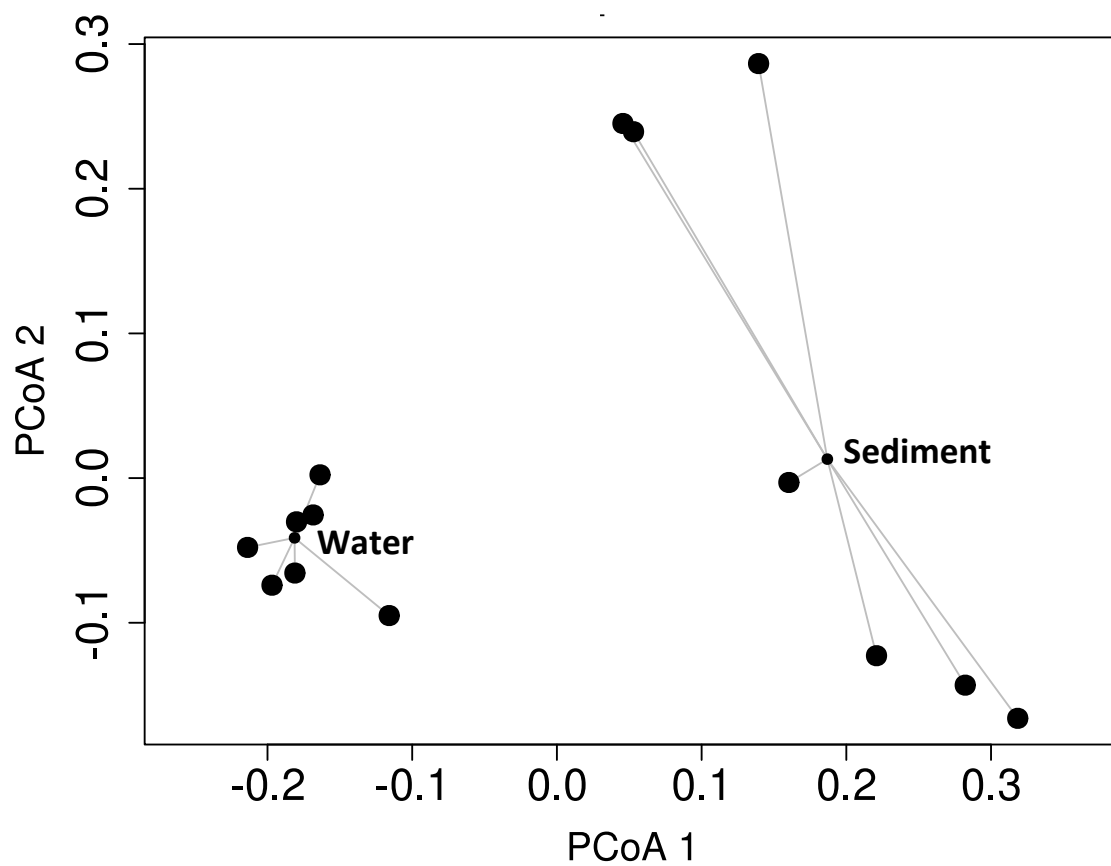
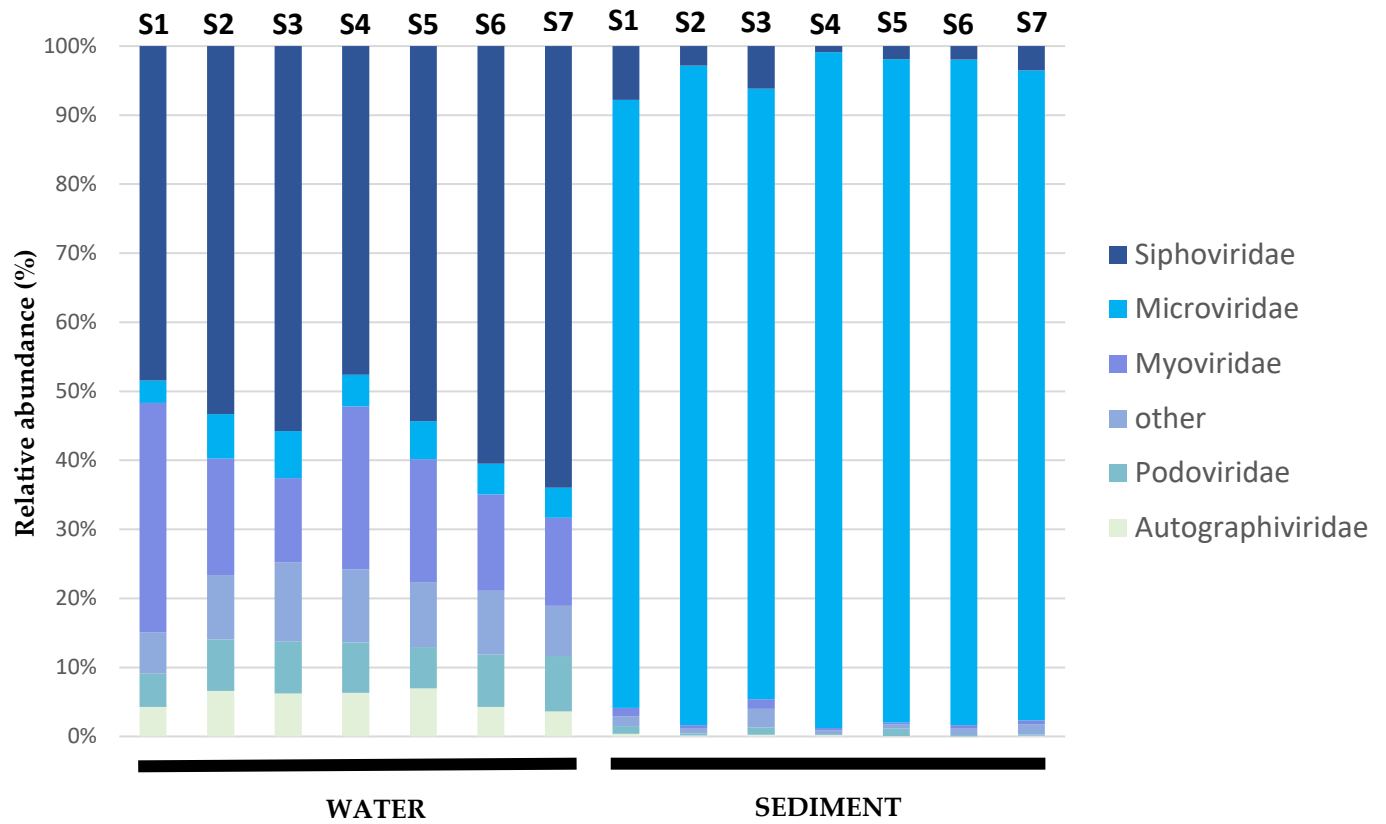


**Figure S1.** Flow chart representing the overview of 16S metabarcoding and host prediction analyses



**Figure S2.** Principal coordinates plot (PCoA) representing the multivariate homogeneity of group dispersions (betadisper) in the water and sediment compartments. Each point represents a single station (seven per compartment). PCoA1 and PCoA2 are the first and second sort axes in the "betadisper" analysis, respectively.



**Figure S3.** Bar plot showing the relative abundance (%) of the top 5 phage taxa at family level in the sediment and water samples of the seven stations (S1-S7). Viral families are represented by a color code.