

Colonization kinetics and implantation follow-up of the sewage microbiome in an urban wastewater treatment plant

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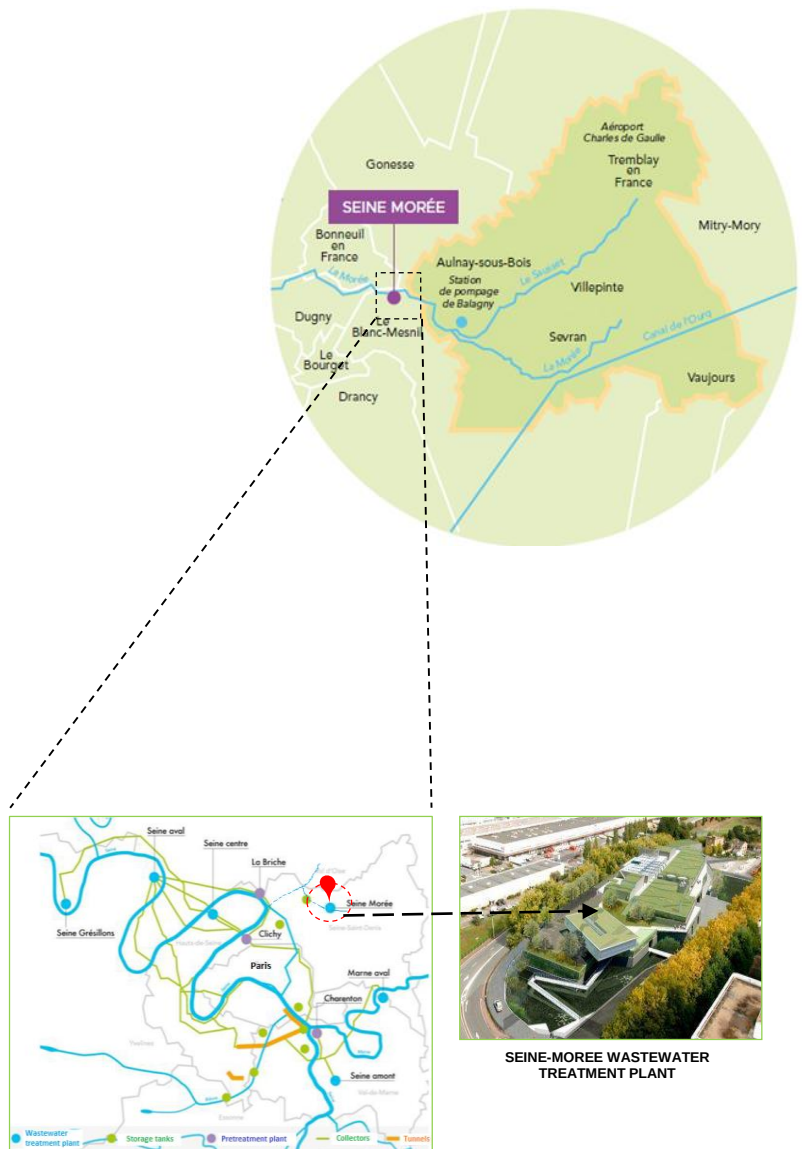


Fig. S1. SM_WWTP geolocalization

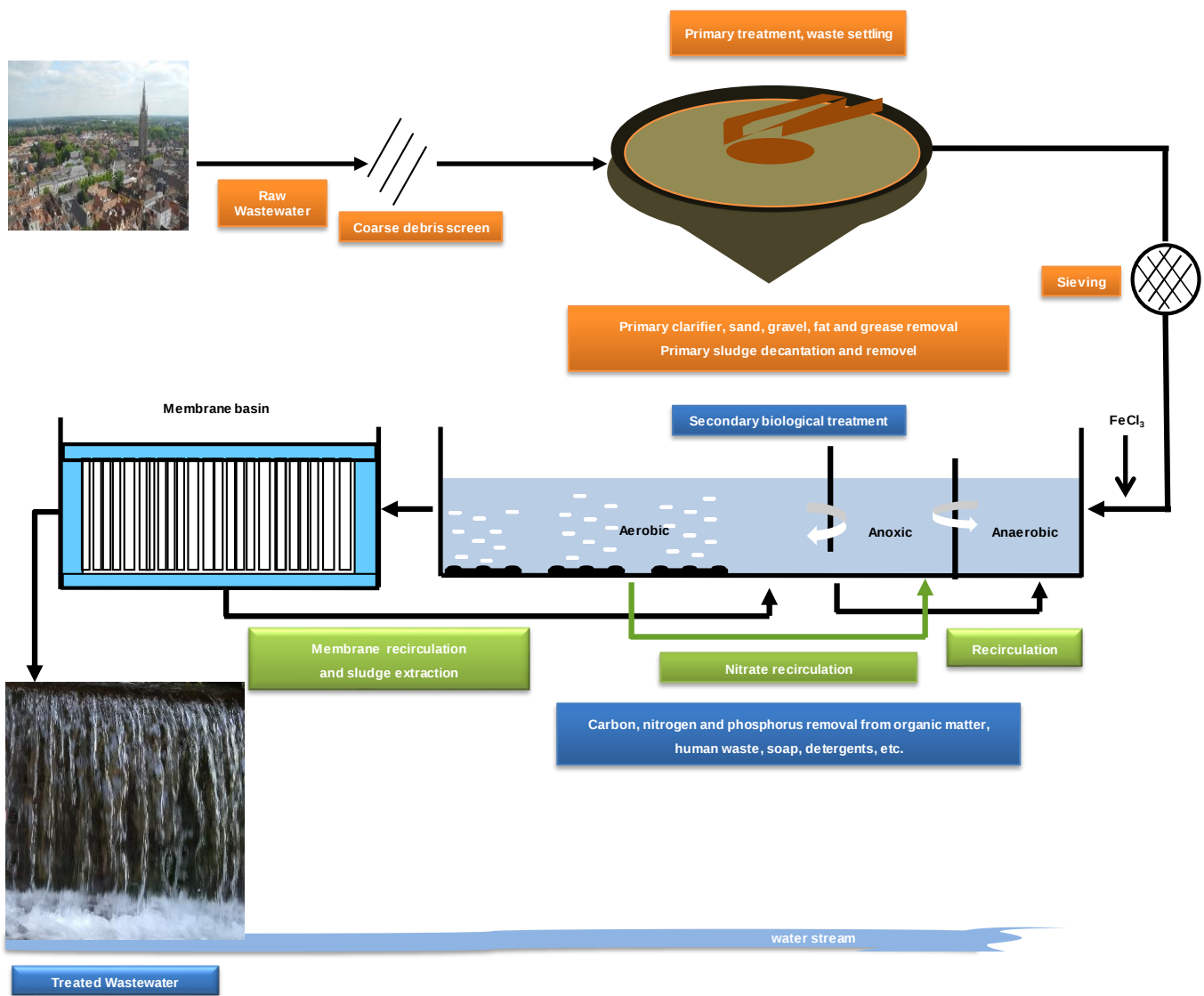


Fig. S2. SM_WWTP plant description

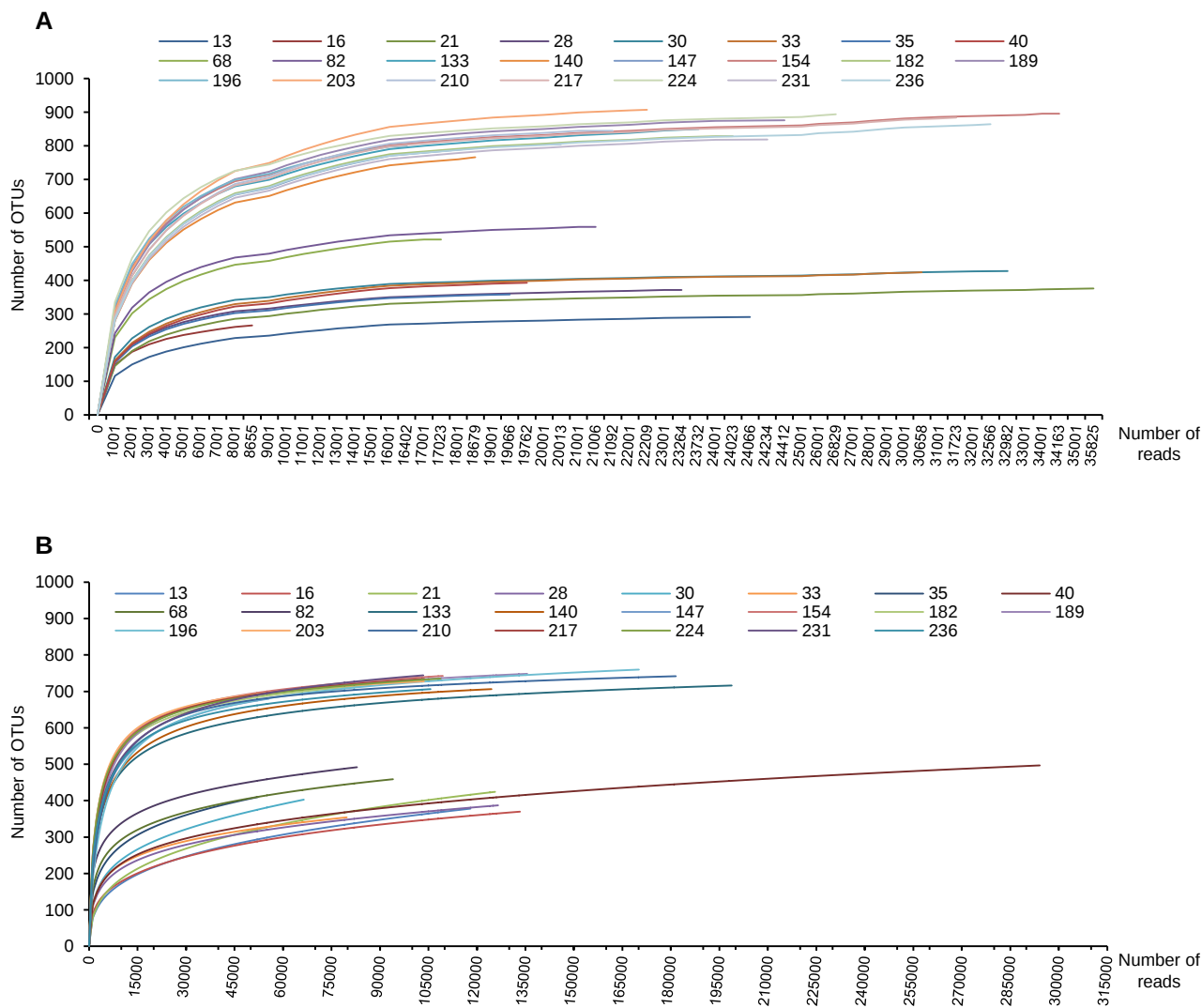


Fig. S3. Bacterial and eukaryotic rarefaction curves describing microbial richness of the time series SM_WWTP samples. Rarefaction curves describing bacterial **(A)** and eukaryotic **(B)** richness and of the 23 times series SM_WWTP samples.

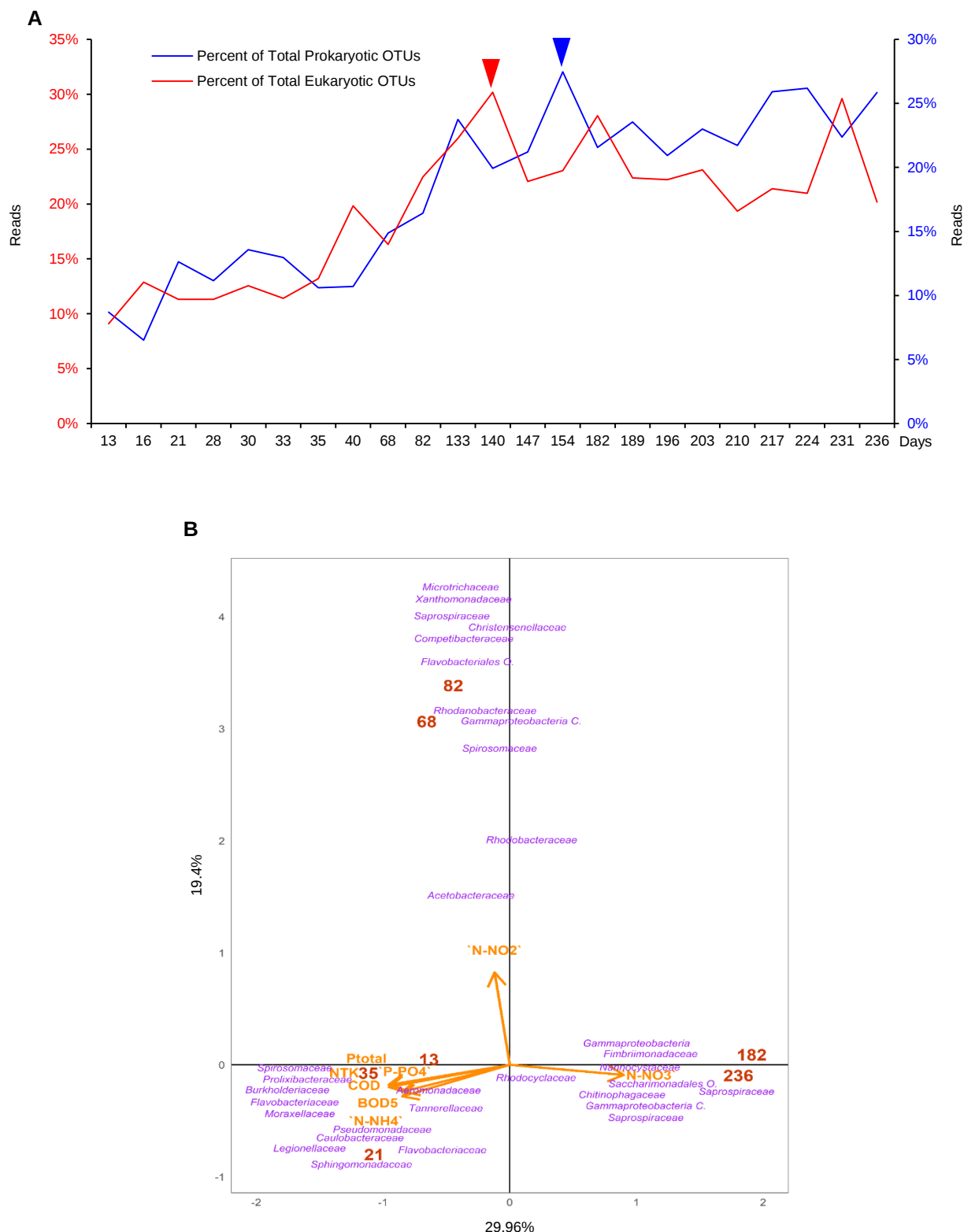


Fig. S4. (A) OTUs colonization kinetics within the aerobic basin of SM_WWTP. Scale colors: blue represent bacterial OTUs and red, Eukaryotic OTUs. **(B)** Canonical correspondence analysis (CCA) describing the relationship between bacterial community compositions and physicochemical properties of the time series wastewater samples.

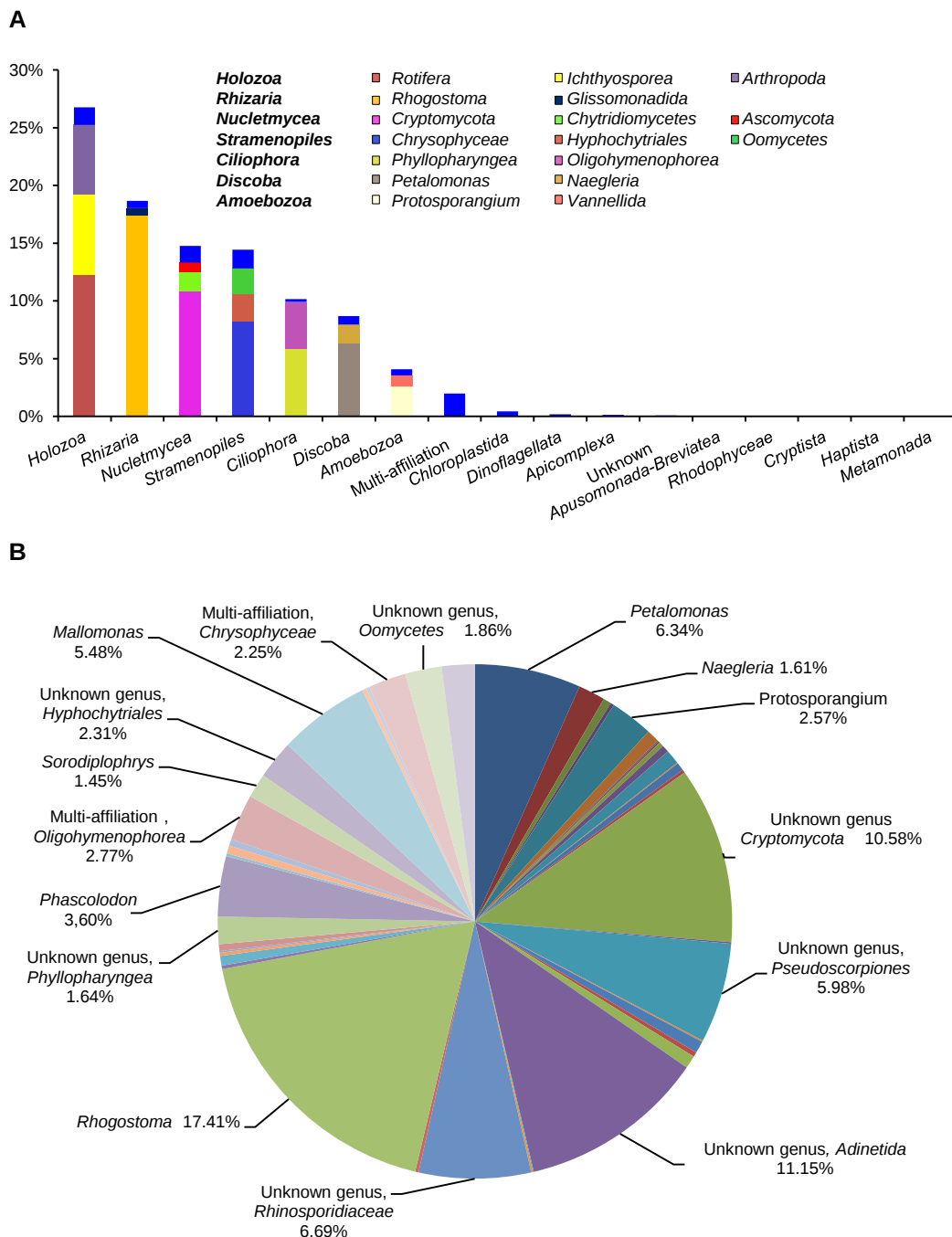


Fig. S6. Global relative abundance average (% of reads) of the eukaryotic phyla and genera within the 23 time-series SM_WWTP samples. (A) Relative abundance average (%) of eukaryotic phyla reads. Each bar includes subphyla and/or genera displayed with different colors. The top blue color represent the sum of the remaining subphyla in the corresponding phylum. From bottom to top, the bars represent subphyla. (B) Relative abundance average (%) of eukaryotic genera reads. Genera were filtered for those that display an abundance rate $\geq 1\%$ in at least one of the 23 samples. Unaffiliated sequences depicted as "Unknown genus" were grouped together within the nearest known taxonomic rank, i.e. family, order, or class. The same applies to those depicted as "Multi-affiliation" sequences.

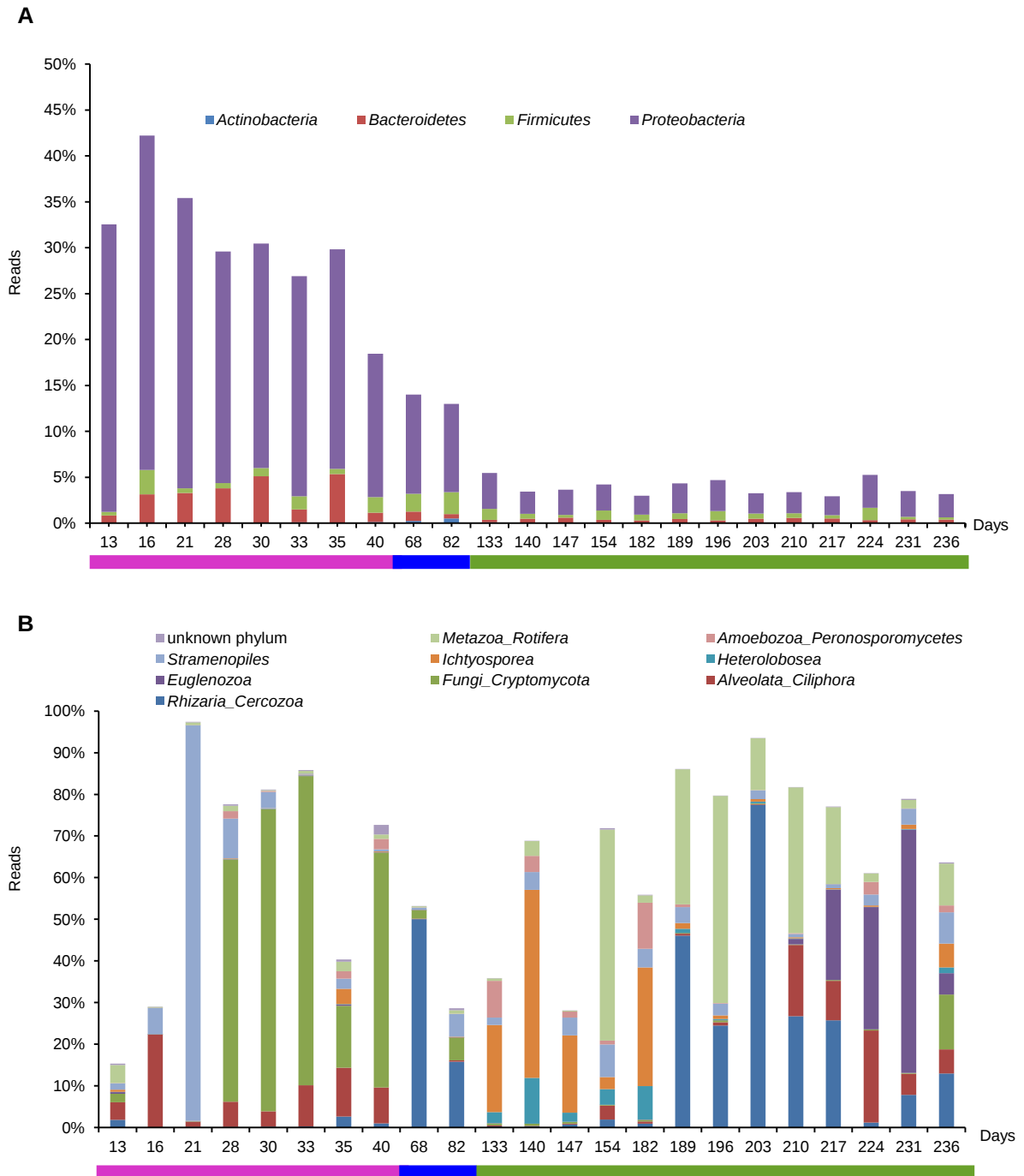


Fig. S7. Relative abundance (%) and kinetics of persistent bacterial (**A**) and eukaryotic (**B**) phyla of the 23 time-series SM_WWTP samples. Colored lines delimit the three periods of physicochemical parameters and microbiota evolution: Pink represent the first period, blue, the intermediate period, and green represent the third period.