Accepted Manuscript

Submission Date: 2021-03-26
Accepted Date: 2022-05-20
Publication Date: 2022-05-20

International Journal of Sports Medicine

Fecal microbiota monitoring in elite soccer players along the 2019-2020 competitive season

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DOI: 10.1055/a-1858-1810

Please cite this article as: Viciani E, Barone M, Bongiovanni T et al. Fecal microbiota monitoring in elite soccer players along the 2019-2020 competitive season. International Journal of Sports Medicine 2022. doi: 10.1055/a-1858-1810

Conflict of Interest: The authors declare that they have no conflict of interest.

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Keywords: gut microbiota, athletes, soccer, longitudinal, 16S rRNA sequencing

1. Introduction

The human gut microbiota is the rich and diverse microbial community that inhabits the distal section of the human intestinal tract. Research in this field has flourished over the past two decades thanks to technological advances in next-generation sequencing and other high-throughput molecular profiling approaches[1]. These advances have allowed the scientific community to highlight the high level of association between the gut microbiota compositional structure with the host's physiology and health. The gut microbiota actively contributes to maintaining the function of the immune system and inflammatory balance, metabolic homeostasis, as well as endocrine and central nervous system functionality[2,3]. Correlations have been proposed with gut microbiota composition for many human-associated variables, starting with age, gender, genetic background, dietary and lifestyle habits, as well as geographical origins, ethnicity, and socio-economic status[4–6].

Physical exercise intensity and pattern have been reported to affect the composition of the human gut microbiota and associated metabolites[7–10], although it is undeniably difficult to separate the effect of exercise from that of other variables, nutrition above all[11,12]. Recently, the composition and functionality of the gut microbiota in professional athletes have been the focus of numerous studies[11,13–19]. Such interest has several drivers: first, the gut microbiota is strongly involved in the regulation of energy storage and production[20], an aspect of utmost importance for maintaining optimal performances during the different phases of training[21]. Indeed, it has been proposed that the microbiota may be a potential predictor of athletes' response to nutritional strategies[22], actively contributing to the optimal use and absorption of energy from food components, as well as producing vitamins and essential amino acids for the host[23]. Second, various aspects of the peculiar life of professional athletes can affect the gut ecosystem through different mechanisms. For instance, high-intensity exercise can jeopardize the integrity of the gastrointestinal epithelium, promoting inflammatory patterns, which can affect the composition of the locally resident

microbiota[21]. Professional athletes are also subject to high psychological stress, for example due to constant pressure for optimal performances and frequent travels, known to have an impact on the gut microbiota[21,24,25].

A suboptimal gut microbiota configuration, as a result of the aforementioned stressors, has been proposed to influence various aspects of an athlete's performance. Indeed, gastrointestinal health has been estimated as suboptimal in 30-50% of athletes, who frequently report gastrointestinal symptoms[24,26]. By undermining immunological and inflammatory homeostasis, both at local and systemic levels[27], an altered microbiota can help in promoting illnesses and delaying recovery after injuries and intense training[21,28]. Furthermore, being involved in the regulation of the hypothalamic-pituitary axis, a compromised gut microbiota structure can affect the levels of neurotransmitters and neurotransmitters-like substances[29,30], indirectly contributing to the promotion of stress-related disorders and overtraining syndrome[24,28,31].

In this scenario, it has been proposed that microbiota research could contribute significantly to sports and exercise medicine and that, in future, microbiota-related indicators could enter the plethora of measurements for fitness, health and the well-being of athletes[32]. Nowadays, elite athletes undergo continuous monitoring of workload, nutrition, as well as the measurement of many parameters of fitness and health, as a comprehensive strategy of diseases prevention and maintenance of performance. Laboratory medicine is becoming essential in the modern conception of professional sports in order to ensure top performances and success in competitions[33–35]. However, there are still no personalized approaches that include microbiota optimization for maintaining athlete performance, and our current understanding of how the gut microbiota of professional athletes changes along with the different phases of training during a competitive season is still far from complete. To date, the literature that takes this longitudinal aspect into account is scant. Ultra-endurance athletes were monitored longitudinally during prolonged intense exercise, *i.e*. an "extreme" situation, reporting an increase in gut microbial biodiversity during the competitive event[36]. Hampton-Marcell and colleagues[17] reported gut microbiota compositional

changes and decreased biodiversity proportional to the reduction in training volume during the active season for collegiate competitive swimmers. On the other hand, it was highlighted that microbiota composition and metabolic pattern changed among elite athletes of different types of sports, underlining the need for further, sport-targeted research with the aim of linking microbiota and performances[19].

To further enrich the amount of knowledge on microbiota variations in different phases of training, and shed some light on the microbiota peculiarities of elite athletes in a sport that consists of high-intensity intermittent exercises[37], here we characterize the stool microbiota in a group of elite soccer players of an Italian professional team during the 2019-2020 competitive season. We monitored the gut microbiota composition of enrolled athletes, using 16S rRNA gene targeted sequencing, after the off-season summer period, pre-season high-intensity training retreat and the first part of the competitive soccer season. The 2019-2020 Italian soccer season was interrupted by the COVID-19 pandemic, forcing a rigorous 8-week lockdown during which sporting events were banned. The athletes were then forced into an unnatural situation of isolation and home-training. The microbiota analysis before the resumption of the competitive season allowed us to investigate the lockdown effects. Our study aims to provide sports medicine with augmented knowledge on the progressive gut microbiota variations that occur during lifestyle and workload changes during the competitive season of one of the most followed sports worldwide. Although further longitudinal studies on larger cohorts are needed to bolster our findings, herein we provide insights for the development of innovative and customized training and nutrition plans, aimed at maximizing performance and optimizing the microbiome.

2. Materials and methods

2.1 Study design and fecal samples collection

Thirty-eight professional male soccer players of the Parma Calcio team (Italy), aged 18-37 years with average weight and height of 79.5 ± 7.5 Kg and 185.0 ± 0.1 cm respectively, were initially recruited at the beginning of the 2019/2020 competitive season (July 8th, 2019). An age below 18 constituted the only exclusion criterion. All subjects received an explanation of the study and were asked to read and sign a written informed consent. The study protocol was approved by the Ethics Committee of the Sant'Orsola-Malpighi Hospital, University of Bologna (ref. number, 118/2015/U/Tess). The longitudinal study design, with the fecal sampling time points in relation to the different phases of the Italian soccer competitive season, is depicted in **Fig. 1**. Briefly, the samples were collected from players returning from the summer holidays (off-season, 6 weeks, from May 25th to July 7th, 2019) (T0). During off-season, footballers recovered from the in-season fatigue, training intensity was low to moderate, and food intake was free. The subjects then began their preparation for the competitive season (pre-season, from July 8th to August 23rd, 2019). The first part of the pre-season phase (4 weeks) was held in a mountain refuge and was characterized by intense training (11-12 hours per week on average), co-living (2 people per hotel room) and strictly controlled nutrition (menu pre-established by the club nutritionist, consisting of 6 meals consumed in the same restaurant). The second fecal sample was collected after the 4-week retreat (T1). During the second part of the pre-season (3 weeks) the athletes returned to training at the club's sports center, ate breakfast and lunch together, and consumed the other 3 meals at home, following the nutritionist's instructions. Once the championship started (in-season, from August 24th, 2019), the players were exposed to 7-8 hours of training per week plus the weekly match; they had breakfast and lunch at the training center and consumed the remaining 3 meals at home, with the nutritional guidelines provided by the team nutritionist. The athletes shared the same spaces and the same menu both the evening before and the day of the match. Fecal samples were collected after 20 weeks of the competitive season (T2), corresponding approximately to the first half of the championship. The COVID-19 pandemic forced players into an 8-week lockdown (from March 9th to May 4th, 2020), during which athletes trained at home and were nutritionally assisted with

individual guidelines. The last fecal samples were collected once the training and competitive season were allowed to resume (T3). Please, see **Supplementary materials (Supplementary Tables 1-5)** for additional information on the training regime and nutritional guidelines for professional soccer players during the different phases of the observation period.

Fecal samples were self-collected by each participant using Fe-Col (Alpha Laboratories Ltd, Eastleigh, United Kingdom), a disposable paper device to prevent sample contamination, and SMART eNAT (Copan SpA, Brescia, Italy) for fecal sampling and preservation. All specimens were delivered to the laboratory of the Unit of Microbiome science and Biotechnology (Dept. Pharmacy and Biotechnology, University of Bologna, Bologna, Italy) where they were stored at -20°C until processing. Samples were processed within 1 month of arrival.

2.2 DNA extraction from feces

Total bacterial DNA was extracted from each stool sample using the DNeasy Blood and Tissue kit (Qiagen, Hilden, Germany) with previously described modifications[38]. Briefly, 500 µl of the feces and storage medium mix were resuspended in lysis buffer (500 mM NaCl, 50 mM Tris-HCl pH 8, 50 mM EDTA, 4% (w/v) SDS). Four 3-mm glass beads and 0.5 g of 0.1-mm zirconia beads (BioSpec Products, Bartlesville, OK, USA) were added to the sample. Homogenization was performed using a FastPrep instrument (MP Biomedicals, Irvine, CA, USA) with 3 beating steps at 5.5 movements/sec for 1 min, and 5-min on ice between steps. Samples were incubated at 95°C for 15 min, then centrifuged at 14,000 rpm for 5 min to remove stool particles. Nucleic acids were precipitated using subsequently 10 M ammonium acetate and isopropanol. The nucleic acids pellets were washed with 70% ethanol and resuspended in TE buffer. RNA was removed by treatment with DNase-free RNase. Protein removal and DNA purification were performed following the manufacturer's instructions (Qiagen). DNA quantification was performed using the NanoDrop ND-1000 spectrophotometer (NanoDrop Technologies, Wilmingot, DE, USA).

2.3 16S rRNA gene amplification and sequencing

12.5 ng of the extracted DNA were used as a template for PCR amplification of the V3-V4 region of the 16S rRNA gene using the S-D-Bact-0341-b-S-17/S-D-Bact-0785-a-A-21 primers[39] with Illumina overhang adapter sequences (Illumina, San Diego, CA, USA). Amplification was carried on in a final volume of 25 µl, containing 200 nM of each primer, and 2X KAPA HiFi HotStart ReadyMix (Kapa Biosystems, Roche, Basel, Switzerland). The thermal cycle was set as follows: 5 min at 95°C, 25 cycles of 95°C for 30 sec, 55°C for 30 sec and 72°C for 30 sec, and a final extension at 72°C for 5 min. PCR products of approximately 460 bp were purified using Agencourt AMPure XP (Beckman Coulter, Brea, CA, USA) and sequenced on Illumina MiSeq platform using the 2 × 250 bp paired-end protocol, according to the manufacturer's instructions. Indexed libraries were prepared by limited-cycle PCR using Nextera technology, and further purified as described above. A pool at equimolar concentrations was prepared, denatured with 0.2 N NaOH, and diluted to 6 pM before loading onto the MiSeq flow cell. Sequencing reads were deposited in the National Center for Biotechnology Information Sequence Read Archive (NCBI SRA: BioProject ID PRJNA708166).

2.4 Bioinformatics and statistics

Raw sequences were processed using a pipeline combining PANDAseq[40] and QIIME 2[41]. High-quality reads (min/max length = 350/550 bp) were binned into amplicon sequence variants (ASVs) using DADA2[42]. Taxonomy was assigned using the vsearch classifier[43] and the Greengenes database as a reference. Alpha diversity was measured using the number of observed ASVs. The statistical analyses were performed using the package "stats" of R Studio software version 1.0.136 running on R (v3.1.3; https://www.r-project.org/), implemented with the libraries vegan and made4. Beta diversity was estimated by computing weighted UniFrac distances and visualized by principal coordinates analyses (PCoAs). The significance of separation among groups of samples was tested by permutational multivariate analysis of variance using the function

"Adonis" of the vegan package. Bacterial phylogenetic groups that showed a minimum relative abundance of 0.5% in at least 10% of the samples were kept for graphical visualization and further analysis. Linear discriminant analysis (LDA) effect size (LEfSE) algorithm[44], a tool which is hosted on the Galaxy web application at https://huttenhower.sph.harvard.edu/galaxy/, was used to discover potential bacterial biomarkers associated to each diet. LEfSe uses the two-tailed nonparametric Kruskal-Wallis test to evaluate the significance of differences in ASVs in two or more groups. Ultimately, LDA was performed to estimate the effect size of each differentially abundant ASV at the genus level. Spearman rank correlation test was used to evaluate associations between gut microbiota profiles of the longitudinal dataset. The samples were considered significantly different if their differences had a p-value < 0.05 and an LDA score (log10) > 2.0. The Kendall rank correlation coefficient (Kendall's tau) between the relative abundance (RA%) of taxa at the genus level at different time points (T1, T2, and T3) was calculated using the function 'cor.test' of the package 'Stats' of R. p-values lower than 0.01 were considered significant and only correlations with Kendall's tau absolute values >= 0.25 were considered. Correlograms were displayed using the R package 'corrplot'.

3. Results

Of the 38 subjects initially enrolled, 26 (aged 27.3 ± 4.8 years, **Supplementary Table S5**) provided at least 2 of the 4 planned fecal samples for each individual (**Fig. 1**). The missing fecal samples were mainly due to players being moved to another soccer team after transfer window. The final set of 82 fecal samples had the following distribution: 22 samples at T0 (before pre-season retreat), 23 samples at T1 (after pre-season retreat), 19 samples at T2 (in season) and 18 samples at T3 (after COVID-19 lockdown). Of these 26 subjects, 12 provided the complete set of 4 fecal samples.

Microbiota characterization of the 82 fecal samples by 16S rRNA gene sequencing using Illumina technology yielded a total of 614,791 reads, with an average value of 7,497 ± 1,973 reads per sample.

The 12 subjects for whom the complete sample set of 4 samples was available were used in a first longitudinal description of the fecal microbiota dynamics along the soccer competitive season (**Fig. 2**). Samples from all other subjects were used for pairwise comparing consecutive time points and identify the most consistent changes in microbiota composition over the season (**Fig. 3**).

In terms of microbiota composition (**Fig. 2C**), our data indicate that the most relevant changes in fecal microbiota occurred at pre-season retreat (between T0 and T1), when exercise load and nutritional guidance were at their maximum (please see **Supplementary Table S6 and Materials: "Supplemental information about training and nutrition in the professional soccer players involved in the study"**). Indeed, samples taken at T0 (before the pre-season retreat) clustered separately in the PCoA based on weighted UniFrac distances, whereas all other samples overlapped (**Fig. 2A**) (Adonis, $P = 0.02 – R^2 = 0.09074$), indicating that the changes induced by the pre-season retreat were maintained during the competitive season. Samples from T0 were also characterized by a significantly greater dispersion on the PCoA plane (**Fig. 2A**), hinting at a higher inter-individual variability compared to samples taken at other time points (weighted UniFrac distances among samples from the same time point, mean ± standard deviation: T0, 0.45 ± 0.08; T1 0.39 ± 0.08; T2, 0.42 ± 0.07; T3, 0.41 ± 0.07) (**Supplementary Figure S1**). According to the multivariate analysis (**Fig. 2A**), T0 samples were on average characterized by higher abundances of *Collinsella* and *Bifidobacterium*. The decrease in relative abundance of *Collinsella* and *Bifidobacterium* across the pre-season retreat could not be confirmed by the LDA LEfSE analysis, when considering all subjects in the cohort who provided fecal samples at both T0 and T1 (19 subjects) (**Fig. 3A**). In fact, the relative abundance of bacteria belonging to the genera *Paraprevotella* and *Blautia* increased from T0 to T1, displaying a positive association with the pre-season diet as shown in **Fig. 3A and Fig. 4B**. At the same time, two bacterial genera showed a positive correlation with the off-season

dietary regimen: *Clostridium* and an unknown genus belonging to the Christensenellaceae family (**Fig. 3A and Fig. 4B**). To evaluate taxa coexistence under each dietary regimen, we calculated the Kendall tau rank correlation between the bacterial genera. A negative correlation (Kendall's tau < -0.25, p-value <= 0.01) between *Faecalibacterium* and *Akkermansia*, *Bacteroides* and *Prevotella*, and *Oscillospira* and *Ruminococcus* were detected when players were given pre-seasonal diet (**Fig. 5A**). At the same time, a positive correlation (Kendall's tau > 0.25, p-value <= 0.01) was found between the genera of the Unclassified S24-7 group and *Butyricimonas*, and *Bifidobacterium* and *Acidaminococcus* (**Fig. 5A**).

The 20 weeks of competitive season (between T1 and T2) affected the microbiota composition in terms of average relative abundance at the genus level (**Fig. 2C**) in our longitudinal analysis in a different fashion. The genera *Faecalibacterium*, *Lactobacillus*, and *Pseudomonas* showed a positive association with the pre-season dietary regimen, when all players who provided both T1 and T2 fecal samples were considered (n = 17), with decreasing relative abundance after following the in-season diet (**Fig. 3B and Fig. 4B**). The genus *Eggerthella* instead showed an inverse behavior, demonstrating a positive association with the in-season diet. After following the T2 diet, different correlations were found among the bacterial taxa. Briefly, a negative correlation (Kendall's tau < -0.25, p-value <= 0.01) was present between the genus of the Unclassified Coriobacteriaceae and *Parabacteroides*, *Streptococcus* and *Bilophila*, and a genus belonging to the Unclassified [Barnesiellaceae] and *Blautia* (**Fig. 5B**). Positive correlations (Kendall's tau > 0.25, p-value <= 0.01) were found between [Prevotella] and *Roseburia*, *Prevotella* and *Desulfovibrio*, *Oscillospira* and *Bilophila*, a genus belonging to the Unclassified Clotridiales and a genus belonging to the Alfaproteobacteria RF32, and between a genus of the Unclassified Coriobacteriaceae and *Dialister* (**Fig. 5B**). Finally, the last fecal samples collected after COVID-19 lockdown (*i.e.*, T3) showed a significant increase in the relative abundance of *Sutterella* and *Lachnospira* genera, if compared to samples at T2, while the unknown genus belonging to the order Mollicutes/RF39 appeared to be positively associated with the in-season diet regimen (**Fig. 3C and Fig. 4B**). After T3, only positive

bacterial correlations (Kendall's tau > 0.25, p-value <= 0.01) were found between *Prevotella* and *Dialister*, *Lachnobacterium* and *Dialister*, a genus of the Unclassified Coriobacteriaceae and a genus of the Unclassified Ruminococcaceae, a genus of the Unclassified [Barnesiellaceae] and a genus of the Unclassified Erysipelotrichaceae, which was also correlated with Parabacteroides abundance (**Fig. 5C**).

A significant decrease in terms of gut microbiota richness (*i.e.* alpha diversity, measured using the number of observed ASV per sample) was also observed after COVID-19 lockdown (T3), compared to both T0 and T1 values (**Fig. 2B**) (corrected paired Wilcoxon rank sum test, P = 0.03 and P = 0.02, respectively), which could reflect an expansion in the relative abundance of specific bacterial groups (**Fig. 2C**) and which is consistent with the loss of negative correlations between taxa at T3 (**Fig. 5C**), since at lower alpha-diversity competition tends to become weaker.[45] Monitoring over time the taxonomic profiles of individual athletes with complete trajectory (*i.e.*, longitudinal dataset), higher correlation coefficients were found between timepoints T1 and T2, as well as between T2 and T3 (mean rho, respectively 0.581 and 0.601). Compared to the pre-season (T0), less marked correlation values were observed at T2 and T3 (mean rho ≤ 0.571), suggesting a more pronounced rearrangement of the gut microbiota composition of athletes.

4. Discussion

High-level, professional athletes possess remarkable physiological and metabolic adaptation and may represent an interesting model for providing unique insights into gut microbiota research [8]. In our pilot study, the first available – to the best of our knowledge – on the fecal microbiota of elite soccer players that spans much of an entire competitive season, we observed that the most notable changes in microbiota composition and inter-individual variability occurred during the pre-season retreat. The enrolled athletes provided the first samples after 6 weeks of vacations, during which they did not observe strict rules neither on nutrition nor physical exercise. Also, during the off-

season, there may have been recreational travel. Since lifestyle, diet and travel are among the most relevant variables affecting the microbiota composition[46], the freedom in diet, exercise and environment granted to players during the off-season may explain the significantly higher inter-individual variability in microbiota composition observed in samples collected at the first time point. The combination of high exercise load, nutritional guidance (**Fig. 4A**), and co-living that characterized the pre-season phase (T1), showed a relevant impact on the athletes' gut microbiota layout, significantly reducing inter-individual variability and inducing significant compositional changes. Interestingly, according to the available literature, the observed changes can be considered positive for the health promotion of enrolled players. Indeed, after the off-season retreat, we observed a significant and consistent decrease in the relative abundance of *Clostridium*. The absence of a nutritional guidance and regular physical activity of the athletes during this time could have contributed to this change, as the abundance of *Clostridium* has been shown to increase in association with moderate-intensity continuous training[47]. Another variation induced by the pre-season retreat, with consistency among players, was the increased abundance of *Blautia*, a health-promoting short chain fatty acids (SCFAs) producer[48,49] that has been associated with a high intake of polyphenols-rich foods[50,51]. Indeed, the diet plans provided to the players during the pre-season retreat included a high amount of polyphenols-rich foods, such as cherries, berries, watermelon, pomegranate and extra-virgin olive oil. The *Paraprevotella* genus was also found increased in the pre-season time. Of note, this genus has been inversely associated with a Western dietary pattern[52], which is also consistent with the lower intake of proteins in pre-season meal plans.

The microbial changes listed above were not maintained throughout the 20 weeks of competitive season occurring between the second and the third fecal samples. In fact, a decrease in the relative abundance of *Faecalibacterium, Lactobacillus and Pseudomonas* and an increase in *Eggerthella* have been observed. *Faecalibacterium* is a well-known biomarker of health in the human microbiota[53], usually associated with the absence of inflammatory disorders, a healthy diet, and a

physically active lifestyle[8,54,55]. It is worth mentioning that the dietary plans suggested to the soccer players during the competitive season provided individuals with a considerably lower intake of fibers (see **Fig. 4A**) than the diet administered during the pre-season retreat (please, see **Supplementary Materials: "Supplemental information about training and nutrition in the professional soccer players involved in the study"**) and the fiber load is one of the dietary components that most affects the abundance of *Faecalibacterium* in the human gut[56,57]. As for the possible impact of physical exercise on *Faecalibacterium* abundance, in one of the very few longitudinal studies performed on the microbiota of athletes, it was reported that the abundance of *Faecalibacterium* decreased along with the reduced training volume in swimmers[17]. Therefore, its consistent decrease in the soccer players involved in our studies could be related to the fact that during the competitive season the training volume is lower than in the pre-season phase. Although it is difficult to separate the effect of changes in nutritional habits and changes in training volume, the variation in the abundance of *Faecalibacterium* in different phases of the competitive season, observed in two different type of athletes (*i.e*. soccer players in this study and swimmers in the study by Hampton-Marcell and colleagues[17]), underlines the need to better understand the mechanism by which this important symbiont responds to variations in load and type of exercise. With *Faecalibacterium* being a core health-promoter of the human microbiota[58], the effects of variations in its abundance on health and performance in elite athletes should be explored across larger cohorts and different type of sports, providing essential data for design of next generation probiotics specifically aimed at maintaining the health aspects related to performance. The genus *Lactobacillus* also appeared to be affected by the in-season diet and physical activity; the decrease of this genus has been associated with chronic stress in studies based on animal models[59,60], so it could be plausible that the high level of psychological and physical stress that elite soccer players endure during the in-season time may have had an impact on this bacterial group. The pro-inflammatory genus *Pseudomonas* decreased during the competitive season, when the nutrients intake was poorer in fats (**Fig. 4A**) while the *Eggerthella* genus, which has been previously

associated with depression[52], displayed a higher relative abundance, which could be linked to the very demanding sport activity the elite soccer players are subjected to during the in-season time.

Additional insight on the dynamics of elite athletes' microbiota was offered in our study since the onset of the COVID-19 pandemic and the subsequent lockdown, which has already been shown to have a relevant impact on athletes nutritionally, physically, and psychologically[61]. In the present study, the gut microbiota of professional soccer players showed a significant decrease in richness and a consistent trend towards increasing *Sutterella* abundance. Gut microbiota variations that lead to such an increase have not been thoroughly explored in athletes. However, *Sutterella* has been proposed to be involved in the so-called "gut-brain axis", as higher abundances have been reported in patients with neurological disorders than in healthy controls[62–65]. More importantly, our findings agree with a recent report that identified *Sutterella* as one of the key bacteria involved in the microbial network conversion from active to sedentary lifestyle[66]. The higher fiber intake that characterized the COVID-19 dietary regimen (**Fig. 4A**) instead might be linked to the observed increase of the short-chain fatty acid producer genus *Lachnospira*[67] and the order RF39 (class Mollicutes) that has been associated with a good quality of diet, poor in refined grains and rich in nuts and legumes[68].

As expected, our pilot observational study of elite soccer players confirmed that the gut microbiota undergoes relevant and consistent changes along with the different phases of the competitive season due to variations occurred in dietary regimens and physical activity intensity respect to pre-season retreat. The consistency of these changes among enrolled players, especially during the pre-season retreat where nutritional guidance and training load were at their peak, may also have been favored by the co-living lifestyle of the players during the pre-season retreat[69,70]. The continued nutritional supervision that is possible during the retreat may have contributed to the purported health-promoting features of the microbiota changes observed after pre-season.

Relevant changes (*i.e.* a significant decrease in gut microbiota richness and a consistent increase in *Sutterella*) were also observed after the COVID-19 lockdown, during which athletes were forced to

radically change their training routines and possibly experienced an increase of psychological stress[71,72]. This observation could be relevant not only to the peculiar physiology of athletes, but also to the general population and the effect that COVID-19 lockdown and pandemic stress may have had on various aspects of human health, including our microbial counterpart.

Laboratory medicine in the supervision of athletes is assuming an increasingly important role every day for monitoring performance and preventing injuries and diseases, to the point of envisaging a future sports medicine based on the creation and continuous updating of the "athletes' biological passport"[34]. Being the human gut microbiota a crucial player in maintaining health and fitness, it is natural to foresee the inclusion of gut microbiota monitoring in sports medicine practice, with the aim of optimizing the microbiota profile to increase performance through personalized nutritional strategies[22]. Regarding the movement sports, the gut microbiota could also improve stamina and integrity of skeletal muscles, preventing indirect muscle disorder/injury[73], by regulating the metabolism of glucose and amino acids respectively. Indeed, machine learning approaches could allow, in the future, to integrate data on health biomarkers, microbiota characterization, nutrition and performance of an athlete, in order to uncover associations between microbiota and performance and to compile personalized recommendations[74]. Our longitudinal study, focused on elite soccer players – the most followed sport worldwide and the one that generates the greatest economic impact, with over 240 million active soccer players around the world, of which 165 thousand are professional players[75–77] - provides baseline data for future comparisons and intervention studies that will pursue the goal of personalizing training and dietary approaches for maximizing performances. The major limitations of the study were the limited sample sizes and the need to compare two different groups of soccer players along the season. Unfortunately, the latter was unavoidable since the replacements of players between professional soccer teams during the transfer market change the roster during the season. Hence, more studies with larger sample sizes will be required to further investigate the exploitation of gut microbiota modulation, by training and nutrition, to optimize athletic performances. For instance, next generation biotherapeuthics based on

Faecalibacterium and *Lactobacillus* could be devised to maintain a balanced amount of this key health-promoter throughout the competitive season, in order to maintain health and performance of athletes and promote recovery.

Competing interests.

The authors declare no competing interests.

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Figure legends

Fig. 1. Study design. The competitive season of the Italian professional soccer players from Parma Calcio is depicted with the indication of the duration of each period in weeks. Sampling times are indicated by black arrows. The colors orange, green, grey and blue are associated with the Off-season, Pre-season, In-season, and COVID-19 lockdown periods, respectively.

Fig. 2. Description of the fecal microbiota along the different phases of the soccer competitive season, in terms of beta diversity (A), microbiota richness (B) and genus-level microbiota phylogenetic structure (C). (A) Principal Coordinates Analyses (PCoA) based on weighted Unifrac distances of the fecal microbiota from the 4 longitudinally collected samples. Samples are depicted as dots filled with light blue, pink, green and yellow, based on the sampling time (T0, T1, T2, and T3, respectively). The first and second principal components are shown, explaining 14.95% and 12.96% of the variance in the dataset, respectively. Ellipses for each group of samples include a 95% confidence area based on the standard error of the weighted average of sample coordinates. The biplot of the bacterial coordinates weighted by the corresponding bacterial relative abundance per sample was superimposed on the PCoA plots for abundant bacterial genera that contributed most significantly to the ordination space (envfit, $P<0.001$) (black arrows). **(B)** Levels of alpha diversity calculated as the number of observed amplicon sequence variants (ASVs) for each sample collected in the 4 timepoints for 12 soccer players are depicted as boxplots. The significant difference between the alpha diversity in samples taken at T0 and T3, and at T1 and T3 is indicated by asterisks (Wilcoxon rank sum test for paired samples, $P = 0.03$ and $P = 0.02$, respectively). **(C)** Bar plots of the genus-level composition of the gut microbiota of soccer athletes at each time point (*i.e*. T0, T1, T2, and T3); colors for each genus are reported in the side color legend. Only genera with relative abundance ≥0.5% in at least 10% of the samples are represented (22 subjects at T1, 23 subjects at T1, 19 subjects at T2, and 18 subjects at T3).

Fig. 3. Plot from LDA LEfSE analysis on the fecal samples taken at T0 (off-season), T1(pre-season), T2 (in-season), and T3 (COVID-19 lock down). The plot was generated using the online Galaxy web platform tools at https://huttenhower.sph.harvard.edu/galaxy/[44]. The length of the bar column represents the LDA score. The figure shows the microbial taxa with significant differences between T0 and T1, T1 and T2, and T2 and T3. Below each plot, the relative abundances (%) of each taxon found as a biomarker in the various conditions are shown. The number of subjects used for the comparisons is as follows: 19 for T0 vs. T1 **(A)**, 17 for T1 vs. T2 **(B)** and 16 for T2 vs. T3 **(C)**.

Fig. 4. Bar plots of nutrient intake per time point and streamgraph of significant bacterial taxa abundances changes in time. (A)Bar plots of nutrient intake per day in grams (g/day) for each macronutrient category present in the diet observed by the football players during the various stages of their training (T0, T1, T2, and T3). (B) Streamgraph of bacterial taxa relative abundance percentages that are significantly modulated by the different dietary regimens at the various time points.

Fig. 5. Correlograms of Kendall rank correlation coefficients. Correlograms showing co-abundance correlation analysis based on Kendall rank correlation coefficients measured between the relative abundance (RA%) of taxa at the genus level in pre-season (A), in-season (B) and after COVID-19 pandemic (C).

Fecal microbiota monitoring in elite soccer players along the 2019-2020 competitive season

Supplementary materials

Supplemental information on training and nutrition of the professional soccer players involved in the study.

In elite football (soccer) the annual structure of a season includes three phases: off-season, pre-season and in-season. These phases have specific goals and require different levels of training variation.

The pre-season phase (from T0 to T1), also known as the preparation period, is typically 5-7 weeks and is characterized by higher intensity and volume training in an attempt to compensate for the detraining during the off-season and try to reach the high levels of fitness required for the start of the season in such a short time[1]. The first part of the preparation took place in a mountain retreat (Prato allo Stelvio, Italy; from July 8th to August 4th, 2019). The preparation then continued at the Parma Calcio training center in Collecchio (Italy) from August 5th to August 23rd, 2019. The first two weeks of the preparation phase encompassed extensive endurance/aerobic moderate/high intensity exercise. During the second part (weeks 3 and 4) the players performed high-intensity aerobic and interval anaerobic sessions, with quality sprint training as the overall volume decreases. The last part of the preparation phase (weeks 5 to 7) included a training structure with an emphasis on high-intensity exercise. Overall, during the pre-season phase, the players performed on average between 6 and 8 training sessions per week, with a weekly training exposure of about 11-12 h, and in the second part of the pre-season preparation the players also played one friendly match per week. During this pre-season period, the aim is to develop the physical requirements for championship competition, thus improving high-intensity exercise endurance, modify body composition, increase muscle mass and power[2,3].

In-season training sessions (from T1 to T2) were planned to ensure a balance between weekly training and official matches load and adequate rest and recovery. During in-season, the footballers were exposed to 7-8 h of exercise, plus one match per week. Typically, the in-season length is 42 weeks, but the 2019/2020 championship only lasted 38 weeks due to the COVID-19 pandemic. High-intensity exercise, soccer-specific technical and tactical drills and tactical exercises were the critical components of the in-season training sessions planning as previously described[2].

The overall weekly training plan was as follows:

	Monday	Tuesday	Wednesday	Thursday	Friday	Saturday	Sunday
Playing squad	REST	Aerobic	Strength Anaerobic	Aerobic High	Technical Tactical	Quick feet / agility	GAME
Non-playing squad	REST	Individual Training	Strength Anaerobic	Aerobic High	Technical Tactical	Quick feet / agility	REST

As for the lockdown period, due to the worldwide outbreak of COVID-19 (from T2 to T3), the players were confined at their private home (as well as most of the Italian population) without the possibility of reaching the training center. None of the players could use large gym equipment at home. Home workouts were suggested, consistent with available space and small equipment, but the physical activity load was not comparable to what players were used to during pre-season or in-season periods (from T0 to T2).

From a nutritional point of view, during the first 4 weeks in the mountains (pre-season, T0-T1), a well-balanced diet with a periodization of macronutrients on weekdays based on the extent of the training session (low intensity, moderate, high, and very high) and containing macronutrients, micronutrients and liquids in the proper amounts, was planned, following the current guidelines for athletes and soccer players[4–8]. Daily meals (breakfast, lunch, pre-training snack, dinner and pre-sleep snack) were provided at the hotel restaurant in the form of flexible "buffet-style". Professional nutritional advices to build the "athlete's plate" that ensures the right intake were offered by the club's nutritionist, with advices tailored to the playing position and individual body composition goals, helping athletes to adjust their own intake based on different training sessions needs while achieving key macronutrients goals. Fruit snacks were planned and delivered after morning and/or afternoon training sessions, to ensure recovery after exercise and reduce muscle damage[9].

Supplementary Table S1. Example of dietary meal plans provided to an 80 Kg player engaged in high-intensity training session during the pre-season retreat (T0-T1)

Meal / Time	Meal composition
Breakfast (9.00 am)	Omelet with 150 g of egg's white, 150 g of banana with 20 g of honey and 200 g of porridge (150 g of almond milk and 50 g of oat), 15 g of pistachios
Lunch (1 pm)	250 g of vegetables, 25 g of EVO oil, 150 g of buckwheat pasta, 100 g of chicken
Pre-training snack (5 pm)	40 g of bread, 40 g of turkey, 20 g of fresh dates
Afternoon snack (7 pm)	100 g of cherries, 200 g of watermelon, 100 g of berries, 100 g of pomegranate
Dinner (8.30 pm)	250 g of vegetables, 25 g of EVO oil, 250 g of sea bream, 150 g of black wild rice
Pre-sleep snack (10 pm)	100 g of kiwifruit, 200 g of Greek yogurt and 10 g of nuts
Approximate macronutrient intake	6 g/Kg/day of carbohydrates (480 g/day) (1,920 Kcal=53% of TEI) 1.7 g/Kg/day of proteins (136 g/day) (544 Kcal=15% of TEI) 1.6 g/Kg/day of fats (128 g/day) (1,152 Kcal=32% of TEI) 52 g/day of total fibre 3,616 Kcal TEI=45.2 Kcal/Kg/day

During the latter part of the pre-season and in the season (T1-T2), breakfast and lunch were always planned and consumed at the club restaurant and the general approach mirrored the diet plan described above. The remaining three meals (afternoon snack, dinner and pre-sleep snack) were consumed by the players at home following the guidelines produced by club's nutritionist and based on the most recent evidence[8,10,11]. During the in-season period, players dined together the evening before an official match (MD-1) as well as match day meals following current evidence and recommendations on nutrition in elite football[11]. Below are provided examples of meal composition during rest, training and match days for an 80 Kg player, along with their respective approximate macronutrients intakes listed below each.

Supplementary Table S2. Example of dietary meal plans provided to an 80 Kg player in-season (T1-T2) for rest days

Meal	Meal composition
Breakfast	300 g of Greek yogurt, 300 g of fresh fruit
Snack	15 g of nuts, 120 g of albumen, 50 g of rye bread, 5 g of EVO
Lunch	300 g of raw vegetables, 20 g of EVO, 25 g of lemon juice, 90 g of quinoa, 100 g of clam (shelled), 200 g of courgette, 5 g of spices
Afternoon snack	300 g of fresh fruit
Dinner	500 g of cooked vegetables, 20 g of EVO, 300 g of sea bream, 25 g of lemon juice
Approximate macronutrient intake	2.1 g/Kg/day of carbohydrates (169.7 g/day) (678.7 Kcal=23.4 % of TEI) 1.5 g/Kg/day of proteins (121.6 g/day) (486.6 Kcal=21.1 % of TEI) 1.2 g/Kg/day of fats (95.4 g/day) (858.3 Kcal=37.1 % of TEI) 24.8 g/day of total fibre 2,310 Kcal TEI=28.9 Kcal/Kg/day

Supplementary Table S3. Example of dietary meal plans provided to an 80 Kg player in-season (T1-T2) for training days

Meal	Meal composition
Breakfast	500 g of hazelnut milk, 50 g of whole toasted biscuits, 20 g of jam (reduced in sugars), 15 g of nuts, 25 g of lemon juice
Snack	350 g of fresh fruit
Lunch	300 g of raw vegetables, 20 g of EVO, 25 g of lemon juice, 120 g of whole rice, 300 g of fresh cod, 200 g of courgette, 5 g of spices
Afternoon snack	30 g of whey protein, 300 g of fresh fruit
Dinner	500 g of cooked vegetables, 20 g of EVO, 350 g of fish soup, 200 g of potatoes, 25 g of lemon juice
Approximate macronutrient intake	3.6 g/Kg/day of carbohydrates (290.6 g/day) (1162.3 Kcal=42.2 % of TEI) 1.8 g/Kg/day of proteins (144.4 g/day) (577.6 Kcal=21.0 % of TEI) 1.0 g/Kg/day of fats (83.7 g/day) (753.1 Kcal=27.3 % of TEI) 29.9 g/day of total fibre 2,755 Kcal TEI=34.4 Kcal/Kg/day

Supplementary Table S4. Example of dietary meal plans provided to an 80 Kg player in-season (T1-T2) for match day

Meal	Meal composition
Breakfast	170 g of Greek yogurt, 60 g of oat flakes, 15 g of nuts, 200 g of banana, 20 g of dark chocolate, 15 g of honey, 50 g of bread, 20 g of jam (reduced in sugars)
Snack	-
Lunch	100 g of cooked vegetables, 150 g of spelt pasta, 20 g of EVO, 100 g of bresaola, 25 g of lemon juice
Pre-match snack	150 g of pasta or rice, 100 g of bresaola
Post-match dinner	500 g of cooked vegetables, 20 g of EVO, 150 g of shellfish, 150 g of rice with shellfish, 25 g of lemon juice
Approximate macronutrient intake	5.1 g/Kg/day of carbohydrates (408.8 g/day) (1635.4 Kcal=51.6 % of TEI) 1.9 g/Kg/day of proteins (149 g/day) (596 Kcal=18.8 % of TEI) 1.1 g/Kg/day of fats (85.5 g/day) (769.2 Kcal=24.2 % of TEI) 19.1 g/day of total fibre 3,172 Kcal TEI=39.6 Kcal/Kg/day

Both during the pre-season preparation phase and during the in-season, athletes were supplemented with a personalized approach to promote adaptation processes, repair exercise-induced muscle damage and/or accelerate recovery from close matches, as recently described[12]. In addition, key micronutrients (e.g. Vitamin D, Iron) were regularly tested and supplemented as needed[11,13].
During the COVID-19 lockdown, players were advised to follow a zone diet (19 blocks) provided by the team's nutritionist. It is important to remember that during this period it was not possible to verify the adherence of the players to the provided meal plans. An example of meals composition during this phase for a player of 80Kg is provided below, with the approximate intake of macronutrients.

Supplementary Table S5. Example of dietary meal plans provided to an 80 Kg player engaged during COVID-19 lockdown (T2-T3)

Meal	Meal composition
Breakfast	40 g of whole bread, 60 g of baked ham (degreased), 9 g of pine nut, 200 g of semi-skimmed milk, 250 g of semi-skimmed yogurt

Snack	20 g of Parmesan cheese, 100 g of pear
Lunch	175 g of veal rump, 380 g of green bean, 240 g of carrot, 175 g of blueberry, 100 g of kiwi fruit, 7 g of EVO
Afternoon snack	60 g of bresaola, 345 g of orange, 9 g of almond
Dinner	120 g of fresh tuna, 300 g of lettuce, 680 g of courgette, 180 g of pineapple, 6 g of EVO
Evening snack	Energetic snack (8.7 g of carbohydrates, 7.6 g of protein, 3.9 g of fat)
Approximate macronutrient intake	2.1 g/Kg/day of carbohydrates (169,75 g/day) (679 Kcal=37% of TEI) 2 g/Kg/day of proteins (163.5 g/day) (653.9 Kcal=35.6 % of TEI) 0.7 g/Kg/day of fats (60.2 g/day) (542 Kcal=29.5 % of TEI) 55.8 g/day of total fibre 1,834 Kcal TEI=22 Kcal/Kg/day

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Supplementary Table S6. Enrolled subjects, age and fecal (F) samples available. The subjects who have provided the complete set of 4 fecal samples during the competitive season are highlighted in grey.

Subject ID	Age	T0	T1	T2	T3
PC01	37	F			F
PC02	21		F	F	
PC03	27	F	F		
PC04	31	F	F	F	F
PC05	26		F	F	F
PC07	32	F	F		
PC08	28	F	F	F	F
PC09	26		F	F	
PC10	18	F	F	F	F
PC11	30		F	F	F
PC12	27	F		F	F
PC16	29	F	F	F	F
PC17	34	F	F		
PC18	24	F	F	F	F
PC20	25	F	F	F	
PC21	32	F	F	F	F
PC25	32	F	F	F	F
PC26	19	F	F		F
PC27	30	F	F	F	F
PC29	22	F	F		
PC30	19	F	F		
PC33	26	F	F	F	F
PC36	31	F	F	F	F
PC37	28	F	F	F	F
PC38	31	F		F	F
PC39	26	F	F	F	F

Supplementary Figure S1. Box and whiskers distribution of beta diversity levels, calculated as weighted UniFrac distances, between samples from T0 (light blue), T1 (pink), T2 (green) and T3 (yellow). Asterisks indicate significant differences, calculated using corrected Wilcoxon rank sum test, (*, $P<0.05$; **, $P<0.01$).

Supplementary Table S7.

Sample	Time	Subject	ASV_genus	Abundance RA %
PC01T0	T0	PC01	Uncl_Coriobacteriaceae	6,47
PC01T3	T3	PC01	Uncl_Coriobacteriaceae	10,09
PC01T0	T0	PC01	Prevotella	10,51
PC01T3	T3	PC01	Prevotella	12,81
PC01T3	T3	PC01	Uncl_S24-7	5,92
PC01T3	T3	PC01	[Prevotella]	6,65
PC01T0	T0	PC01	Uncl_Clostridiales	7,66
PC01T3	T3	PC01	Uncl_Lachnospiraceae	7,97
PC01T0	T0	PC01	Uncl_Ruminococcaceae	24,40
PC01T3	T3	PC01	Uncl_Ruminococcaceae	16,25
PC01T0	T0	PC01	Faecalibacterium	11,76
PC01T0	T0	PC01	Sutterella	9,15
PC01T3	T3	PC01	Sutterella	10,72
PC01T0	T0	PC01	Other	30,04
PC01T3	T3	PC01	Other	29,59
PC02T1	T1	PC02	Bifidobacterium	15,18
PC02T2	T2	PC02	Bifidobacterium	14,55
PC02T2	T2	PC02	Uncl_Coriobacteriaceae	6,61
PC02T2	T2	PC02	Adlercreutzia	7,34
PC02T1	T1	PC02	Collinsella	17,44
PC02T1	T1	PC02	Bacteroides	10,82
PC02T2	T2	PC02	Bacteroides	21,86
PC02T2	T2	PC02	Uncl_Rikenellaceae	16,60
PC02T1	T1	PC02	Uncl_Lachnospiraceae	10,23
PC02T1	T1	PC02	Uncl_Peptostreptococcaceae	7,07
PC02T1	T1	PC02	Faecalibacterium	8,35
PC02T1	T1	PC02	Ruminococcus	7,83
PC02T2	T2	PC02	Sutterella	7,97
PC02T1	T1	PC02	Other	23,08
PC02T2	T2	PC02	Other	25,06
PC03T0	T0	PC03	Bacteroides	18,62
PC03T1	T1	PC03	Bacteroides	12,63
PC03T0	T0	PC03	Uncl_Clostridiales	8,35
PC03T1	T1	PC03	Uncl_Clostridiales	17,37
PC03T0	T0	PC03	Uncl_Lachnospiraceae	11,24
PC03T1	T1	PC03	Uncl_Lachnospiraceae	13,92
PC03T0	T0	PC03	Blautia	10,20
PC03T0	T0	PC03	Lachnospira	7,10
PC03T0	T0	PC03	Uncl_Ruminococcaceae	13,02
PC03T1	T1	PC03	Uncl_Ruminococcaceae	10,34
PC03T1	T1	PC03	Faecalibacterium	10,23

PC03T1	T1	PC03	Ruminococcus	8,11
PC03T0	T0	PC03	Uncl_Erysipelotrichaceae	6,65
PC03T0	T0	PC03	Other	24,82
PC03T1	T1	PC03	Other	27,39
PC04T2	T2	PC04	Bifidobacterium	5,15
PC04T0	T0	PC04	Uncl_Coriobacteriaceae	8,60
PC04T1	T1	PC04	Uncl_Coriobacteriaceae	5,53
PC04T0	T0	PC04	Collinsella	14,44
PC04T1	T1	PC04	Collinsella	15,42
PC04T2	T2	PC04	Collinsella	15,59
PC04T3	T3	PC04	Collinsella	11,42
PC04T0	T0	PC04	Bacteroides	12,81
PC04T2	T2	PC04	Bacteroides	16,85
PC04T3	T3	PC04	Bacteroides	6,23
PC04T1	T1	PC04	Prevotella	18,06
PC04T2	T2	PC04	Prevotella	26,52
PC04T3	T3	PC04	Prevotella	25,97
PC04T0	T0	PC04	Uncl_Rikenellaceae	5,22
PC04T2	T2	PC04	Uncl_Rikenellaceae	7,66
PC04T0	T0	PC04	Uncl_Clostridiales	8,11
PC04T3	T3	PC04	Uncl_Clostridiales	8,11
PC04T1	T1	PC04	Uncl_Lachnospiraceae	8,01
PC04T3	T3	PC04	Uncl_Lachnospiraceae	5,92
PC04T0	T0	PC04	Uncl_Ruminococcaceae	9,40
PC04T2	T2	PC04	Uncl_Ruminococcaceae	5,22
PC04T1	T1	PC04	Faecalibacterium	21,30
PC04T2	T2	PC04	Oscillospira	6,68
PC04T0	T0	PC04	Dialister	7,00
PC04T1	T1	PC04	Dialister	5,12
PC04T3	T3	PC04	Dialister	9,50
PC04T1	T1	PC04	Mitsuokella	6,02
PC04T0	T0	PC04	Sutterella	6,96
PC04T3	T3	PC04	Sutterella	12,81
PC04T0	T0	PC04	Other	27,46
PC04T1	T1	PC04	Other	20,54
PC04T2	T2	PC04	Other	16,32
PC04T3	T3	PC04	Other	20,05
PC05T2	T2	PC05	Uncl_Coriobacteriaceae	25,79
PC05T3	T3	PC05	Uncl_Coriobacteriaceae	15,59
PC05T1	T1	PC05	Collinsella	7,45
PC05T2	T2	PC05	Collinsella	20,78
PC05T1	T1	PC05	Bacteroides	5,43
PC05T2	T2	PC05	Bacteroides	12,39
PC05T3	T3	PC05	Bacteroides	7,21

PC05T2	T2	PC05	Prevotella	11,59
PC05T3	T3	PC05	Prevotella	9,92
PC05T3	T3	PC05	Uncl_Rikenellaceae	6,16
PC05T3	T3	PC05	Uncl_S24-7	14,27
PC05T1	T1	PC05	Streptococcus	9,22
PC05T1	T1	PC05	Uncl_Lachnospiraceae	7,41
PC05T2	T2	PC05	Uncl_Ruminococcaceae	5,88
PC05T3	T3	PC05	Uncl_Ruminococcaceae	10,09
PC05T1	T1	PC05	Faecalibacterium	35,36
PC05T3	T3	PC05	Faecalibacterium	15,35
PC05T1	T1	PC05	Ruminococcus	5,43
PC05T1	T1	PC05	Other	29,69
PC05T2	T2	PC05	Other	23,56
PC05T3	T3	PC05	Other	21,41
PC07T0	T0	PC07	Collinsella	6,61
PC07T0	T0	PC07	Bacteroides	5,74
PC07T0	T0	PC07	Prevotella	13,99
PC07T1	T1	PC07	Prevotella	29,31
PC07T0	T0	PC07	Uncl_Clostridiales	6,96
PC07T0	T0	PC07	Other_Lachnospiraceae	8,08
PC07T0	T0	PC07	Uncl_Lachnospiraceae	7,45
PC07T0	T0	PC07	Blautia	5,57
PC07T1	T1	PC07	Blautia	14,65
PC07T0	T0	PC07	Coprococcus	6,16
PC07T1	T1	PC07	Uncl_Ruminococcaceae	6,79
PC07T0	T0	PC07	Faecalibacterium	9,50
PC07T1	T1	PC07	Ruminococcus	8,18
PC07T0	T0	PC07	Sutterella	11,42
PC07T0	T0	PC07	Other	18,52
PC07T1	T1	PC07	Other	41,07
PC08T0	T0	PC08	Bifidobacterium	7,41
PC08T2	T2	PC08	Uncl_Coriobacteriaceae	8,88
PC08T3	T3	PC08	Uncl_Coriobacteriaceae	6,68
PC08T0	T0	PC08	Collinsella	23,42
PC08T1	T1	PC08	Collinsella	7,62
PC08T2	T2	PC08	Collinsella	20,29
PC08T0	T0	PC08	Bacteroides	10,72
PC08T1	T1	PC08	Bacteroides	25,20
PC08T2	T2	PC08	Bacteroides	19,18
PC08T3	T3	PC08	Bacteroides	16,22
PC08T0	T0	PC08	Uncl_Clostridiales	8,25
PC08T1	T1	PC08	Uncl_Clostridiales	6,06
PC08T2	T2	PC08	Uncl_Clostridiales	7,21
PC08T2	T2	PC08	Uncl_Lachnospiraceae	5,01

PC08T1	T1	PC08	Blautia	24,99
PC08T2	T2	PC08	Roseburia	8,28
PC08T0	T0	PC08	Uncl_Ruminococcaceae	14,41
PC08T1	T1	PC08	Uncl_Ruminococcaceae	5,67
PC08T2	T2	PC08	Uncl_Ruminococcaceae	11,87
PC08T3	T3	PC08	Uncl_Ruminococcaceae	12,74
PC08T0	T0	PC08	Faecalibacterium	18,48
PC08T3	T3	PC08	Faecalibacterium	6,20
PC08T1	T1	PC08	Ruminococcus	10,06
PC08T2	T2	PC08	Ruminococcus	5,92
PC08T3	T3	PC08	Ruminococcus	8,04
PC08T3	T3	PC08	Alphaproteobacteria_RF32	17,09
PC08T3	T3	PC08	Sutterella	15,49
PC08T0	T0	PC08	Other	17,30
PC08T1	T1	PC08	Other	20,40
PC08T2	T2	PC08	Other	13,37
PC08T3	T3	PC08	Other	17,54
PC09T2	T2	PC09	Adlercreutzia	13,09
PC09T1	T1	PC09	Collinsella	12,01
PC09T2	T2	PC09	Eggerthella	7,69
PC09T1	T1	PC09	Bacteroides	6,54
PC09T2	T2	PC09	Bacteroides	20,74
PC09T2	T2	PC09	Parabacteroides	9,82
PC09T1	T1	PC09	Prevotella	8,28
PC09T1	T1	PC09	Paraprevotella	5,22
PC09T1	T1	PC09	Uncl_Ruminococcaceae	6,75
PC09T1	T1	PC09	Faecalibacterium	20,43
PC09T2	T2	PC09	Faecalibacterium	6,33
PC09T2	T2	PC09	Uncl_Erysipelotrichaceae	5,36
PC09T1	T1	PC09	Sutterella	6,68
PC09T2	T2	PC09	Sutterella	6,47
PC09T1	T1	PC09	Desulfovibrio	5,15
PC09T1	T1	PC09	Other	28,92
PC09T2	T2	PC09	Other	30,49
PC10T0	T0	PC10	Bifidobacterium	13,23
PC10T1	T1	PC10	Bifidobacterium	5,15
PC10T2	T2	PC10	Bifidobacterium	8,25
PC10T0	T0	PC10	Collinsella	29,27
PC10T1	T1	PC10	Collinsella	22,55
PC10T2	T2	PC10	Collinsella	31,78
PC10T3	T3	PC10	Collinsella	23,77
PC10T1	T1	PC10	Bacteroides	9,71
PC10T2	T2	PC10	Bacteroides	9,99
PC10T3	T3	PC10	Bacteroides	6,13

PC10T0	T0	PC10	Prevotella	5,85
PC10T1	T1	PC10	Prevotella	8,77
PC10T3	T3	PC10	Uncl_Clostridiales	22,76
PC10T2	T2	PC10	Uncl_Lachnospiraceae	9,05
PC10T3	T3	PC10	Blautia	6,75
PC10T2	T2	PC10	Dorea	7,38
PC10T2	T2	PC10	[Ruminococcus]	8,32
PC10T3	T3	PC10	[Ruminococcus]	6,51
PC10T0	T0	PC10	Uncl_Ruminococcaceae	10,76
PC10T1	T1	PC10	Uncl_Ruminococcaceae	9,95
PC10T1	T1	PC10	Faecalibacterium	11,59
PC10T2	T2	PC10	Faecalibacterium	6,65
PC10T3	T3	PC10	Oscillospira	6,23
PC10T0	T0	PC10	Megasphaera	11,00
PC10T1	T1	PC10	Megasphaera	5,50
PC10T0	T0	PC10	Sutterella	5,46
PC10T0	T0	PC10	Other	24,43
PC10T1	T1	PC10	Other	26,77
PC10T2	T2	PC10	Other	18,59
PC10T3	T3	PC10	Other	27,85
PC11T2	T2	PC11	Uncl_Coriobacteriaceae	13,54
PC11T2	T2	PC11	Adlercreutzia	26,35
PC11T3	T3	PC11	Adlercreutzia	12,91
PC11T1	T1	PC11	Collinsella	22,90
PC11T1	T1	PC11	Bacteroides	13,26
PC11T2	T2	PC11	Bacteroides	7,21
PC11T3	T3	PC11	Bacteroides	5,74
PC11T2	T2	PC11	Streptococcus	9,61
PC11T3	T3	PC11	Streptococcus	6,89
PC11T2	T2	PC11	Uncl_Clostridiales	10,86
PC11T3	T3	PC11	Uncl_Clostridiales	25,30
PC11T1	T1	PC11	Uncl_Ruminococcaceae	9,01
PC11T1	T1	PC11	Faecalibacterium	15,38
PC11T2	T2	PC11	Ruminococcus	7,38
PC11T3	T3	PC11	Ruminococcus	18,10
PC11T3	T3	PC11	Alphaproteobacteria_RF32	7,90
PC11T1	T1	PC11	Sutterella	5,92
PC11T1	T1	PC11	Uncl_Enterobacteriaceae	8,28
PC11T1	T1	PC11	Klebsiella	6,02
PC11T1	T1	PC11	Other	19,21
PC11T2	T2	PC11	Other	25,06
PC11T3	T3	PC11	Other	23,15
PC12T3	T3	PC12	Uncl_Coriobacteriaceae	7,59
PC12T0	T0	PC12	Prevotella	10,34

PC12T2	T2	PC12	Prevotella	29,55
PC12T3	T3	PC12	Prevotella	22,76
PC12T2	T2	PC12	Uncl_S24-7	5,22
PC12T0	T0	PC12	Blautia	7,00
PC12T0	T0	PC12	Uncl_Ruminococcaceae	11,70
PC12T2	T2	PC12	Uncl_Ruminococcaceae	9,29
PC12T3	T3	PC12	Uncl_Ruminococcaceae	16,74
PC12T0	T0	PC12	Faecalibacterium	8,21
PC12T2	T2	PC12	Faecalibacterium	10,06
PC12T3	T3	PC12	Faecalibacterium	6,09
PC12T3	T3	PC12	Oscillospira	6,89
PC12T2	T2	PC12	Dialister	7,97
PC12T0	T0	PC12	Catenibacterium	6,61
PC12T0	T0	PC12	Sutterella	7,94
PC12T2	T2	PC12	Sutterella	5,29
PC12T3	T3	PC12	Sutterella	7,76
PC12T0	T0	PC12	Other	48,21
PC12T2	T2	PC12	Other	32,61
PC12T3	T3	PC12	Other	32,16
PC16T0	T0	PC16	Collinsella	7,31
PC16T2	T2	PC16	Collinsella	10,62
PC16T2	T2	PC16	Eggerthella	10,34
PC16T0	T0	PC16	Bacteroides	18,69
PC16T1	T1	PC16	Bacteroides	5,01
PC16T3	T3	PC16	Bacteroides	7,27
PC16T0	T0	PC16	Prevotella	18,24
PC16T1	T1	PC16	Prevotella	18,87
PC16T2	T2	PC16	Prevotella	15,66
PC16T3	T3	PC16	Prevotella	19,67
PC16T1	T1	PC16	Paraprevotella	5,08
PC16T3	T3	PC16	Paraprevotella	6,37
PC16T1	T1	PC16	Uncl_Clostridiales	11,42
PC16T0	T0	PC16	Uncl_Lachnospiraceae	15,45
PC16T3	T3	PC16	Uncl_Lachnospiraceae	8,46
PC16T2	T2	PC16	Blautia	5,85
PC16T1	T1	PC16	Lachnospira	5,78
PC16T3	T3	PC16	Roseburia	7,27
PC16T1	T1	PC16	Uncl_Ruminococcaceae	6,47
PC16T2	T2	PC16	Uncl_Ruminococcaceae	8,28
PC16T2	T2	PC16	Faecalibacterium	14,69
PC16T3	T3	PC16	Faecalibacterium	9,47
PC16T2	T2	PC16	Oscillospira	6,30
PC16T1	T1	PC16	Ruminococcus	11,10
PC16T3	T3	PC16	Ruminococcus	6,44

PC16T0	T0	PC16	Phascolarctobacterium	7,87
PC16T3	T3	PC16	Phascolarctobacterium	8,74
PC16T0	T0	PC16	Sutterella	5,46
PC16T1	T1	PC16	Sutterella	6,30
PC16T2	T2	PC16	Sutterella	7,48
PC16T3	T3	PC16	Sutterella	9,95
PC16T0	T0	PC16	Other	26,98
PC16T1	T1	PC16	Other	29,97
PC16T2	T2	PC16	Other	20,78
PC16T3	T3	PC16	Other	16,36
PC17T0	T0	PC17	Other_Coriobacteriaceae	5,85
PC17T0	T0	PC17	Collinsella	23,49
PC17T1	T1	PC17	Collinsella	15,42
PC17T0	T0	PC17	Bacteroides	5,43
PC17T1	T1	PC17	Bacteroides	10,23
PC17T1	T1	PC17	Prevotella	16,39
PC17T1	T1	PC17	Uncl_Rikenellaceae	5,12
PC17T0	T0	PC17	Blautia	6,58
PC17T1	T1	PC17	Blautia	8,70
PC17T0	T0	PC17	Faecalibacterium	10,89
PC17T1	T1	PC17	Faecalibacterium	8,84
PC17T0	T0	PC17	Ruminococcus	7,27
PC17T1	T1	PC17	Other_Erysipelotrichaceae	6,27
PC17T0	T0	PC17	Other	40,48
PC17T1	T1	PC17	Other	29,03
PC18T0	T0	PC18	Bifidobacterium	6,96
PC18T2	T2	PC18	Uncl_Coriobacteriaceae	11,10
PC18T0	T0	PC18	Collinsella	5,78
PC18T2	T2	PC18	Collinsella	20,95
PC18T3	T3	PC18	Collinsella	6,23
PC18T0	T0	PC18	Bacteroides	25,65
PC18T1	T1	PC18	Bacteroides	22,94
PC18T3	T3	PC18	Bacteroides	9,08
PC18T0	T0	PC18	Prevotella	15,98
PC18T2	T2	PC18	Prevotella	10,51
PC18T3	T3	PC18	Prevotella	13,30
PC18T1	T1	PC18	Paraprevotella	10,58
PC18T2	T2	PC18	Paraprevotella	7,07
PC18T0	T0	PC18	Uncl_Clostridiales	5,57
PC18T0	T0	PC18	Uncl_Lachnospiraceae	9,43
PC18T1	T1	PC18	Uncl_Lachnospiraceae	5,33
PC18T1	T1	PC18	Blautia	10,13
PC18T3	T3	PC18	Lachnobacterium	14,51
PC18T3	T3	PC18	Lachnospira	5,74

PC18T3	T3	PC18	[Ruminococcus]	5,74
PC18T0	T0	PC18	Uncl_Ruminococcaceae	9,71
PC18T2	T2	PC18	Uncl_Ruminococcaceae	10,89
PC18T3	T3	PC18	Uncl_Ruminococcaceae	5,43
PC18T1	T1	PC18	Faecalibacterium	18,52
PC18T2	T2	PC18	Faecalibacterium	6,37
PC18T3	T3	PC18	Faecalibacterium	8,81
PC18T3	T3	PC18	Ruminococcus	9,19
PC18T1	T1	PC18	Dialister	5,57
PC18T2	T2	PC18	Sutterella	7,03
PC18T0	T0	PC18	Other	20,92
PC18T1	T1	PC18	Other	26,94
PC18T2	T2	PC18	Other	26,07
PC18T3	T3	PC18	Other	21,96
PC20T0	T0	PC20	Collinsella	7,00
PC20T0	T0	PC20	Bacteroides	11,70
PC20T1	T1	PC20	Bacteroides	8,95
PC20T2	T2	PC20	Bacteroides	6,44
PC20T1	T1	PC20	Prevotella	10,51
PC20T1	T1	PC20	Uncl_S24-7	5,99
PC20T2	T2	PC20	Uncl_S24-7	9,33
PC20T0	T0	PC20	Uncl_Clostridiales	5,29
PC20T2	T2	PC20	Uncl_Clostridiales	11,10
PC20T0	T0	PC20	Blautia	19,98
PC20T1	T1	PC20	Blautia	18,76
PC20T2	T2	PC20	Blautia	9,36
PC20T0	T0	PC20	[Ruminococcus]	5,64
PC20T0	T0	PC20	Uncl_Ruminococcaceae	7,24
PC20T1	T1	PC20	Uncl_Ruminococcaceae	14,41
PC20T2	T2	PC20	Uncl_Ruminococcaceae	16,39
PC20T0	T0	PC20	Faecalibacterium	8,56
PC20T2	T2	PC20	Ruminococcus	7,55
PC20T1	T1	PC20	Sutterella	10,30
PC20T2	T2	PC20	Sutterella	15,77
PC20T0	T0	PC20	Other	34,60
PC20T1	T1	PC20	Other	31,08
PC20T2	T2	PC20	Other	24,05
PC21T2	T2	PC21	Bifidobacterium	5,46
PC21T3	T3	PC21	Bifidobacterium	7,21
PC21T3	T3	PC21	Uncl_Coriobacteriaceae	18,10
PC21T0	T0	PC21	Collinsella	21,93
PC21T1	T1	PC21	Collinsella	18,34
PC21T3	T3	PC21	Collinsella	28,72
PC21T0	T0	PC21	Prevotella	8,42

PC21T1	T1	PC21	Prevotella	17,23
PC21T2	T2	PC21	Prevotella	16,99
PC21T3	T3	PC21	Prevotella	11,17
PC21T2	T2	PC21	Paraprevotella	5,22
PC21T0	T0	PC21	Uncl_Clostridiales	12,63
PC21T3	T3	PC21	Uncl_Clostridiales	5,26
PC21T1	T1	PC21	Blautia	7,45
PC21T0	T0	PC21	Uncl_Ruminococcaceae	14,20
PC21T2	T2	PC21	Uncl_Ruminococcaceae	11,80
PC21T3	T3	PC21	Uncl_Ruminococcaceae	8,14
PC21T0	T0	PC21	Faecalibacterium	11,03
PC21T1	T1	PC21	Faecalibacterium	7,90
PC21T2	T2	PC21	Faecalibacterium	10,06
PC21T1	T1	PC21	Ruminococcus	9,89
PC21T2	T2	PC21	Ruminococcus	5,50
PC21T3	T3	PC21	Sutterella	5,71
PC21T2	T2	PC21	Desulfovibrio	5,36
PC21T0	T0	PC21	Other	31,78
PC21T1	T1	PC21	Other	39,19
PC21T2	T2	PC21	Other	39,61
PC21T3	T3	PC21	Other	15,70
PC25T0	T0	PC25	Bifidobacterium	5,26
PC25T2	T2	PC25	Uncl_Coriobacteriaceae	5,99
PC25T3	T3	PC25	Uncl_Coriobacteriaceae	21,13
PC25T3	T3	PC25	Adlercreutzia	8,98
PC25T0	T0	PC25	Collinsella	16,71
PC25T2	T2	PC25	Uncl_Bacteroidales	5,12
PC25T0	T0	PC25	Bacteroides	10,93
PC25T1	T1	PC25	Bacteroides	10,55
PC25T2	T2	PC25	Bacteroides	10,86
PC25T3	T3	PC25	Bacteroides	9,99
PC25T0	T0	PC25	Prevotella	8,60
PC25T1	T1	PC25	Prevotella	20,81
PC25T1	T1	PC25	Paraprevotella	5,99
PC25T1	T1	PC25	Uncl_Clostridiales	7,07
PC25T2	T2	PC25	Uncl_Clostridiales	10,37
PC25T1	T1	PC25	Uncl_Lachnospiraceae	8,08
PC25T2	T2	PC25	Uncl_Lachnospiraceae	6,02
PC25T3	T3	PC25	Lachnospira	8,74
PC25T0	T0	PC25	Uncl_Ruminococcaceae	20,08
PC25T2	T2	PC25	Uncl_Ruminococcaceae	25,72
PC25T3	T3	PC25	Uncl_Ruminococcaceae	23,70
PC25T0	T0	PC25	Faecalibacterium	11,28
PC25T1	T1	PC25	Faecalibacterium	5,29

PC25T2	T2	PC25	Ruminococcus	5,40
PC25T2	T2	PC25	Alphaproteobacteria_RF32	6,54
PC25T1	T1	PC25	Akkermansia	7,45
PC25T0	T0	PC25	Other	27,15
PC25T1	T1	PC25	Other	34,77
PC25T2	T2	PC25	Other	23,98
PC25T3	T3	PC25	Other	27,46
PC26T0	T0	PC26	Bacteroides	30,53
PC26T1	T1	PC26	Bacteroides	6,09
PC26T3	T3	PC26	Bacteroides	18,27
PC26T3	T3	PC26	Uncl_Rikenellaceae	8,70
PC26T0	T0	PC26	Uncl_Clostridiales	9,47
PC26T1	T1	PC26	Uncl_Clostridiales	5,64
PC26T3	T3	PC26	Uncl_Clostridiales	6,40
PC26T0	T0	PC26	Uncl_Lachnospiraceae	6,02
PC26T1	T1	PC26	Uncl_Lachnospiraceae	15,87
PC26T3	T3	PC26	Uncl_Lachnospiraceae	12,32
PC26T3	T3	PC26	Lachnospira	6,93
PC26T1	T1	PC26	Uncl_Ruminococcaceae	8,77
PC26T3	T3	PC26	Uncl_Ruminococcaceae	7,83
PC26T0	T0	PC26	Faecalibacterium	20,88
PC26T1	T1	PC26	Faecalibacterium	30,42
PC26T3	T3	PC26	Faecalibacterium	6,09
PC26T0	T0	PC26	Ruminococcus	5,46
PC26T3	T3	PC26	Ruminococcus	10,86
PC26T0	T0	PC26	Phascolarctobacterium	6,09
PC26T0	T0	PC26	Other	21,55
PC26T1	T1	PC26	Other	33,21
PC26T3	T3	PC26	Other	22,59
PC27T3	T3	PC27	Collinsella	8,42
PC27T2	T2	PC27	Bacteroides	8,21
PC27T3	T3	PC27	Bacteroides	7,07
PC27T0	T0	PC27	Prevotella	10,16
PC27T3	T3	PC27	Prevotella	7,62
PC27T0	T0	PC27	Uncl_S24-7	14,10
PC27T0	T0	PC27	[Prevotella]	6,86
PC27T2	T2	PC27	[Prevotella]	12,60
PC27T3	T3	PC27	[Prevotella]	5,88
PC27T1	T1	PC27	Uncl_Clostridiales	5,64
PC27T2	T2	PC27	Uncl_Clostridiales	10,41
PC27T3	T3	PC27	Uncl_Clostridiales	8,60
PC27T0	T0	PC27	Uncl_Lachnospiraceae	5,71
PC27T1	T1	PC27	Uncl_Lachnospiraceae	10,37
PC27T2	T2	PC27	Uncl_Lachnospiraceae	9,40

PC27T0	T0	PC27	Blautia	11,14
PC27T1	T1	PC27	Blautia	5,40
PC27T0	T0	PC27	Lachnospira	6,16
PC27T3	T3	PC27	Lachnospira	10,76
PC27T2	T2	PC27	Roseburia	13,47
PC27T0	T0	PC27	Uncl_Ruminococcaceae	6,06
PC27T1	T1	PC27	Uncl_Ruminococcaceae	7,21
PC27T2	T2	PC27	Uncl_Ruminococcaceae	6,58
PC27T3	T3	PC27	Uncl_Ruminococcaceae	15,52
PC27T0	T0	PC27	Faecalibacterium	15,94
PC27T1	T1	PC27	Faecalibacterium	24,30
PC27T2	T2	PC27	Faecalibacterium	6,33
PC27T1	T1	PC27	Ruminococcus	8,25
PC27T3	T3	PC27	Ruminococcus	6,37
PC27T0	T0	PC27	Sutterella	6,82
PC27T1	T1	PC27	Sutterella	5,26
PC27T0	T0	PC27	Other	17,06
PC27T1	T1	PC27	Other	33,59
PC27T2	T2	PC27	Other	33,00
PC27T3	T3	PC27	Other	29,76
PC29T0	T0	PC29	Collinsella	21,16
PC29T1	T1	PC29	Collinsella	15,32
PC29T0	T0	PC29	Bacteroides	10,34
PC29T1	T1	PC29	Bacteroides	15,38
PC29T1	T1	PC29	Uncl_Clostridiales	6,20
PC29T1	T1	PC29	Uncl_Lachnospiraceae	7,24
PC29T1	T1	PC29	Blautia	5,29
PC29T0	T0	PC29	Uncl_Ruminococcaceae	16,99
PC29T1	T1	PC29	Uncl_Ruminococcaceae	10,86
PC29T0	T0	PC29	Faecalibacterium	17,51
PC29T1	T1	PC29	Faecalibacterium	20,99
PC29T0	T0	PC29	Sutterella	8,25
PC29T0	T0	PC29	Other	25,76
PC29T1	T1	PC29	Other	18,73
PC30T0	T0	PC30	Collinsella	17,51
PC30T1	T1	PC30	Collinsella	16,92
PC30T0	T0	PC30	Bacteroides	9,29
PC30T1	T1	PC30	Bacteroides	13,16
PC30T0	T0	PC30	Uncl_Clostridiales	7,03
PC30T1	T1	PC30	Blautia	5,40
PC30T0	T0	PC30	Uncl_Ruminococcaceae	14,55
PC30T1	T1	PC30	Uncl_Ruminococcaceae	12,01
PC30T0	T0	PC30	Faecalibacterium	6,40
PC30T1	T1	PC30	Faecalibacterium	14,55

PC30T0	T0	PC30	Ruminococcus	11,94
PC30T0	T0	PC30	Other	33,28
PC30T1	T1	PC30	Other	37,97
PC33T0	T0	PC33	Collinsella	11,59
PC33T3	T3	PC33	Bacteroides	7,38
PC33T0	T0	PC33	Prevotella	6,40
PC33T1	T1	PC33	Prevotella	6,23
PC33T2	T2	PC33	Prevotella	8,70
PC33T3	T3	PC33	Prevotella	11,07
PC33T0	T0	PC33	Uncl_S24-7	8,56
PC33T1	T1	PC33	Uncl_S24-7	9,68
PC33T2	T2	PC33	Uncl_S24-7	22,76
PC33T3	T3	PC33	Uncl_S24-7	6,61
PC33T1	T1	PC33	Uncl_Clostridiales	12,18
PC33T2	T2	PC33	Uncl_Clostridiales	13,92
PC33T2	T2	PC33	Uncl_Lachnospiraceae	5,57
PC33T3	T3	PC33	Blautia	7,07
PC33T0	T0	PC33	Uncl_Ruminococcaceae	20,78
PC33T1	T1	PC33	Uncl_Ruminococcaceae	17,47
PC33T2	T2	PC33	Uncl_Ruminococcaceae	9,47
PC33T1	T1	PC33	Faecalibacterium	13,30
PC33T3	T3	PC33	Ruminococcus	5,92
PC33T2	T2	PC33	Dialister	6,89
PC33T0	T0	PC33	Uncl_Erysipelotrichaceae	6,51
PC33T3	T3	PC33	Uncl_Erysipelotrichaceae	18,03
PC33T0	T0	PC33	Alphaproteobacteria_RF32	5,46
PC33T1	T1	PC33	Alphaproteobacteria_RF32	5,12
PC33T1	T1	PC33	Sutterella	7,10
PC33T3	T3	PC33	Sutterella	7,48
PC33T0	T0	PC33	Other	40,69
PC33T1	T1	PC33	Other	28,92
PC33T2	T2	PC33	Other	32,68
PC33T3	T3	PC33	Other	36,44
PC36T0	T0	PC36	Uncl_Coriobacteriaceae	5,92
PC36T2	T2	PC36	Uncl_Coriobacteriaceae	13,30
PC36T3	T3	PC36	Uncl_Coriobacteriaceae	9,64
PC36T0	T0	PC36	Collinsella	28,54
PC36T1	T1	PC36	Collinsella	16,39
PC36T2	T2	PC36	Collinsella	12,18
PC36T0	T0	PC36	Bacteroides	9,89
PC36T1	T1	PC36	Bacteroides	5,08
PC36T2	T2	PC36	Bacteroides	14,41
PC36T3	T3	PC36	Bacteroides	13,12
PC36T1	T1	PC36	Parabacteroides	5,19

PC36T0	T0	PC36	Prevotella	6,82
PC36T1	T1	PC36	Prevotella	18,45
PC36T2	T2	PC36	Prevotella	12,70
PC36T3	T3	PC36	Prevotella	6,93
PC36T2	T2	PC36	Uncl_Rikenellaceae	10,09
PC36T3	T3	PC36	Uncl_[Barnesiellaceae]	6,27
PC36T3	T3	PC36	Uncl_Clostridiales	16,32
PC36T3	T3	PC36	Uncl_Lachnospiraceae	5,19
PC36T1	T1	PC36	Blautia	5,05
PC36T2	T2	PC36	Blautia	6,33
PC36T0	T0	PC36	Uncl_Ruminococcaceae	8,91
PC36T1	T1	PC36	Uncl_Ruminococcaceae	8,88
PC36T2	T2	PC36	Uncl_Ruminococcaceae	5,05
PC36T3	T3	PC36	Uncl_Ruminococcaceae	6,30
PC36T0	T0	PC36	Faecalibacterium	13,51
PC36T1	T1	PC36	Faecalibacterium	19,84
PC36T2	T2	PC36	Faecalibacterium	15,35
PC36T3	T3	PC36	Faecalibacterium	9,61
PC36T0	T0	PC36	Ruminococcus	5,43
PC36T1	T1	PC36	Dialister	5,57
PC36T3	T3	PC36	Sutterella	5,92
PC36T0	T0	PC36	Other	20,99
PC36T1	T1	PC36	Other	15,56
PC36T2	T2	PC36	Other	10,58
PC36T3	T3	PC36	Other	20,71
PC37T3	T3	PC37	Other_Coriobacteriaceae	5,01
PC37T0	T0	PC37	Collinsella	9,54
PC37T1	T1	PC37	Collinsella	7,66
PC37T3	T3	PC37	Collinsella	7,90
PC37T1	T1	PC37	Bacteroides	18,20
PC37T2	T2	PC37	Bacteroides	11,94
PC37T3	T3	PC37	Bacteroides	13,40
PC37T2	T2	PC37	Parabacteroides	5,05
PC37T3	T3	PC37	Parabacteroides	8,56
PC37T2	T2	PC37	Prevotella	9,43
PC37T3	T3	PC37	Prevotella	7,87
PC37T2	T2	PC37	Uncl_Rikenellaceae	10,06
PC37T1	T1	PC37	Uncl_Clostridiales	8,01
PC37T3	T3	PC37	Uncl_Clostridiales	10,86
PC37T1	T1	PC37	Uncl_Lachnospiraceae	5,29
PC37T2	T2	PC37	Uncl_Lachnospiraceae	5,64
PC37T1	T1	PC37	Blautia	8,25
PC37T0	T0	PC37	Uncl_Ruminococcaceae	9,33
PC37T1	T1	PC37	Uncl_Ruminococcaceae	12,77

PC37T2	T2	PC37	Uncl_Ruminococcaceae	14,62
PC37T3	T3	PC37	Uncl_Ruminococcaceae	6,58
PC37T0	T0	PC37	Faecalibacterium	34,04
PC37T1	T1	PC37	Oscillospira	5,67
PC37T0	T0	PC37	Ruminococcus	10,44
PC37T3	T3	PC37	Ruminococcus	5,67
PC37T1	T1	PC37	Phascolarctobacterium	8,25
PC37T2	T2	PC37	Phascolarctobacterium	7,87
PC37T3	T3	PC37	Phascolarctobacterium	5,36
PC37T0	T0	PC37	Other	36,65
PC37T1	T1	PC37	Other	25,90
PC37T2	T2	PC37	Other	35,40
PC37T3	T3	PC37	Other	28,79
PC38T0	T0	PC38	Bifidobacterium	7,38
PC38T0	T0	PC38	Collinsella	8,08
PC38T2	T2	PC38	Collinsella	15,18
PC38T3	T3	PC38	Collinsella	5,53
PC38T0	T0	PC38	Bacteroides	9,15
PC38T3	T3	PC38	Bacteroides	18,45
PC38T0	T0	PC38	Prevotella	5,95
PC38T2	T2	PC38	Prevotella	10,06
PC38T0	T0	PC38	Uncl_S24-7	5,78
PC38T2	T2	PC38	Uncl_S24-7	7,27
PC38T2	T2	PC38	Uncl_Clostridiales	9,68
PC38T3	T3	PC38	Uncl_Clostridiales	6,02
PC38T0	T0	PC38	Uncl_Peptostreptococcaceae	7,62
PC38T0	T0	PC38	Uncl_Ruminococcaceae	8,81
PC38T2	T2	PC38	Uncl_Ruminococcaceae	20,99
PC38T3	T3	PC38	Uncl_Ruminococcaceae	12,08
PC38T0	T0	PC38	Ruminococcus	7,45
PC38T3	T3	PC38	Phascolarctobacterium	9,15
PC38T0	T0	PC38	Catenibacterium	6,16
PC38T3	T3	PC38	Catenibacterium	8,21
PC38T0	T0	PC38	[Eubacterium]	14,79
PC38T2	T2	PC38	[Eubacterium]	8,25
PC38T3	T3	PC38	[Eubacterium]	13,89
PC38T0	T0	PC38	Other	18,83
PC38T2	T2	PC38	Other	28,58
PC38T3	T3	PC38	Other	26,66
PC39T0	T0	PC39	Bifidobacterium	7,38
PC39T0	T0	PC39	Collinsella	12,91
PC39T1	T1	PC39	Collinsella	13,51
PC39T2	T2	PC39	Collinsella	9,99
PC39T3	T3	PC39	Collinsella	26,45

PC39T1	T1	PC39	Bacteroides	11,90
PC39T2	T2	PC39	Bacteroides	21,30
PC39T3	T3	PC39	Bacteroides	18,73
PC39T2	T2	PC39	Uncl_Rikenellaceae	5,33
PC39T3	T3	PC39	Paraprevotella	7,07
PC39T2	T2	PC39	Uncl_Clostridiales	12,95
PC39T0	T0	PC39	Blautia	5,74
PC39T3	T3	PC39	Blautia	5,99
PC39T1	T1	PC39	Uncl_Ruminococcaceae	14,62
PC39T2	T2	PC39	Uncl_Ruminococcaceae	8,01
PC39T0	T0	PC39	Faecalibacterium	53,53
PC39T1	T1	PC39	Faecalibacterium	16,57
PC39T2	T2	PC39	Faecalibacterium	15,32
PC39T2	T2	PC39	Oscillospira	5,60
PC39T2	T2	PC39	Alphaproteobacteria_RF32	5,71
PC39T1	T1	PC39	Sutterella	8,70
PC39T3	T3	PC39	Sutterella	14,10
PC39T0	T0	PC39	Other	20,43
PC39T1	T1	PC39	Other	34,70
PC39T2	T2	PC39	Other	15,80
PC39T3	T3	PC39	Other	27,67