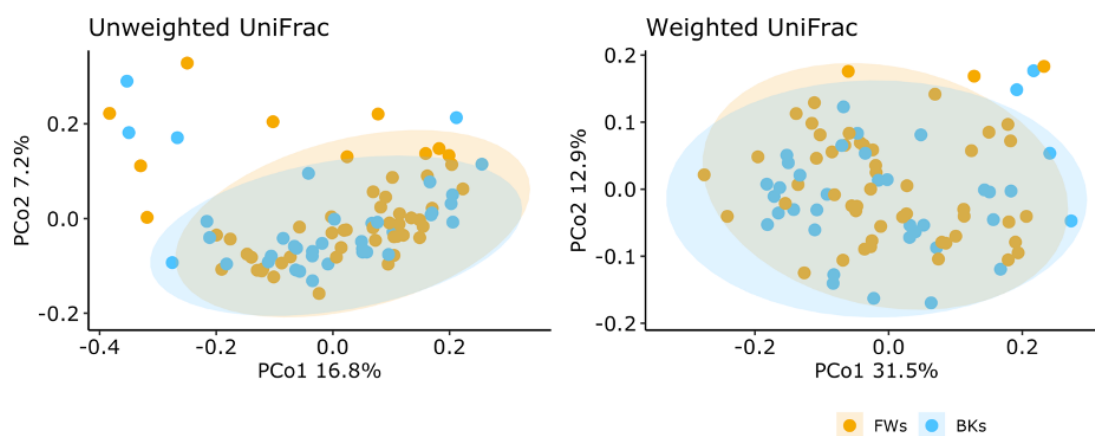


Supplementary Table S1. Alpha diversity indices of the microbiotas in fecal samples from university rugby players

Index	FWs		BKs		P-value
Chao1	161.18	± 47.78	169.91	± 48.11	0.36
Shannon	4.54	± 0.50	4.52	± 0.55	0.79

Team positions: FWs, forwards.; BKs, backs

Significance (* $P < 0.05$ and ** $P < 0.01$) was analyzed using the Welch's t-test.



Supplementary Figure S1. PCoA analysis of the microbiotas in fecal samples from university rugby players, based on unweighted and weighted UniFrac distances. Ellipses enclosing clusters indicate 95% confidence interval. Significance was analyzed by PERMANOVA. Team positions: FWs, Forwards; BKs, Backs

Supplementary Table S2. Bacterial genera that differed in fecal samples of the control and URP groups (average abundance < 0.1%)

Taxonomy			Control			URP			P-value	
Order	Family	Genus								
Clostridiales	<i>Lachnospiraceae</i>	Unclassified	0.092	±	0.132	0.083	±	0.243	0.028	*
Erysipelotrichales	<i>Erysipelotrichaceae</i>	<i>Coprobacillus</i>	0.097	±	0.167	0.051	±	0.194	0.003	**
Bacteroidales	S24-7	Unclassified	0.034	±	0.077	0.102	±	0.677	<0.001	**
Clostridiales	<i>Christensenellaceae</i>	Unclassified	0.082	±	0.239	0.039	±	0.235	0.001	**
Clostridiales	Unclassified	Unclassified	0.022	±	0.044	0.073	±	0.103	0.028	*
Bacillales	<i>Bacillaceae</i>	<i>Bacillus</i>	0.004	±	0.009	0.080	±	0.158	0.029	*
Clostridiales	<i>Lachnospiraceae</i>	<i>Defluviitalea</i>	0.065	±	0.096	0.016	±	0.042	0.003	**
Pasteurellales	<i>Pasteurellaceae</i>	<i>Aggregatibacter</i>	0.002	±	0.007	0.062	±	0.207	0.016	*
Enterobacteriales	<i>Enterobacteriaceae</i>	<i>Citrobacter</i>	0.004	±	0.014	0.057	±	0.217	0.021	*
Lactobacillales	<i>Streptococcaceae</i>	<i>Lactococcus</i>	0.003	±	0.011	0.053	±	0.300	0.006	**
Actinomycetales	<i>Micrococcaceae</i>	<i>Rothia</i>	0.012	±	0.023	0.044	±	0.089	0.005	**
Clostridiales	<i>Ruminococcaceae</i>	<i>Anaerotruncus</i>	0.040	±	0.062	0.008	±	0.019	<0.001	**
Lactobacillales	<i>Carnobacteriaceae</i>	<i>Granulicatella</i>	0.007	±	0.006	0.030	±	0.054	0.007	**
Lactobacillales	<i>Lactobacillaceae</i>	<i>Pediococcus</i>	0.015	±	0.060	0.019	±	0.164	0.040	*
Erysipelotrichales	<i>Erysipelotrichaceae</i>	cc_115	0.010	±	0.017	0.002	±	0.005	<0.001	**
Bacteroidales	<i>Rikenellaceae</i>	<i>Rikenella</i>	0.010	±	0.031	<0.001			0.002	**
Streptophyta	Unclassified	Unclassified	0.001	±	0.002	0.007	±	0.025	0.033	*
Clostridiales	<i>Peptococcaceae</i>	rc4-4	0.005	±	0.014	0.003	±	0.019	0.038	*
Clostridiales	<i>Christensenellaceae</i>	<i>Christensenella</i>	0.006	±	0.012	0.001	±	0.004	0.005	**
Clostridiales	<i>Christensenellaceae</i>	Unclassified	0.005	±	0.010	0.001	±	0.003	0.001	**
Clostridiales	<i>Eubacteriaceae</i>	<i>Anaerofustis</i>	0.003	±	0.004	0.001	±	0.004	0.005	**
Clostridiales	<i>Dehalobacteriaceae</i>	<i>Dehalobacterium</i>	0.003	±	0.009	0.001	±	0.006	0.030	*
Actinomycetales	<i>Corynebacteriaceae</i>	<i>Corynebacterium</i>	0.003	±	0.009	0.001	±	0.009	0.036	*
Pseudomonadales	<i>Moraxellaceae</i>	<i>Acinetobacter</i>	0.003	±	0.006	<0.001			<0.001	**
Sphingomonadales	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>	<0.001			0.003	±	0.004	<0.001	**
Bacteroidales	<i>Porphyromonadaceae</i>	<i>Dysgonomonas</i>	0.002	±	0.007	<0.001			0.033	*
Deferribacteriales	<i>Deferribacteraceae</i>	<i>Mucispirillum</i>	0.001	±	0.003	<0.001			<0.001	**
Clostridiales	[<i>Tissierellaceae</i>]	WAL_1855D	0.001	±	0.002	0.000	±	0.003	<0.001	**
Campylobacteriales	<i>Helicobacteraceae</i>	<i>Flexispira</i>	<0.001			0.001	±	0.002	0.023	*
Campylobacteriales	<i>Helicobacteraceae</i>	Unclassified	<0.001			0.001	±	0.002	0.047	*
Bacteroidales	Unclassified	Unclassified	0.000	±	0.002	<0.001			0.033	*
Pseudomonadales	<i>Moraxellaceae</i>	<i>Enhydrobacter</i>	0.000	±	0.001	<0.001			0.033	*

Genera with relative abundances lower than 0.1% and having significant differences between groups are listed. Significance (* P <0.05 and ** P <0.01) was analyzed using the Wilcoxon rank sum test.