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Comparison of metagenomes from EBPR wastewater treatment plants to other environments shows a conserved functional potential

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Introduction

Metagenomics can provide comprehensive information about the entire microbial community of a certain ecosystem, e.g. a wastewater treatment plant. Such studies on full-scale plants are needed to improve the understanding of key microorganisms in the EBPR process and the entire community in order to improve the process for efficient phosphorus removal and recovery.

Objectives

- Compare the functional potential of two full-scale EBPR plants to other environments by the use of metagenomics.
- Investigate, in detail, similarities and differences between selected available reference genomes and the bacteria present in the full-scale EBPR plants.

Methods

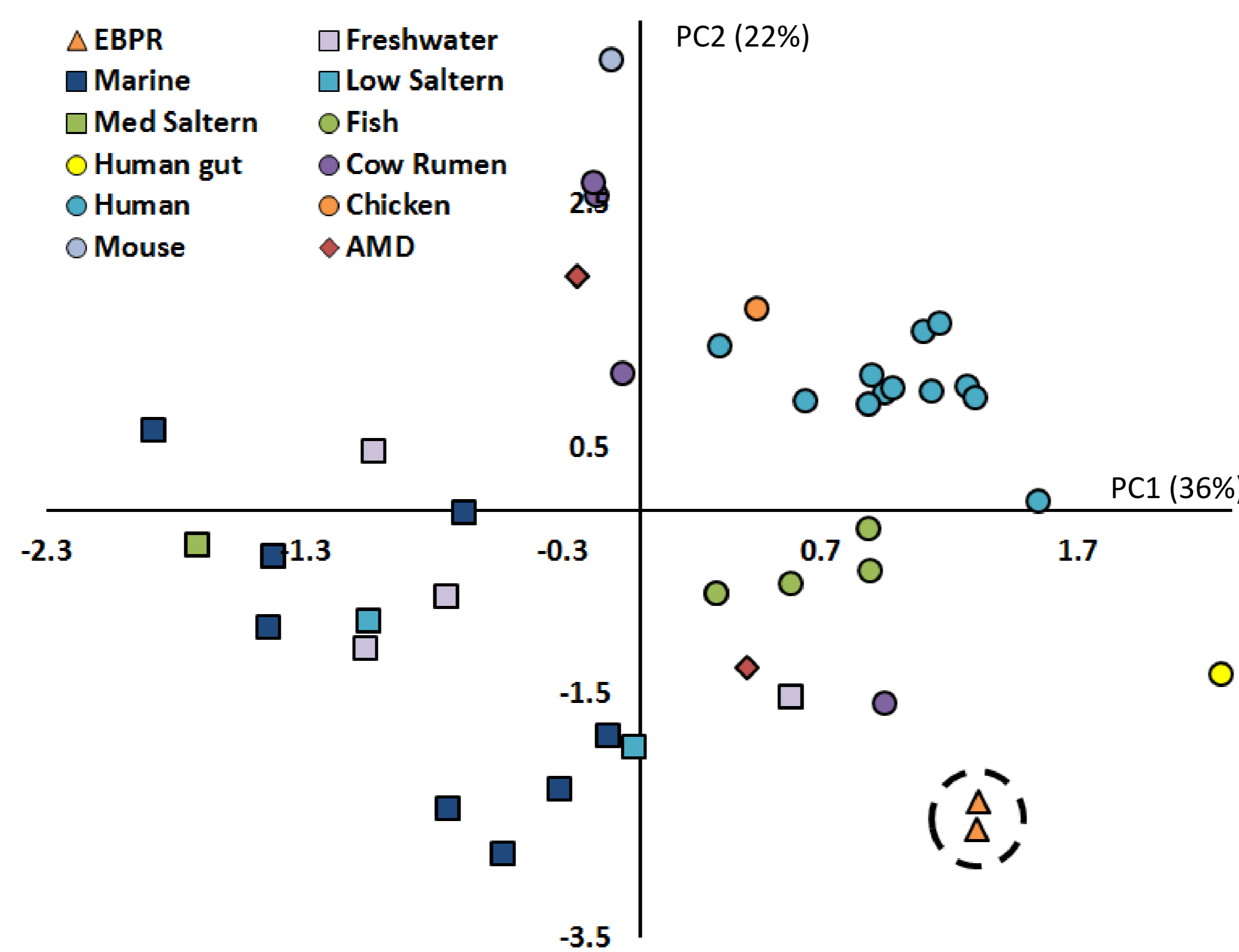
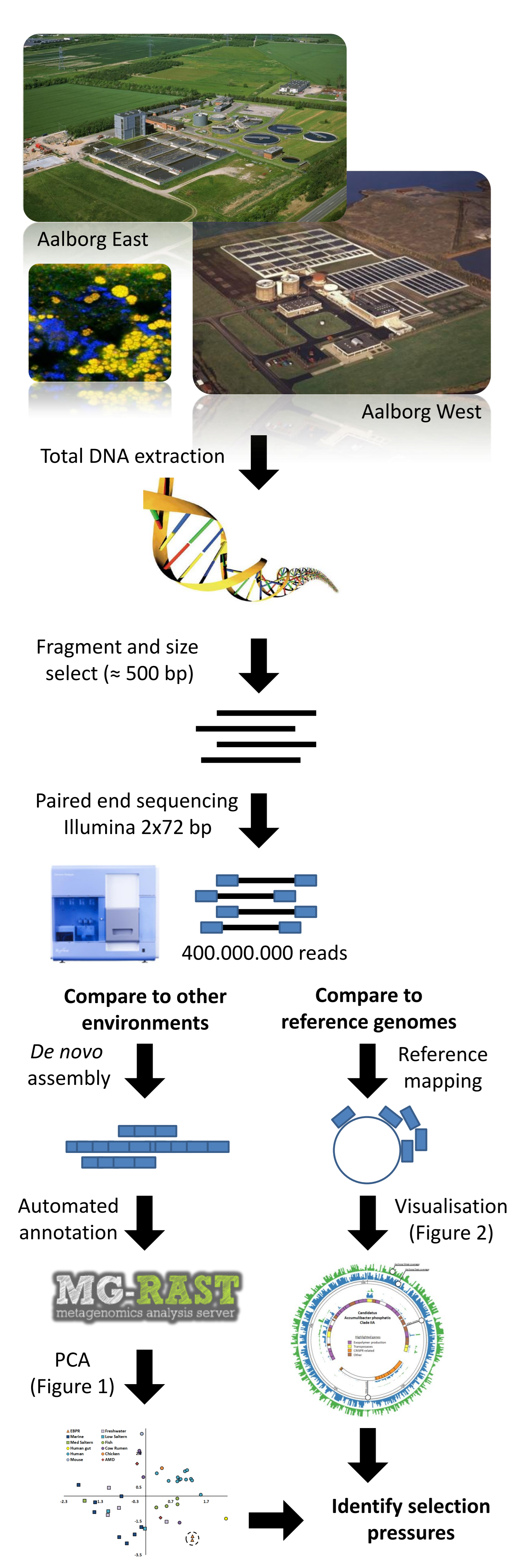
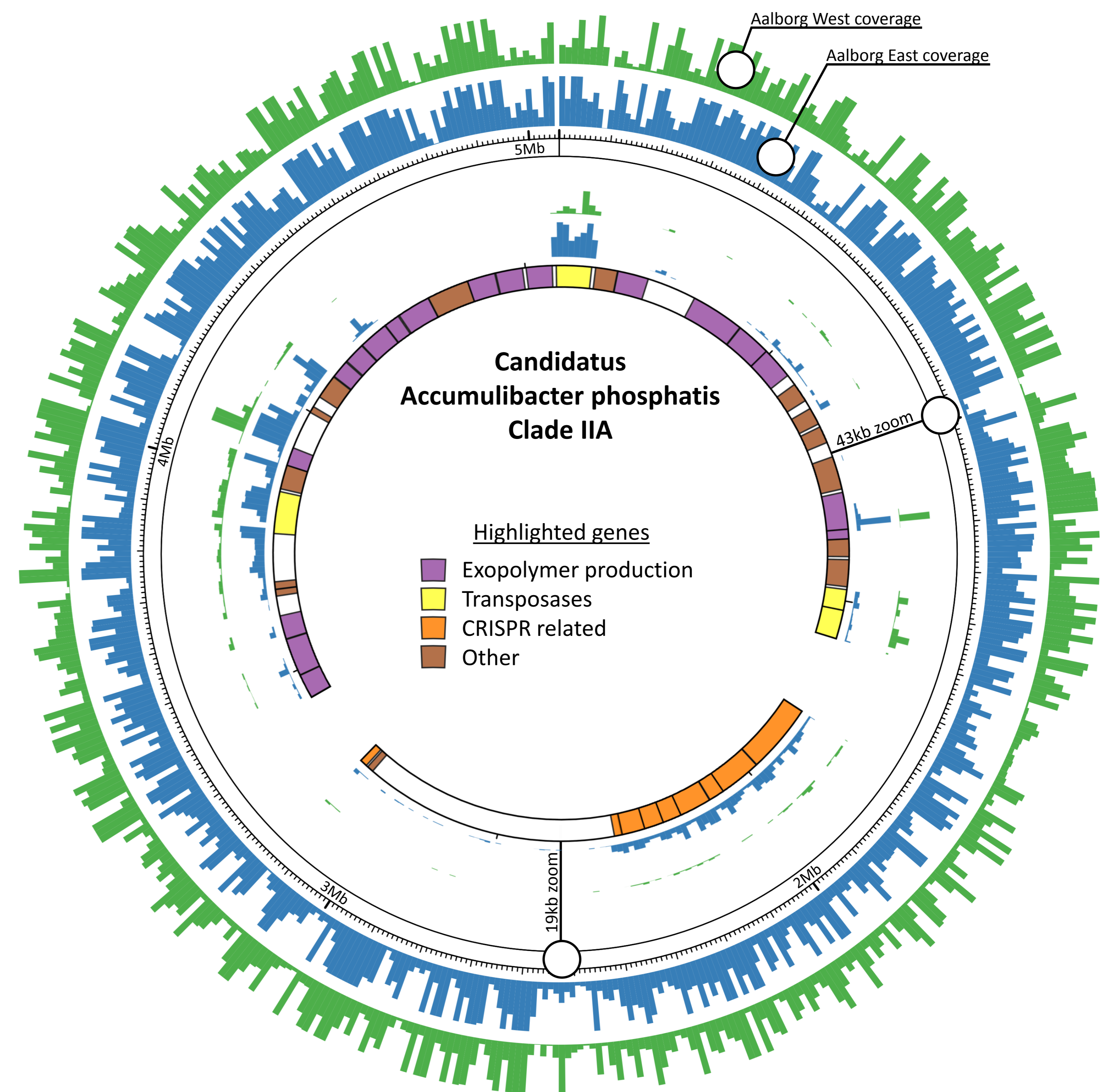


Figure 1. Principle coordinate analysis (PCA) of the functional potential of the two EBPR metagenomes and 39 metagenomes selected to represent a wide range of environments.

The EBPR metagenomes form a distinct cluster when compared to the other environments. However, no single factor could be identified that explained the groupings, underlining the complex selection pressures that form the different microbial communities.

Figure 2. Identification of selection pressures on one of the key P-removal bacteria by mapping metagenome reads to the genome.

It can be seen that several parts of the genome have low coverage in both the Aalborg West and East metagenomes (examples highlighted by inserts). Low coverage indicates that these genes are not present in the genomes of the species in the wastewater treatment plants. Many genes involved in exopolymer production and CRISPR phage defense had very low coverage. This indicates that not only CRISPR genes are involved in the direct phage defense, but also the structure of the extracellular matrix is altered in response to phage attacks.



Conclusions and Further Work

- EBPR wastewater treatment plants show a conserved functional potential when compared to a wide range of environments. However, no single factors could be attributed to the clustering. More metagenomes will enable more detailed investigations.
- The hyper-variability of genes involved in exopolymer production indicates a very active phage defence. Phages might play a large role in shaping the microbial community and the dynamic interplay of bacteria and phages in full-scale EBPR wastewater treatment plants will be interesting to investigate in further details.
- More reference genomes from wastewater treatment plants are needed to make in-depth analysis. We are currently generating the needed genomes by a combination of single cell genomics and metagenomics.