

# Cataloguing Metagenome Assembled Genomes and microbial genes from the athlete gut microbiome.

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**Abstract:**

The gut microbiome plays a crucial role in host physiology, and in recent years the fitness-microbiome paradigm has gained much research attention. As previously reported, the gut microbiomes of elite athletes are more diverse than that of non-athletes, with the changes in certain microbial taxa accounting for this increased diversity. To assess the gut microbiome of elite athletes, we have used various bioinformatic pipelines to recover Metagenome Assembled Genomes (MAGs), construct a phylogenomic tree of recovered MAGs, and to assess the genomic content predicted within the MAGs. This study recovered approximately 10,000 MAGs, from which 1,327 were deemed High-Quality and were brought forward for further analysis. The average nucleotide identity (ANI) of recovered MAGs was assessed for potential novel taxa. Our approach has recovered and established a catalogue of bacterial taxa genomes associated with fitness and several clusters of bacterial taxa that could be attributed to specific sports. *Bacteroides* spp., and *Eubacterium* spp. clusters were concluded to be associated with rugby players, while, *Faecalibacterium* spp., *Prevotella* spp. and *Roseburia* spp. clusters were attributed to cyclists and runners respectively. To assess the gene content of recovered MAGs, we scored genes to phenotypes (in this case sports), and discovered differences in gene content between the sports. This study highlights the potential of this MAG recovery strategy to expand our understanding of the specific roles that the microbes and their genes play in fitness, as well as providing us with the direction for further investigation of the complex microbiome-fitness paradigm.