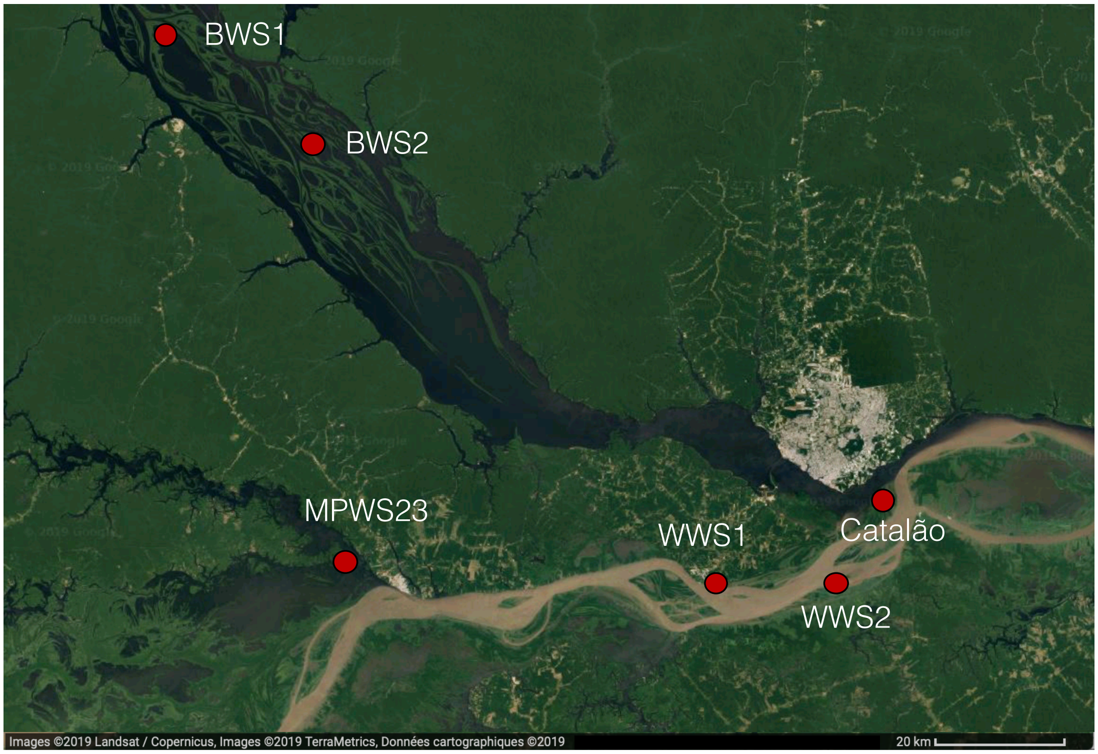
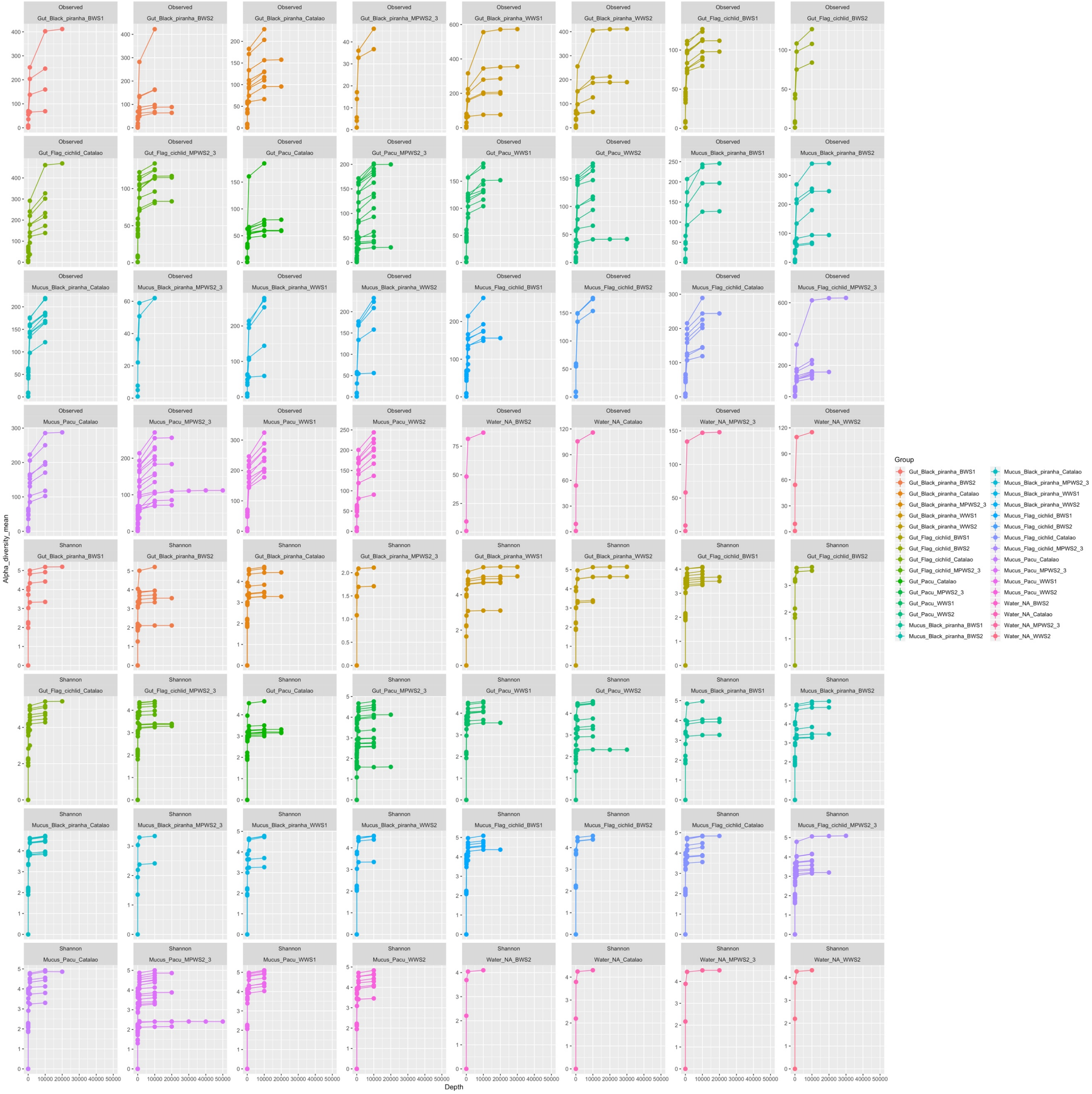
Fish skin and gut microbiomes show contrasting signatures of host species and habitat

François-Étienne Sylvain, Aleicia Holland, Sidki Bouslama, Émie Audet-Gilbert, Camille Lavoie, Adalberto Luis Val, Nicolas Derome

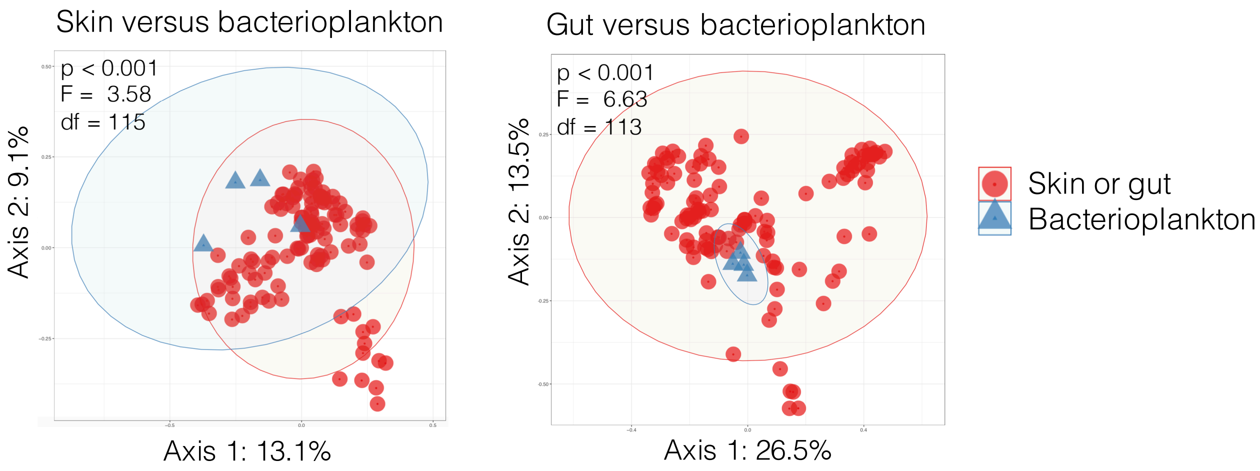
Supplementary figures



Supplementary figure 1: Map of sampling sites in the study.



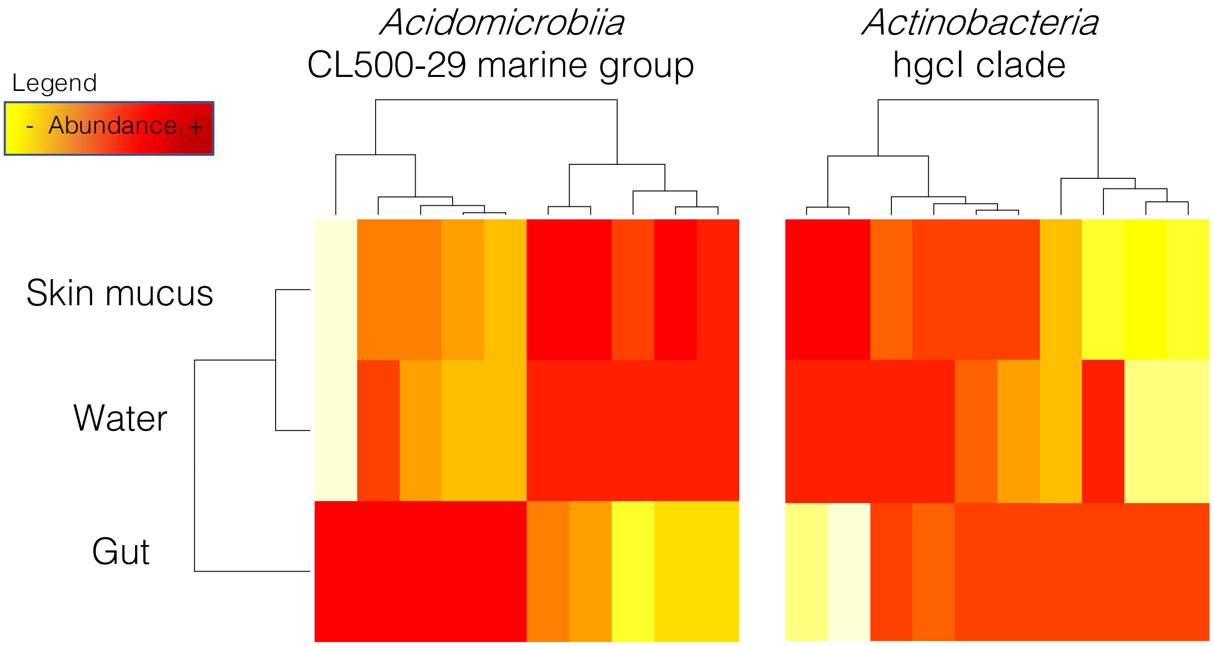
Supplementary figure 2: Rarefaction plots of all samples, for each sample group (i.e. each species*site*tissue combination). The rarefaction analysis was based on the observed counts and the Shannon diversity for each sample group.



Total = 22.2 %

Total = 40.0%

Supplementary figure 3: The phylogenetic structure of the skin mucus community is closer to bacterioplankton than to gut community. Principal components analysis show the clustering of all environmental bacterioplankton communities versus all skin or gut communities. Results of PERMANOVA tests between groups are indicated on the top left corner of each PCA plot.



Supplementary figure 4: The ASVs from two of the most abundant genera in bacterioplankton share co-abundance with the same ASVs in the fish skin mucus microbiome, but not in the gut microbiome. Heatmaps show the clustering of 10 ASVs from each of the two most important genera in bacterioplankton (CL500-29 marine group and hgcI clade), based on their mean relative abundance in fish skin mucus, gut and bacterioplankton samples.