0.154	.556	.872
Acinetobacter johnsonii	0.000	1.000	1.000
Acinetobacter venetianus	0.334	.191	.798
Actinobacillus parahaemolyticus	0.298	.245	.829
Actinomadura vinacea	0.370	.144	.798
Aggregatibacter pneumotropica	0.035	.893	.962
Aggregatibacter segnis	0.158	.544	.872
Akkermansia muciniphila	0.177	.496	.867
Alcaligenes faecalis	-0.412	.100	.798
Alkaliphilus transvaalensis	0.026	.921	.976
Anaerophaga thermohalophila	0.370	.144	.798
Aneurinibacillus migulanus	-0.257	.320	.829
Arthrobacter scleromae	0.000	1.000	1.000
Atopobium rimae	0.154	.555	.872

Species	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Bacillus badius	0.334	.191	.798
Bacillus cereus	0.176	.499	.867
Bacillus endophyticus	0.000	1.000	1.000
Bacillus flexus	-0.530	.029	.798
Bacteroides acidifaciens	0.398	.113	.798
Bacteroides barnesiae	0.205	.431	.832
Bacteroides caccae	0.182	.484	.867
Bacteroides coprophilus	-0.300	.242	.829
Bacteroides coprosuis	0.421	.092	.798
Bacteroides eggerthii	-0.409	.103	.798
Bacteroides fragilis	-0.063	.811	.943
Bacteroides kribbi	-0.151	.563	.876
Bacteroides ovatus	-0.242	.350	.829
Bacteroides plebeius	0.004	.989	1.000
Bacteroides uniformis	0.442	.075	.798
Baumannia cicadellinicola	-0.103	.695	.907
Bifidobacterium adolescentis	-0.058	.825	.943
Bifidobacterium animalis	-0.334	.190	.798
Bifidobacterium bifidum	0.402	.110	.798
Bifidobacterium breve	-0.252	.329	.829
Bifidobacterium eulemuris	0.000	1.000	1.000
Bifidobacterium longum	-0.217	.403	.832
Bifidobacterium pseudolongum	-0.026	.920	.976
Bifidobacterium thermacidophilum	-0.136	.603	.896
Bilophila sp.	0.317	.215	.829
Blautia obeum	0.067	.800	.943
Blautia producta	0.228	.379	.832
Bradyrhizobium elkanii	-0.017	.950	.989
Brenneria rubrifaciens	-0.158	.544	.872
Brevibacillus invocatus	-0.334	.191	.798
Brevibacillus reuszeri	0.334	.191	.798
Brevibacterium casei	-0.070	.788	.943
Brevibacterium paucivorans	0.205	.429	.832
Brevundimonas diminuta	0.000	1.000	1.000
Bulleidia moorei	-0.177	.497	.867
Bulleidia p-1630-c5	-0.270	.294	.829
Burkholderia bryophila	0.000	1.000	1.000
Burkholderia gladioli	-0.103	.695	.907
Campylobacter ureolyticus	0.257	.320	.829
Candidatus Aquiluna rubra	-0.070	.788	.943
Capnocytophaga ochracea	0.103	.695	.907
Clostridium acetobutylicum	0.325	.204	.804

Species	r_s	***p*-value**	**FDR-adjusted *p*-value**
Clostridium algidixylanolyticum	0.457	.065	.798
Clostridium bowmanii	-0.024	.927	.980
Clostridium butyricum	-0.257	.320	.829
Clostridium celerecrescens	0.440	.077	.798
Clostridium clostridioforme	0.399	.112	.798
Clostridium colinum	0.154	.555	.872
Clostridium hiranonis	-0.242	.350	.829
Clostridium intestinale	-0.154	.555	.872
Clostridium islandicum	-0.411	.102	.798
Clostridium metallolevans	-0.205	.429	.832
Clostridium neonatale	-0.257	.320	.829
Clostridium perfringens	0.232	.371	.832
Clostridium piliforme	-0.200	.441	.835
Clostridium purinilyticum	0.103	.695	.907
Clostridium sartagoforme	-0.453	.068	.798
Clostridium sphenoides	0.444	.074	.798
Collinsella aerofaciens	0.265	.304	.829
Collinsella stercoris	0.159	.542	.872
Coprobacillus cateniformis	-0.334	.190	.798
Coprococcus catus	-0.288	.262	.829
Coprococcus eutactus	0.087	.738	.928
Corynebacterium durum	0.103	.695	.907
Corynebacterium stationis	0.334	.191	.798
Corynebacterium variabile	0.257	.320	.829
Cronobacter sakazakii	0.127	.626	.907
Cryobacterium psychrophilum	0.103	.695	.907
Defluviitalea saccharophila	-0.228	.378	.832
Desulfosporosinus meridiei	-0.051	.845	.943
Desulfovibrio aminophilus	-0.447	.072	.798
Desulfovibrio C21_c20	-0.070	.791	.943
Desulfovibrio D168	0.057	.827	.943
Desulfovibrio dechloracetivorans	-0.339	.183	.798
Dickeya zeae	0.103	.695	.907
Dorea formicigenerans	0.177	.496	.867
Eggerthella lenta	-0.097	.712	.918
Enterobacter aerogenes	0.485	.048	.798
Enterobacter cloacae	-0.359	.157	.798
Enterobacter kobei	-0.011	.967	.998
Enterobacter ludwigii	0.000	1.000	1.000
Enterococcus haemoperoxidus	0.154	.555	.872
Erwinia soli	0.363	.152	.798
Escherichia coli	0.475	.054	.798

Species	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Faecalibacterium prausnitzii	0.296	.249	.829
Gemmiger formicilis	0.246	.340	.829
Haemophilus influenzae	0.028	.916	.976
Haemophilus parainfluenzae	-0.308	.229	.829
Halomonas anticariensis	0.141	.590	.889
Janthinobacterium lividum	0.045	.864	.954
Kitasatospora pitsanulaokmensis	-0.205	.429	.832
Klebsiella oxytoca	0.522	.032	.798
Kocuria rhizophila	0.334	.191	.798
Lactobacillus delbrueckii	0.332	.193	.798
Lactobacillus mucosae	-0.103	.695	.907
Lactobacillus zeae	0.405	.107	.798
Lactococcus garvieae	0.334	.191	.798
Leclercia adecarboxylata	0.334	.191	.798
Lysinibacillus boronitolerans	-0.103	.695	.907
Marinobacter hydrocarbonoclasticus	-0.103	.695	.907
Megamonas hypermegale	0.056	.830	.943
Methylotenera mobilis	0.477	.053	.798
Microbispora rosea	0.200	.441	.835
Micrococcus luteus	-0.158	.544	.872
Mitsuokella multacida	-0.154	.554	.872
Morganella morganii	0.334	.191	.798
Nocardiopsis exhalans	-0.334	.191	.798
Oscillospira guilliermondii	0.304	.236	.829
Oxalobacter formigenes	-0.205	.431	.832
Pantoea agglomerans	-0.082	.754	.932
Pantoea ananatis	0.334	.191	.798
Pantoea dispersa	-0.127	.627	.907
Parabacteroides distasonis	0.264	.306	.829
Parabacteroides gordonii	-0.017	.950	.989
Paracoccus aminovorans	0.288	.262	.829
Paracoccus marcusii	0.205	.429	.832
Pasteurella multocida	0.334	.191	.798
Pedobacter cryoconitis	0.174	.503	.867
Photorhabdus temperata	-0.257	.319	.829
Plesiomonas shigelloides	0.274	.287	.829
Porphyromonas endodontalis	0.200	.440	.835
Prevotella copri	-0.201	.440	.835
Prevotella intermedia	-0.221	.393	.832
Prevotella melaninogenica	-0.053	.840	.943
Prevotella nanceiensis	-0.332	.193	.798
Prevotella nigrescens	-0.309	.227	.829

Species	***r*$_s$**	***p*-value**	**FDR-adjusted *p*-value**
Prevotella pallens	-0.331	.195	.798
Prevotella stercorea	-0.598	.011	.798
Propionibacterium acnes	-0.085	.746	.928
Propionibacterium granulosum	0.334	.191	.798
Pseudoalteromonas piscicida	0.158	.544	.872
Pseudobutyrivibrio xylanivorans	-0.237	.359	.832
Pseudomonas fragi	0.103	.695	.907
Pseudomonas stutzeri	0.363	.152	.798
Pseudomonas veronii	0.071	.788	.943
Rathayibacter caricis	-0.103	.695	.907
Rhizobium leguminosarum	-0.103	.695	.907
Rhodococcus fascians	0.000	1.000	1.000
Rhodococcus ruber	-0.205	.429	.832
Roseburia faecis	-0.561	.019	.798
Rothia dentocariosa	0.157	.547	.872
Rothia mucilaginosa	0.117	.656	.907
Ruminococcus albus	-0.365	.149	.798
Ruminococcus bromii	0.450	.070	.798
Ruminococcus callidus	0.180	.489	.867
Ruminococcus flavefaciens	0.142	.587	.889
Salinispora tropica	-0.359	.156	.798
Salmonella enterica	0.173	.507	.868
Selenomonas noxia	-0.060	.819	.943
Selenomonas ruminantium	0.387	.125	.798
Serratia marcescens	0.226	.383	.832
Serratia proteamaculans	0.132	.612	.903
Serratia symbiotica	-0.259	.315	.829
Shewanella benthica	0.334	.191	.798
Shigella flexneri	0.239	.356	.829
Sorangium cellulosum	0.246	.340	.829
Sphingobacterium faecium	0.326	.202	.803
Sphingobacterium multivorum	0.257	.320	.829
Sphingobium yanoikuyae	-0.103	.695	.907
Sporomusa polytropa	-0.103	.695	.907
Staphylococcus epidermidis	-0.088	.737	.928
Stenotrophomonas geniculata	0.359	.157	.798
Stenotrophomonas retroflexus	-0.359	.157	.798
Streptococcus alactolyticus	-0.359	.157	.798
Streptococcus anginosus	0.000	1.000	1.000
Streptococcus infantis	0.252	.329	.829
Streptococcus luteciae	0.410	.102	.798
Streptococcus sobrinus	0.023	.930	.980

Species	r_s	***p*-value**	**FDR-adjusted *p*-value**
Streptomyces ahygroscopicus	-0.205	.429	.832
Thermoanaerobacter uzonensis	-0.257	.320	.829
Thermoanaerobacterium saccharolyticum	-0.161	.536	.872
Trabulsiella farmeri	0.326	.202	.803
Vagococcus salmoninarum	0.334	.191	.798
Variovorax paradoxus	-0.359	.157	.798
Veillonella dispar	-0.285	.268	.829
Veillonella parvula	0.208	.424	.832
Vestibaculum illigatum	-0.154	.555	.872
Vibrio atlanticus	-0.359	.157	.798
Vibrio cholerae	-0.359	.157	.798
Vibrio fortis	0.334	.191	.798
Vibrio harveyi	0.299	.243	.829
Vibrio rumoiensis	0.103	.695	.907
Virgibacillus marismortui	0.009	.973	.999
Xanthomonas campestris	-0.252	.329	.829
Xenorhabdus nematophila	0.103	.695	.907
sRPE			
[Clostridium] bifermentans	-0.398	.113	.798
[Clostridium] sordellii	0.140	.592	.889
[Eubacterium] biforme	0.262	.309	.829
[Eubacterium] dolichum	0.437	.080	.798
[Prevotella] tannerae	-0.198	.446	.838
[Ruminococcus] gnavus	0.299	.244	.829
[Ruminococcus] torques	-0.091	.729	.928
Achromobacter xylosoxidans	0.207	.425	.832
Acinetobacter johnsonii	0.051	.846	.943
Acinetobacter venetianus	0.357	.159	.798
Actinobacillus parahaemolyticus	0.261	.312	.829
Actinomadura vinacea	0.350	.168	.798
Aggregatibacter pneumotropica	-0.070	.789	.943
Aggregatibacter segnis	0.105	.688	.907
Akkermansia muciniphila	0.089	.734	.928
Alcaligenes faecalis	-0.218	.400	.832
Alkaliphilus transvaalensis	0.101	.699	.907
Anaerophaga thermohalophila	0.385	.127	.798
Aneurinibacillus migulanus	-0.255	.323	.829
Arthrobacter scleromae	0.051	.846	.943
Atopobium rimae	-0.102	.697	.907
Bacillus badius	0.357	.159	.798
Bacillus cereus	0.070	.789	.943
Bacillus endophyticus	0.031	.907	.971

Species	r_s	*p*-value	FDR-adjusted *p*-value
Bacillus flexus	-0.138	.597	.893
Bacteroides acidifaciens	0.264	.307	.829
Bacteroides barnesiae	0.037	.889	.962
Bacteroides caccae	0.206	.428	.832
Bacteroides coprophilus	-0.368	.146	.798
Bacteroides coprosuis	0.502	.040	.798
Bacteroides eggerthii	-0.323	.206	.810
Bacteroides fragilis	0.034	.896	.963
Bacteroides kribbi	-0.365	.150	.798
Bacteroides ovatus	-0.179	.492	.867
Bacteroides plebeius	0.093	.722	.924
Bacteroides uniformis	0.294	.252	.829
Baumannia cicadellinicola	-0.204	.432	.832
Bifidobacterium adolescentis	-0.289	.260	.829
Bifidobacterium animalis	-0.524	.031	.798
Bifidobacterium bifidum	0.259	.315	.829
Bifidobacterium breve	-0.300	.242	.829
Bifidobacterium eulemuris	-0.051	.846	.943
Bifidobacterium longum	-0.242	.350	.829
Bifidobacterium pseudolongum	-0.127	.628	.907
Bifidobacterium thermacidophilum	-0.042	.872	.958
Bilophila sp.	0.105	.688	.907
Blautia obeum	0.113	.667	.907
Blautia producta	0.377	.135	.798
Bradyrhizobium elkanii	0.132	.614	.904
Brenneria rubrifaciens	-0.385	.127	.798
Brevibacillus invocatus	-0.357	.159	.798
Brevibacillus reuszeri	0.357	.159	.798
Brevibacterium casei	-0.101	.701	.907
Brevibacterium paucivorans	0.408	.104	.798
Brevundimonas diminuta	0.051	.846	.943
Bulleidia moorei	0.057	.828	.943
Bulleidia p-1630-c5	-0.206	.427	.832
Burkholderia bryophila	0.051	.846	.943
Burkholderia gladioli	0.051	.846	.943
Campylobacter ureolyticus	0.153	.557	.872
Candidatus Aquiluna rubra	-0.035	.894	.962
Capnocytophaga ochracea	-0.051	.846	.943
Clostridium acetobutylicum	0.537	.026	.798
Clostridium algidixylanolyticum	0.141	.591	.889
Clostridium bowmanii	-0.176	.499	.867
Clostridium butyricum	-0.255	.323	.829

Species	r_s	***p*-value**	**FDR-adjusted *p*-value**
Clostridium celerecrescens	0.111	.671	.907
Clostridium clostridioforme	0.497	.042	.798
Clostridium colinum	0.306	.232	.829
Clostridium hiranonis	-0.451	.069	.798
Clostridium intestinale	-0.306	.232	.829
Clostridium islandicum	0.000	1.000	1.000
Clostridium metallolevans	-0.204	.432	.832
Clostridium neonatale	-0.153	.557	.872
Clostridium perfringens	0.250	.333	.829
Clostridium piliforme	-0.192	.460	.855
Clostridium purinilyticum	-0.051	.846	.943
Clostridium sartagoforme	-0.452	.069	.798
Clostridium sphenoides	0.234	.366	.832
Collinsella aerofaciens	-0.091	.729	.928
Collinsella stercoris	-0.056	.830	.943
Coprobacillus cateniformis	-0.420	.093	.798
Coprococcus catus	-0.306	.233	.829
Coprococcus eutactus	-0.039	.881	.962
Corynebacterium durum	-0.051	.846	.943
Corynebacterium stationis	0.306	.232	.829
Corynebacterium variabile	0.153	.557	.872
Cronobacter sakazakii	0.217	.402	.832
Cryobacterium psychrophilum	-0.051	.846	.943
Defluviitalea saccharophila	-0.110	.675	.907
Desulfosporosinus meridiei	-0.284	.270	.829
Desulfovibrio aminophilus	-0.145	.579	.888
Desulfovibrio C21_c20	-0.175	.503	.867
Desulfovibrio D168	0.227	.382	.832
Desulfovibrio dechloracetivorans	-0.258	.317	.829
Dickeya zeae	-0.051	.846	.943
Dorea formicigenerans	0.137	.599	.894
Eggerthella lenta	-0.186	.474	.864
Enterobacter aerogenes	0.507	.038	.798
Enterobacter cloacae	-0.357	.159	.798
Enterobacter kobei	-0.031	.907	.971
Enterobacter ludwigii	0.051	.846	.943
Enterococcus haemoperoxidus	-0.102	.697	.907
Erwinia soli	0.206	.428	.832
Escherichia coli	0.490	.046	.798
Faecalibacterium prausnitzii	0.297	.248	.829
Gemmiger formicilis	0.350	.168	.798
Haemophilus influenzae	-0.228	.378	.832

Species	r_s	*p*-value	FDR-adjusted *p*-value
Haemophilus parainfluenzae	-0.272	.291	.829
Halomonas anticariensis	0.283	.271	.829
Janthinobacterium lividum	0.258	.318	.829
Kitasatospora pitsanulaokmensis	-0.408	.104	.798
Klebsiella oxytoca	0.586	.013	.798
Kocuria rhizophila	0.357	.159	.798
Lactobacillus delbrueckii	0.212	.414	.832
Lactobacillus mucosae	-0.204	.432	.832
Lactobacillus zeae	0.333	.192	.798
Lactococcus garvieae	0.357	.159	.798
Leclercia adecarboxylata	0.357	.159	.798
Lysinibacillus boronitolerans	0.051	.846	.943
Marinobacter hydrocarbonoclasticus	0.051	.846	.943
Megamonas hypermegale	0.175	.503	.867
Methylotenera mobilis	0.362	.153	.798
Microbispora rosea	0.314	.219	.829
Micrococcus luteus	-0.280	.276	.829
Mitsuokella multacida	0.129	.622	.906
Morganella morganii	0.306	.232	.829
Nocardiopsis exhalans	-0.306	.232	.829
Oscillospira guilliermondii	0.278	.280	.829
Oxalobacter formigenes	-0.186	.474	.864
Pantoea agglomerans	-0.043	.870	.957
Pantoea ananatis	0.306	.232	.829
Pantoea dispersa	-0.243	.347	.829
Parabacteroides distasonis	0.132	.613	.903
Parabacteroides gordonii	-0.036	.890	.962
Paracoccus aminovorans	0.109	.678	.907
Paracoccus marcusii	0.408	.104	.798
Pasteurella multocida	0.357	.159	.798
Pedobacter cryoconitis	0.400	.112	.798
Photorhabdus temperata	-0.241	.352	.829
Plesiomonas shigelloides	0.160	.539	.872
Porphyromonas endodontalis	0.053	.839	.943
Prevotella copri	-0.076	.772	.943
Prevotella intermedia	-0.300	.242	.829
Prevotella melaninogenica	0.078	.765	.940
Prevotella nanceiensis	-0.342	.180	.798
Prevotella nigrescens	-0.252	.328	.829
Prevotella pallens	-0.203	.434	.835
Prevotella stercorea	-0.538	.026	.798
Propionibacterium acnes	-0.176	.499	.867

Species	**r_s**	***p*-value**	**FDR-adjusted *p*-value**
Propionibacterium granulosum	0.357	.159	.798
Pseudoalteromonas piscicida	0.105	.688	.907
Pseudobutyrivibrio xylanivorans	-0.208	.423	.832
Pseudomonas fragi	-0.051	.846	.943
Pseudomonas stutzeri	0.206	.428	.832
Pseudomonas veronii	0.009	.973	.999
Rathayibacter caricis	0.051	.846	.943
Rhizobium leguminosarum	-0.204	.432	.832
Rhodococcus fascians	-0.051	.846	.943
Rhodococcus ruber	-0.408	.104	.798
Roseburia faecis	-0.250	.333	.829
Rothia dentocariosa	0.123	.637	.907
Rothia mucilaginosa	0.136	.604	.896
Ruminococcus albus	-0.277	.282	.829
Ruminococcus bromii	0.395	.117	.798
Ruminococcus callidus	0.185	.476	.866
Ruminococcus flavefaciens	0.093	.722	.924
Salinispora tropica	-0.074	.779	.943
Salmonella enterica	0.241	.352	.829
Selenomonas noxia	-0.051	.847	.943
Selenomonas ruminantium	0.525	.030	.798
Serratia marcescens	0.387	.125	.798
Serratia proteamaculans	0.089	.734	.928
Serratia symbiotica	-0.257	.320	.829
Shewanella benthica	0.357	.159	.798
Shigella flexneri	0.240	.354	.829
Sorangium cellulosum	0.350	.168	.798
Sphingobacterium faecium	0.206	.428	.832
Sphingobacterium multivorum	0.153	.557	.872
Sphingobium yanoikuyae	-0.204	.432	.832
Sporomusa polytropa	-0.204	.432	.832
Staphylococcus epidermidis	0.035	.894	.962
Stenotrophomonas geniculata	0.357	.159	.798
Stenotrophomonas retroflexus	-0.357	.159	.798
Streptococcus alactolyticus	-0.408	.104	.798
Streptococcus anginosus	-0.051	.846	.943
Streptococcus infantis	0.209	.420	.832
Streptococcus luteciae	0.298	.245	.829
Streptococcus sobrinus	0.036	.890	.962
Streptomyces ahygroscopicus	-0.204	.432	.832
Thermoanaerobacter uzonensis	-0.153	.557	.872
Thermoanaerobacterium saccharolyticum	-0.193	.458	.855

Species	***r_s***	***p*-value**	**FDR-adjusted *p*-value**
Trabulsiella farmeri	0.206	.428	.832
Vagococcus salmoninarum	0.357	.159	.798
Variovorax paradoxus	-0.255	.323	.829
Veillonella dispar	-0.252	.328	.829
Veillonella parvula	0.301	.241	.829
Vestibaculum illigatum	0.102	.697	.907
Vibrio atlanticus	-0.357	.159	.798
Vibrio cholerae	-0.357	.159	.798
Vibrio fortis	0.357	.159	.798
Vibrio harveyi	0.175	.502	.867
Vibrio rumoiensis	-0.051	.846	.943
Virgibacillus marismortui	-0.179	.491	.867
Xanthomonas campestris	-0.347	.172	.798
Xenorhabdus nematophila	-0.051	.846	.943

FDR, False Discovery Rate; sRPE, Session-Rating of Perceived Exertion. The variation variable was calculated by subtracting the relative abundance of taxa at baseline from the relative abundance at the end of the tournament. The FDR-adjusted *p*-values were assumed to be statistically significant when < 0.05.