



Fig. S1. Factor analysis of mixed data (FAMD), was built to verify correlation between the viral genome segments, fish species, temperature and geographic area. The first two principal components of the FAMD accounted for 26% of the variance. No correlation between the viral genome segments, fish species, sampling season or geographic area could be established. (A) correlation circle showing the relationship between quantitative variables (Temperature, positive proportion, and frequency), as well as the contribution and the correlation between variables and the dimensions. (B) plot of the correlation and the contribution of the qualitative variables (Area, station, genotype, temperature and species) to the dimensions. (C) Scatterplot of the scores from Dim1 and Dim2 of individual based on (i) Area, (ii) viral genome segment and (iii) temperature