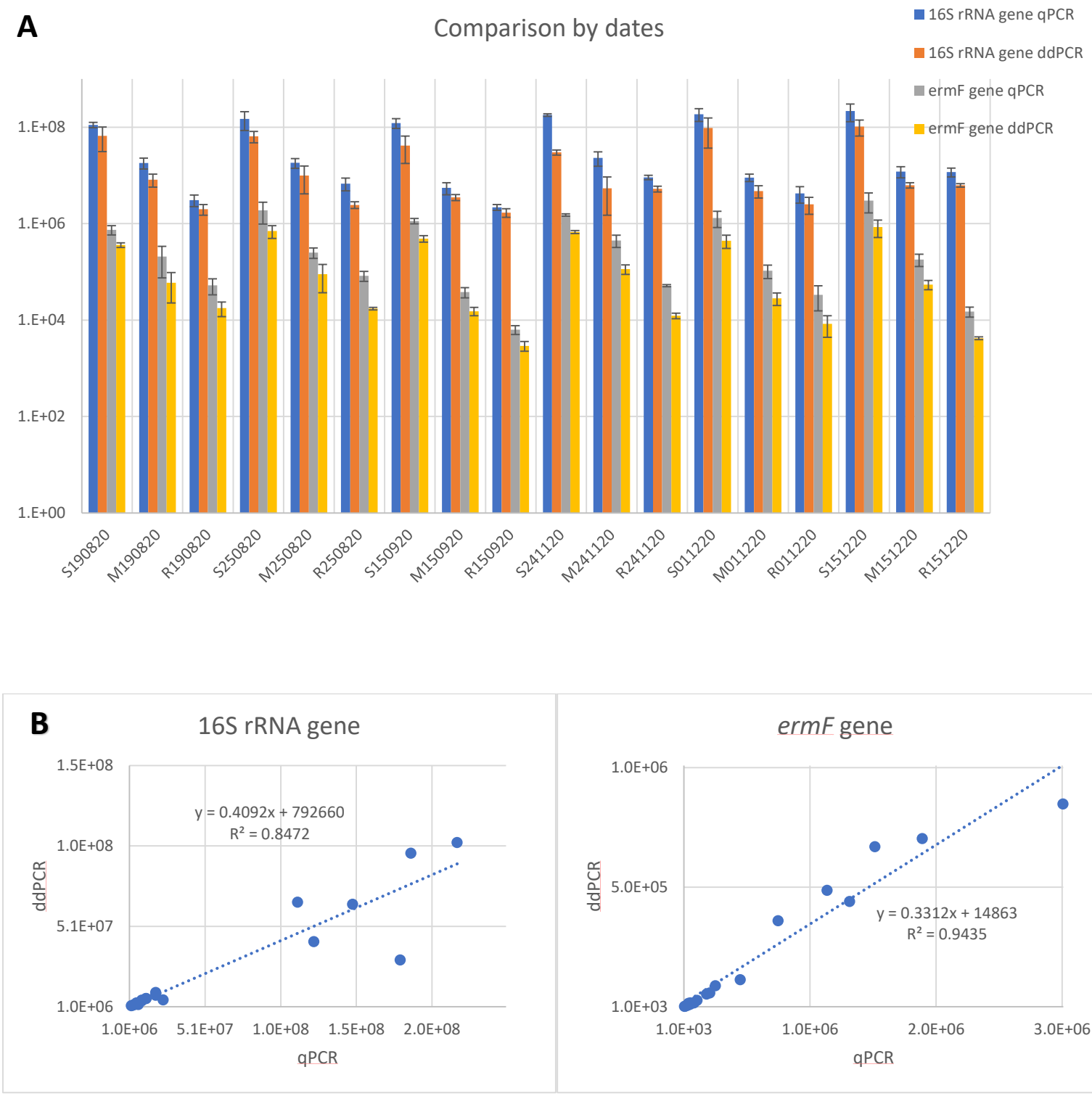

Figure S1. Comparison of quantification by qPCR and ddPCR. A) Absolute abundances of 16S rRNA and *ermF* genes over time. B) Linear regressions of qPCR *vs* ddPCR datas for 16S rRNA (left panel) and *ermF* (right panel) genes.

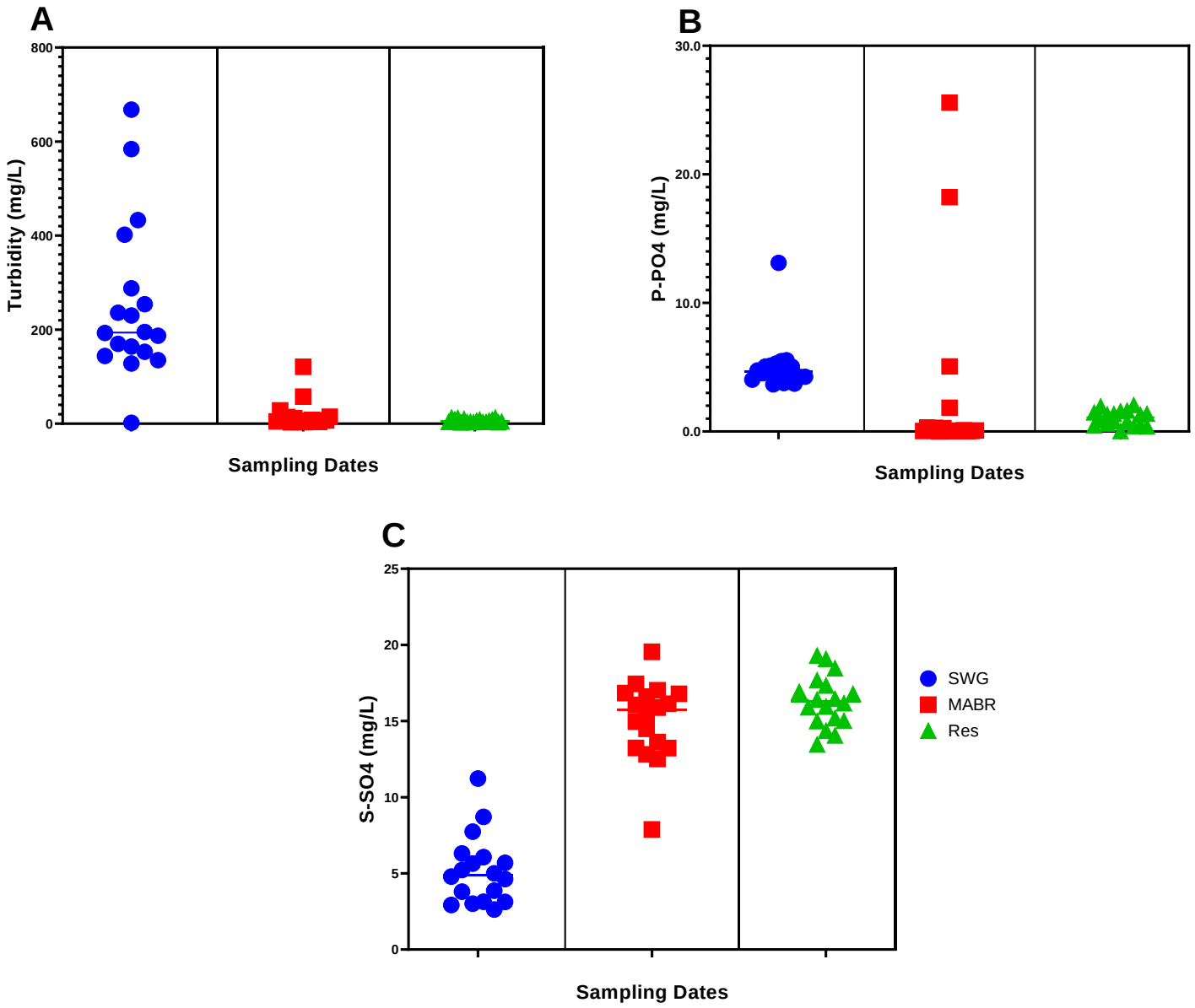

Figure S2. Physicochemical analyses in the raw sewage (blue circles), MABR (red boxes) and reservoir (green triangles). Turbidity (A); Phosphate (B); Sulfate (C)

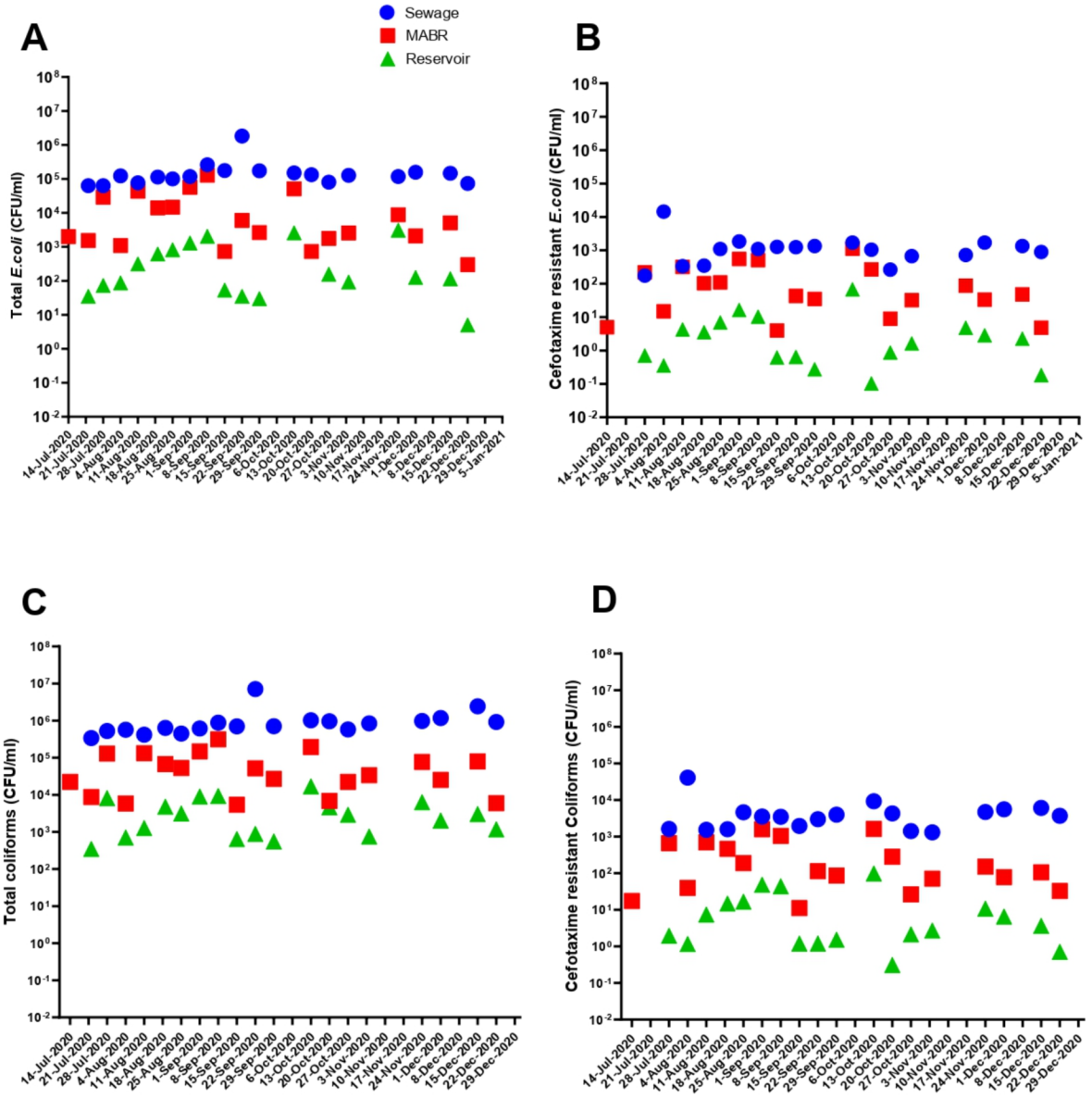

Figure S3. Total (A) and cefotaxime-resistant (B) *E.coli* and total coliforms(C)and cefotaxime-reisistant coliforms (D)in the raw sewage (blue circles), MABR(red boxes) and resservoir (green triangles).

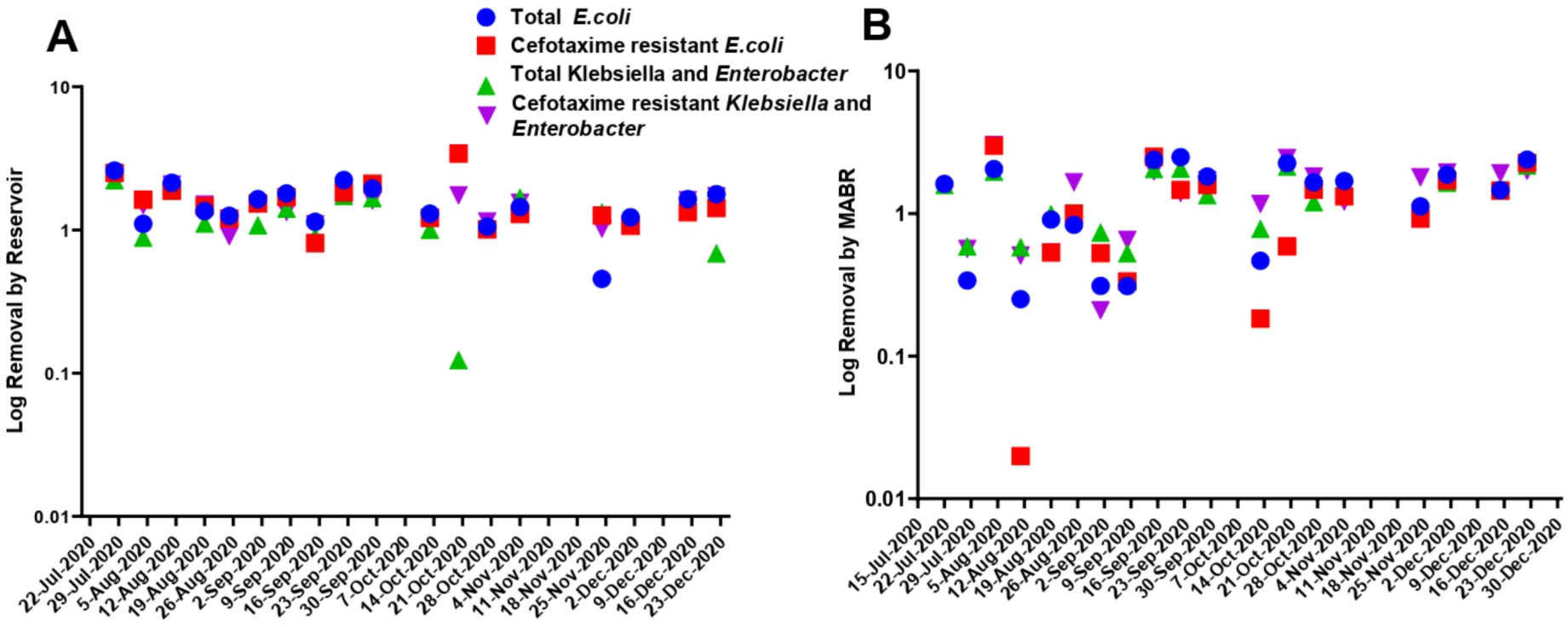

Figure S4. Microbial Log removal by Reservoir (A) and by MABR (B) for total *E.coli* (blue cirlces), Cefotaxime resistant *E.coli* (red squares), total *Klebsiella* and *Enterobacter* (green triangles) and Cefotaxime resistant *Klebsiella* and *Enterobacter* (violet triangles)

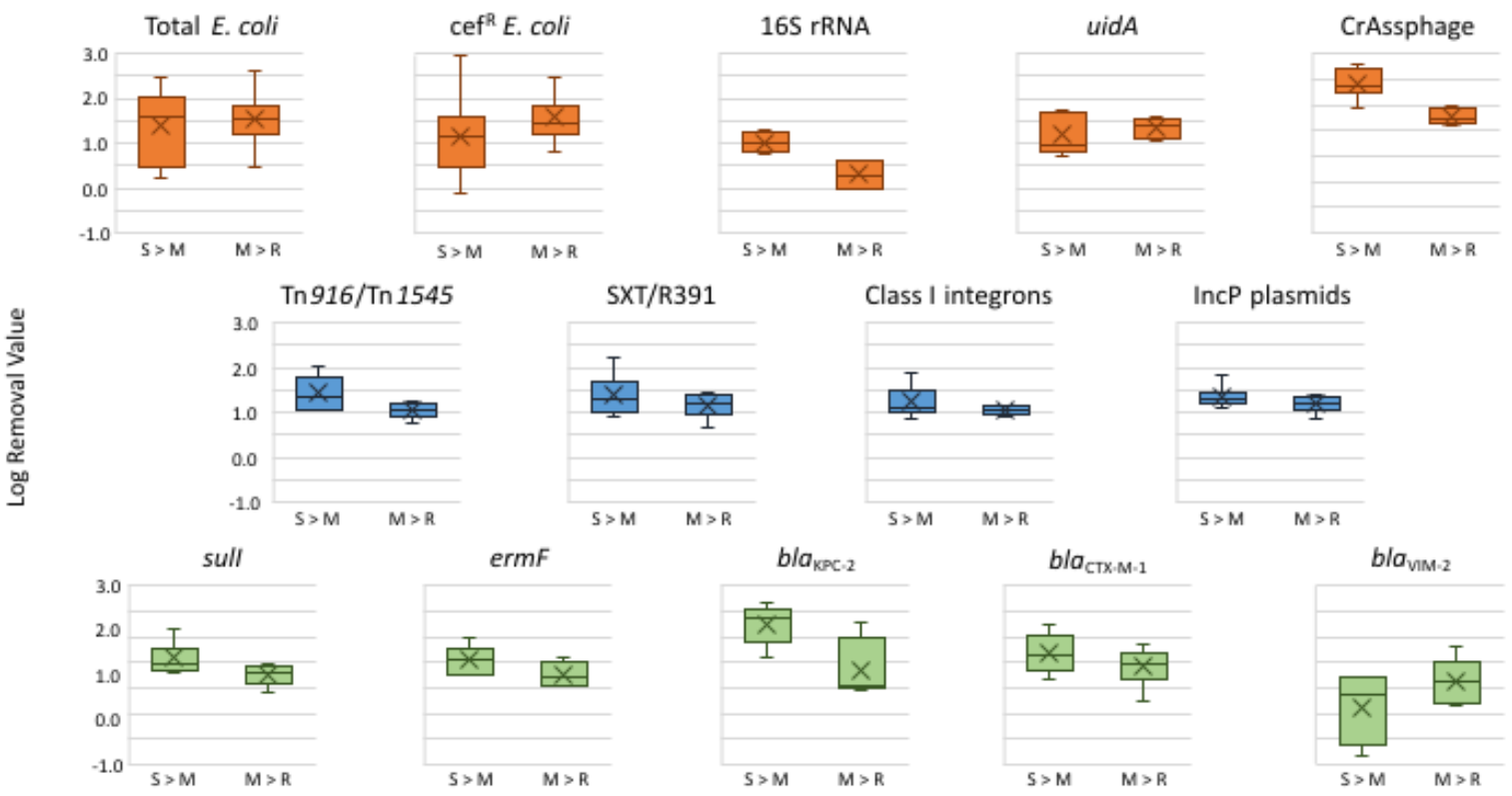

Figure S5. Log removal values (LRV) of ARGs & MGEs monitored. Colors represented different groups: blue = MGEs, green = ARGs and orange = 16S rRNA, uidA and CrAssphage (CPQ_056).

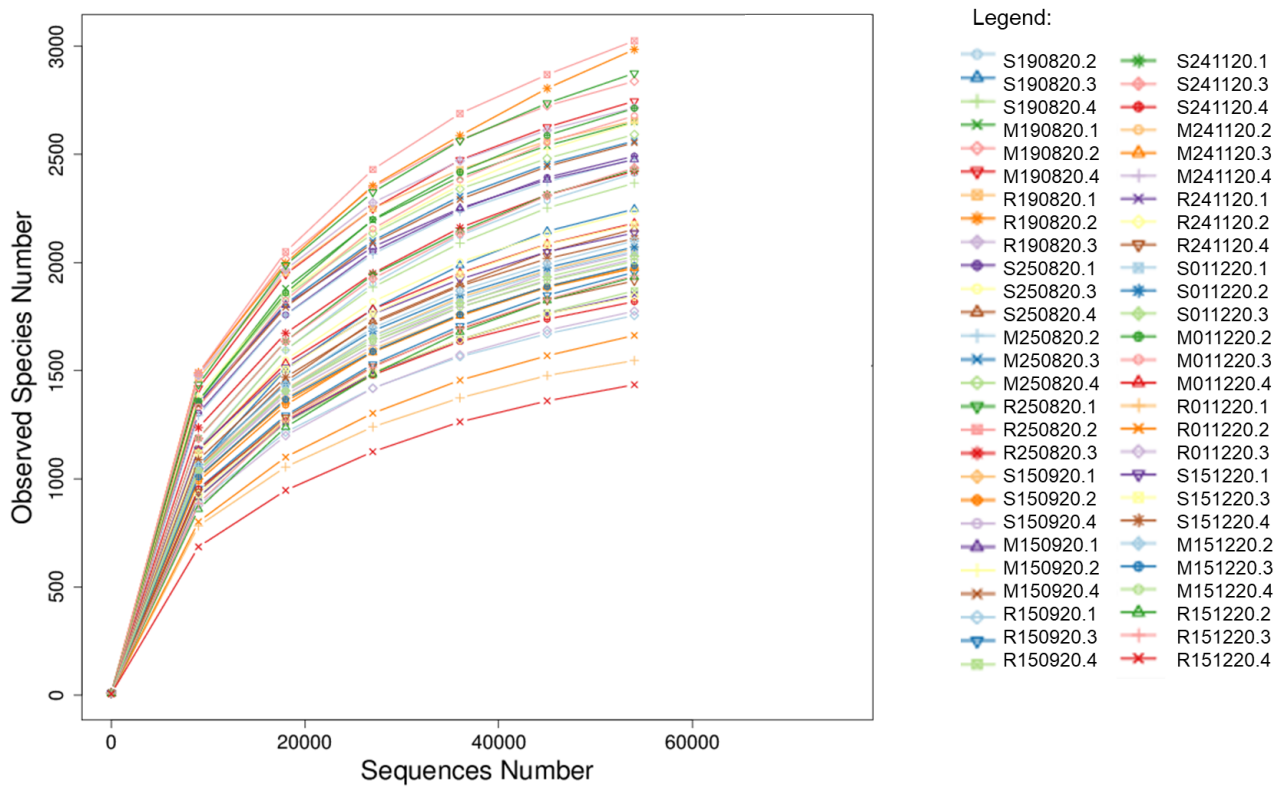

Figure S6. Rarefaction Curves (observed species vs. number of sequences) for 16S rRNA amplicon (V3-V4 hypervariable region) sequencing based community analysis. A total of 18 (6 of each S, M, R) were analysed in triplicate. Operational taxonomic Units (OTU) were defined at a level ≥97%. The number of reads varied between 91 582 (S250820.4) and 119 322 (M151220.2), and sequences were rarefied according to the sample with the lowest effective number of sequences (after filtering chimera).

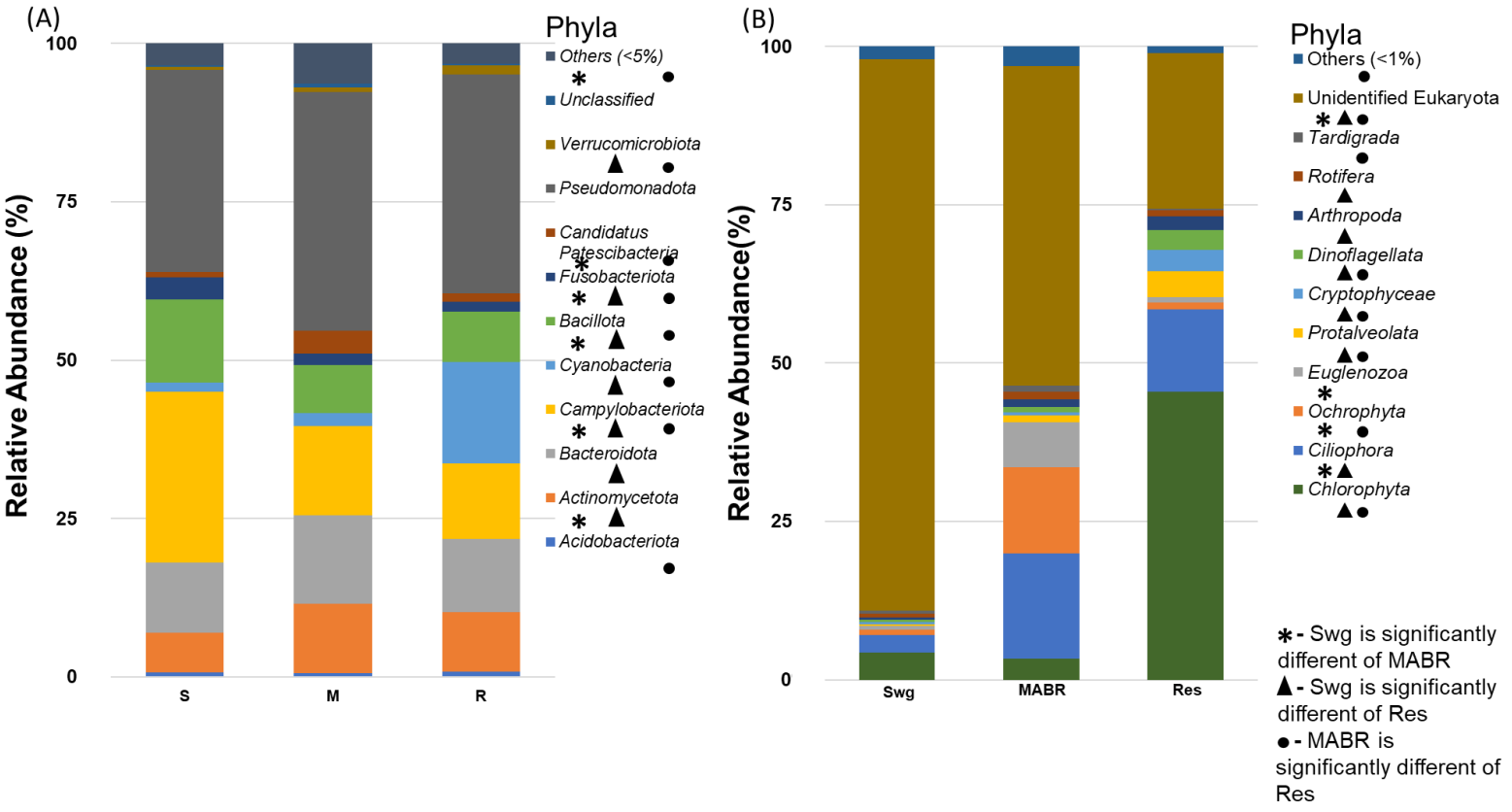

Figure S7. Microbial community analyses based on 16S rRNA V3-V4 region (A) or 18S rRNA V9 region (B), represented at the phyla level for relative abundance values >5% and >1%, respectively. Significantly different ($p<0.01$) relative abundance values estimated based on three replicated of each of 18 samples (Prokaryotic analysis) and all the replicated (Eukaryotic analysis) of Swg, MABR and Res are indicated below the phylum legend.

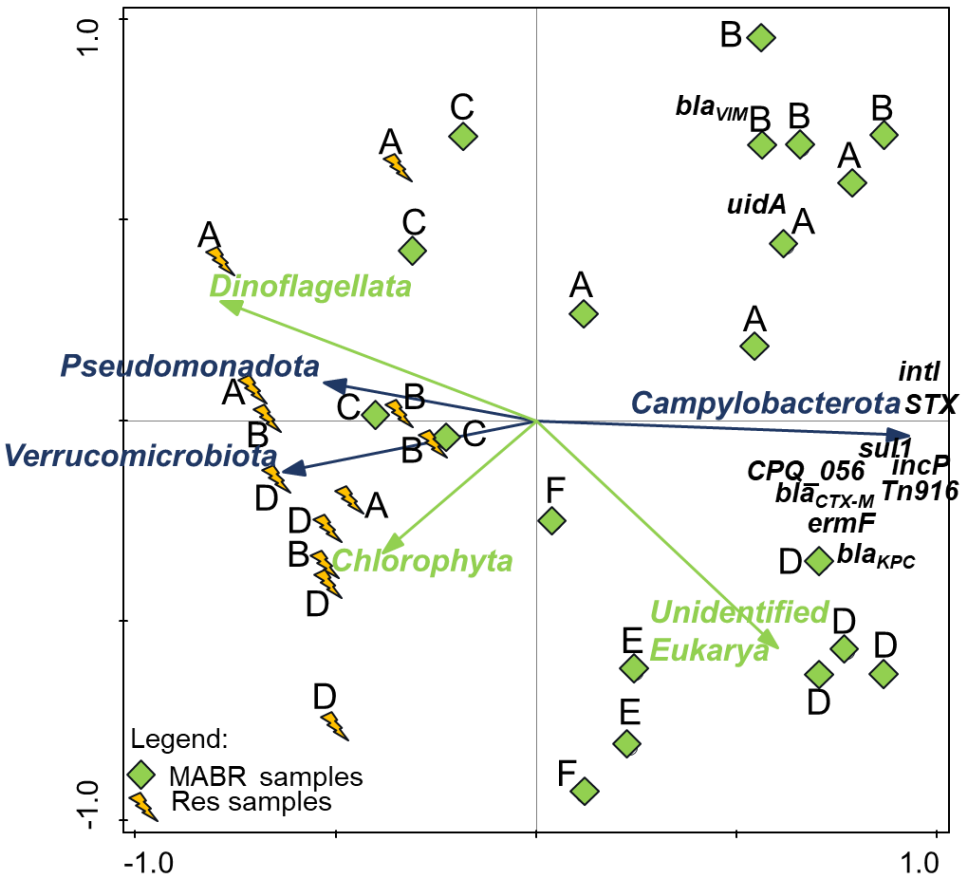

Figure S8. Redundancy analysis (RDA) of the variation of ARGs, MGEs and uidA in the MABR and Reservoir in function of the prokaryotic and eukaryotic community phyla members with relative abundance >5% and >1% respectively, summed as others (E, eukaryote or P, prokaryote) for lower values. The test variables (ARGs, MGEs and uidA) are represented in black and the explanatory variables in blue (prokaryote) or green (eukaryotes). Sampling dates from 2020 are identified from A to F: A – August 19th, B – August 25th, C – September 15th, D – November 24th, E – December 1st and F – December 15th. Total variation was 456.691 and 78.7% could be associated with the explanatory variables.

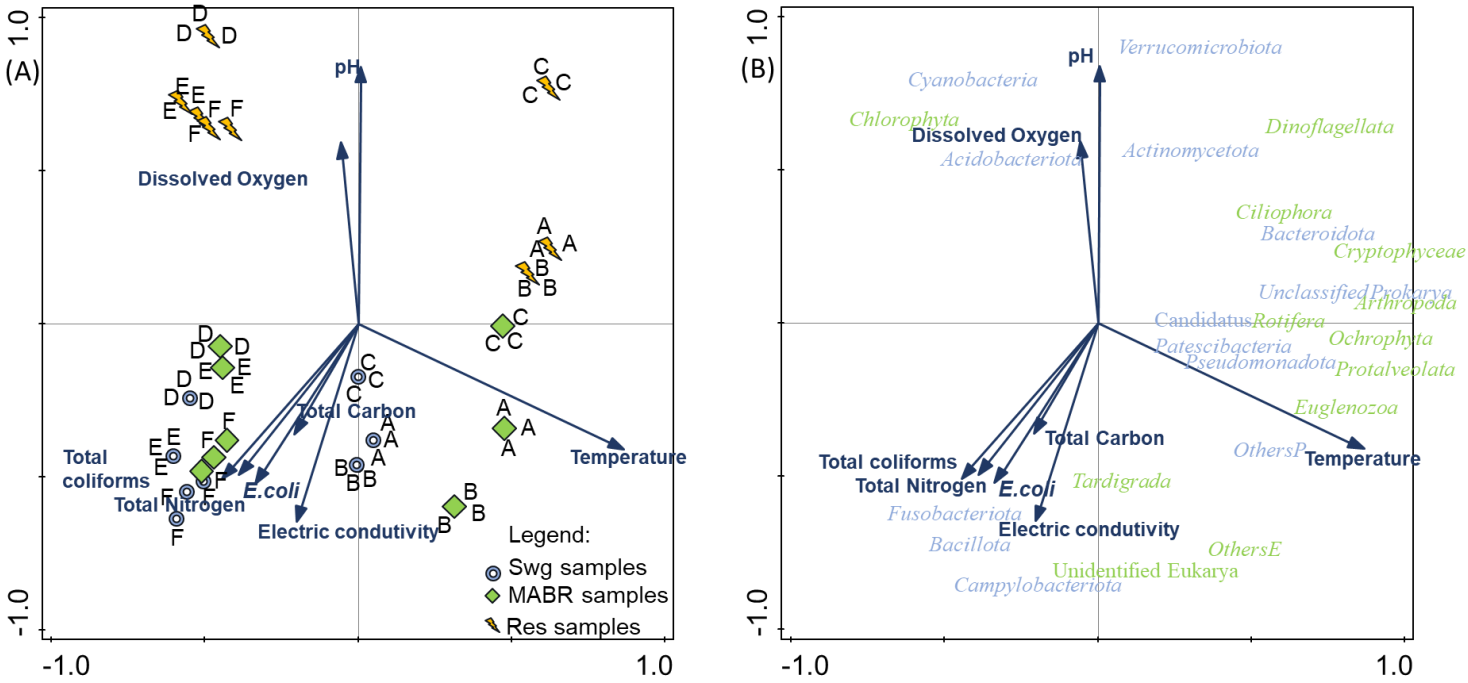

Figure S9. Redundancy analysis (RDA) of the variation of the prokaryotic and eukaryotic community phyla members with relative abundance >5% and >1%, respectively and summed as others (E, eukaryote or P, prokaryote) for lower value in function of the physico-chemical parameters measured. Sampling dates from 2020 are identified from A to F: A – August 19th, B – August 25th, C – September 15th, D – November 24th, E – December 1st and F – December 15th. The test variables are represented in light blue (prokaryotes) or green (eukaryotes) and the explanatory variables in dark blue (physico-chemical parameters). Total variation was 1863.824 and 86.3% could be associated with the explanatory variables. “Unidentified Eukaryota” refers to eukaryotic microorganisms with no hits with >80% confidence in similarity to any sequences in the database used– (A) Samples and Environmental variables; (B) – Test variables and Environmental variables.