

Microbiome variation at the clam-sediment interface may explain changes in the local productivity of *Chamelea gallina* in the North Adriatic Sea

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Supplementary figures

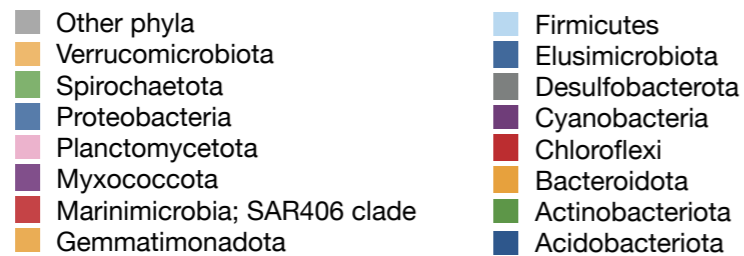
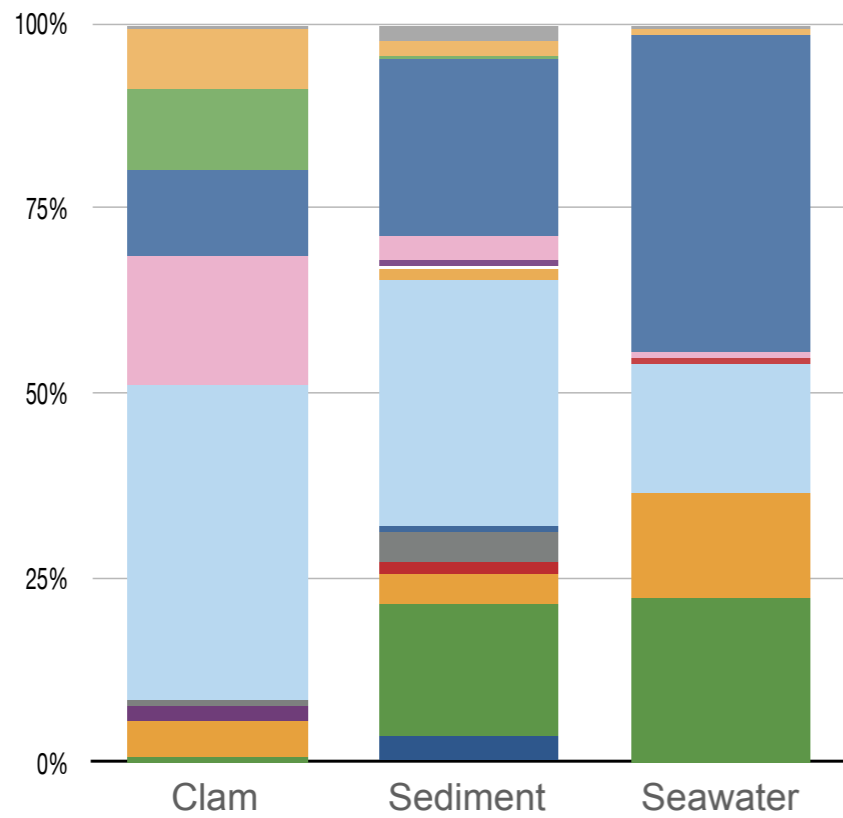
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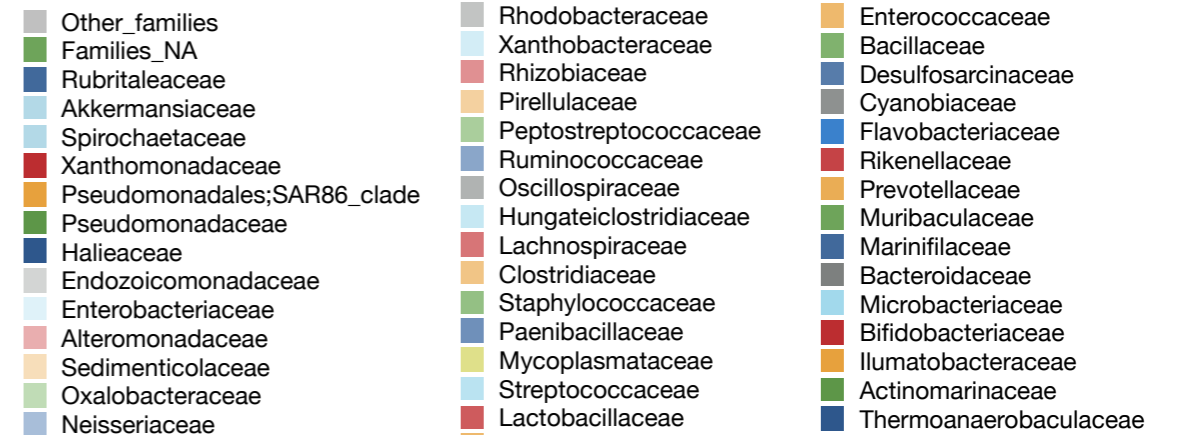
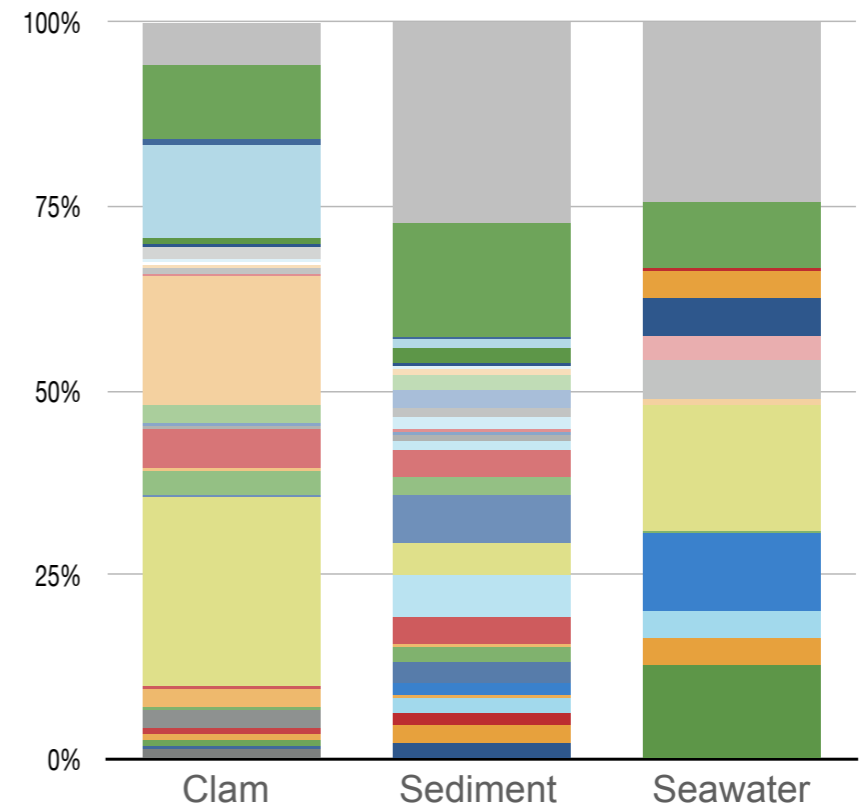
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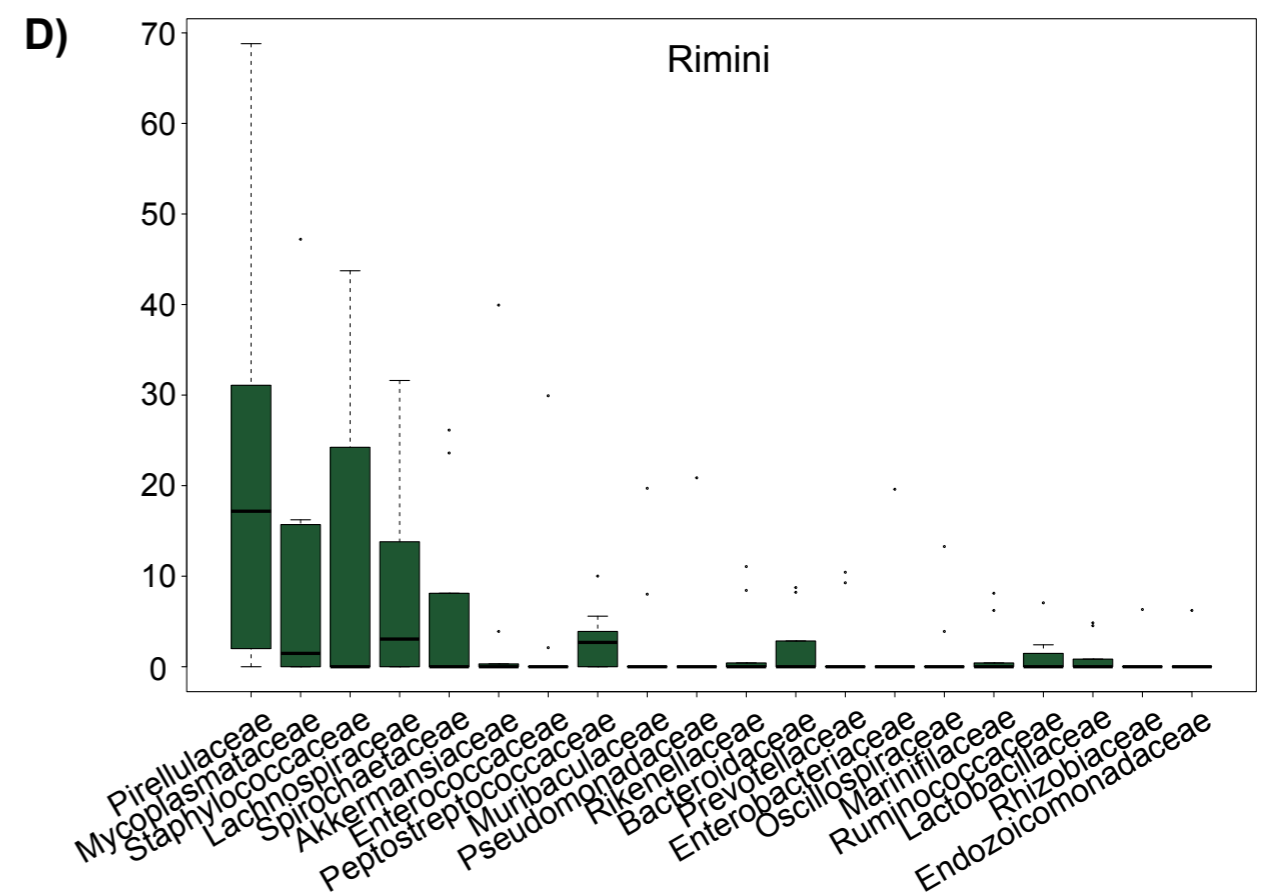
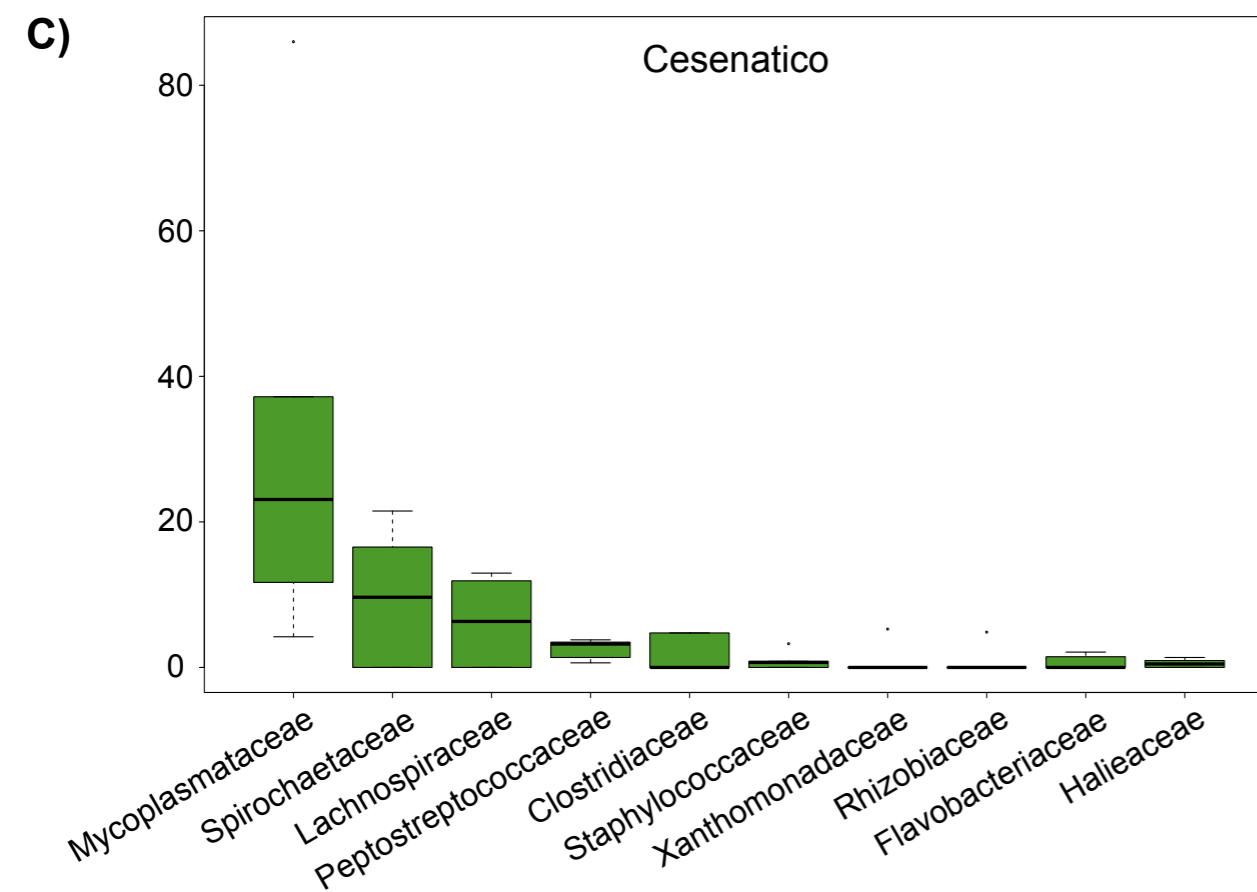
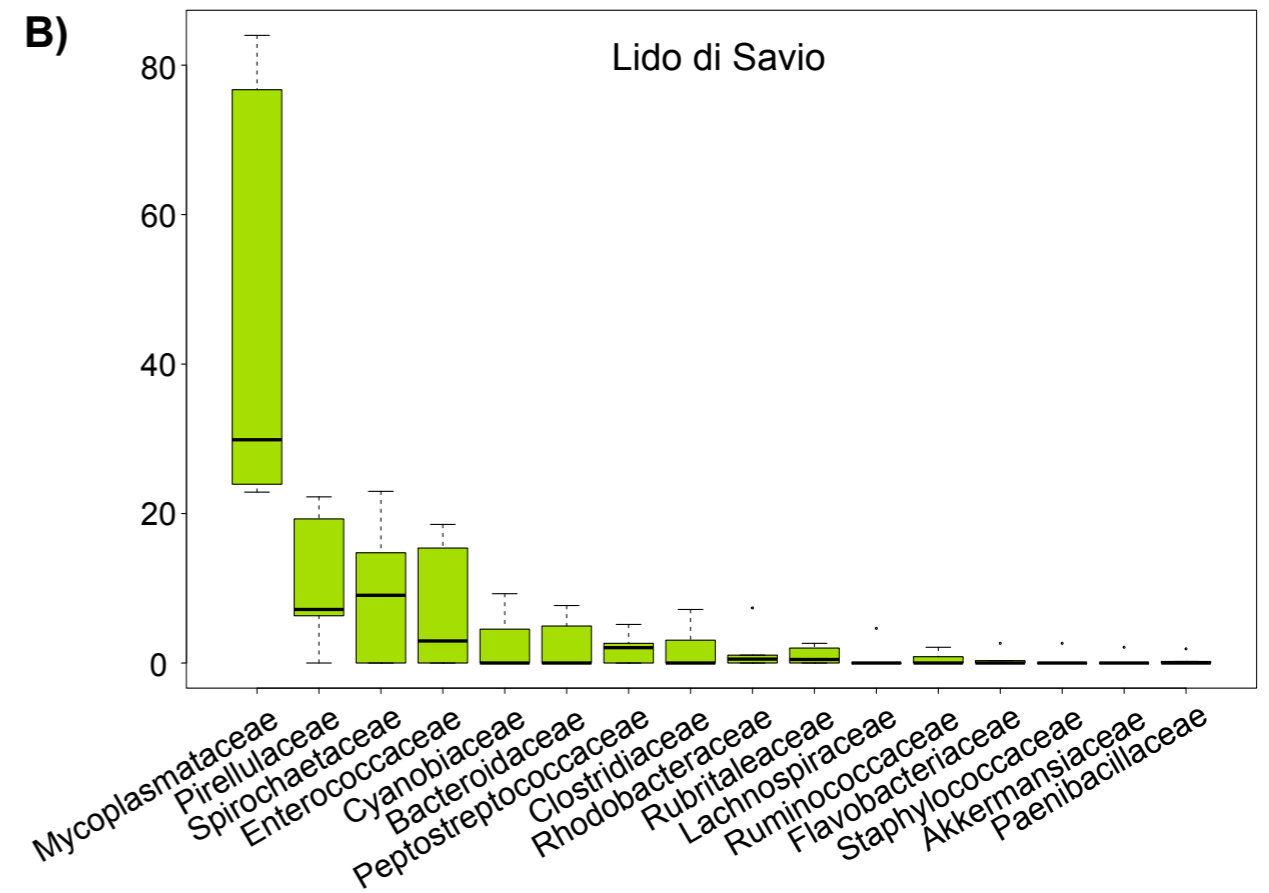
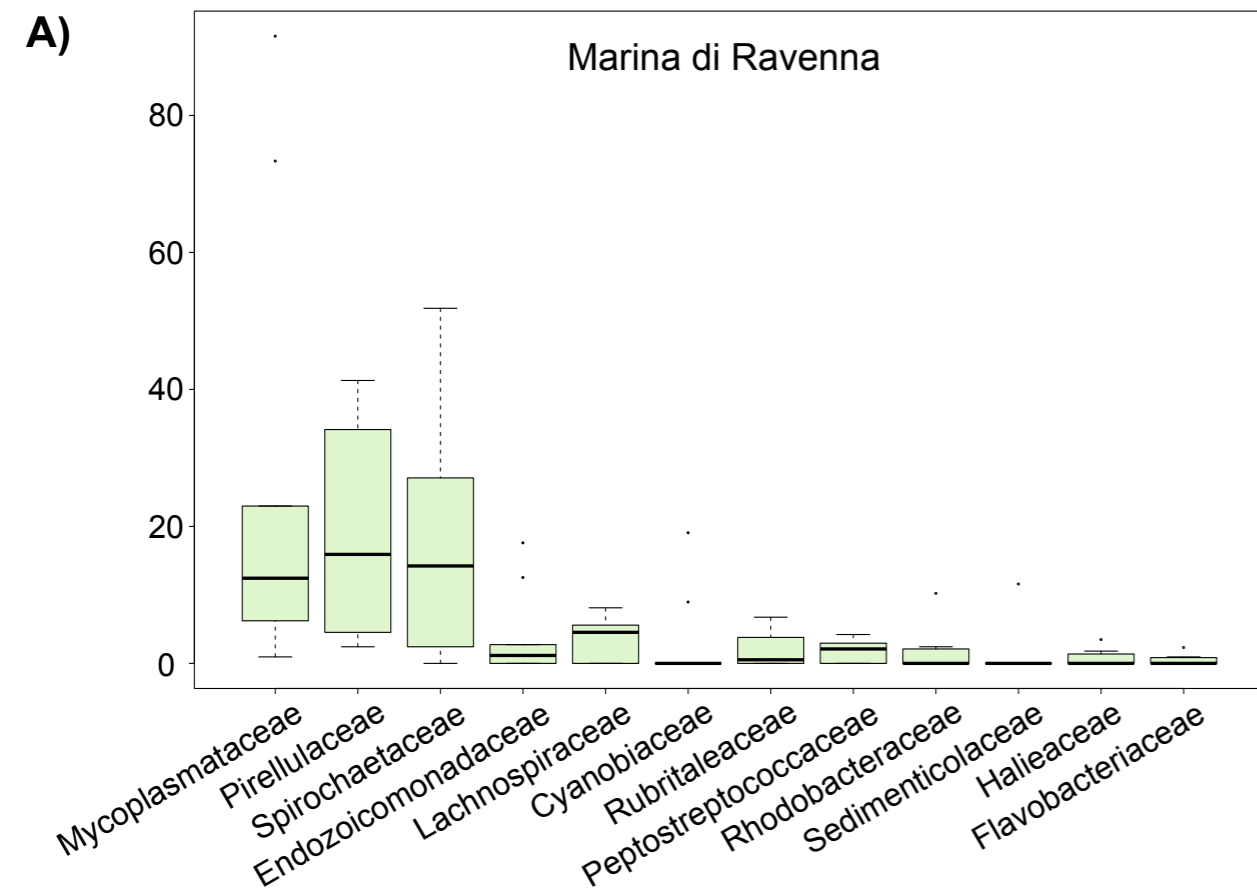
A)



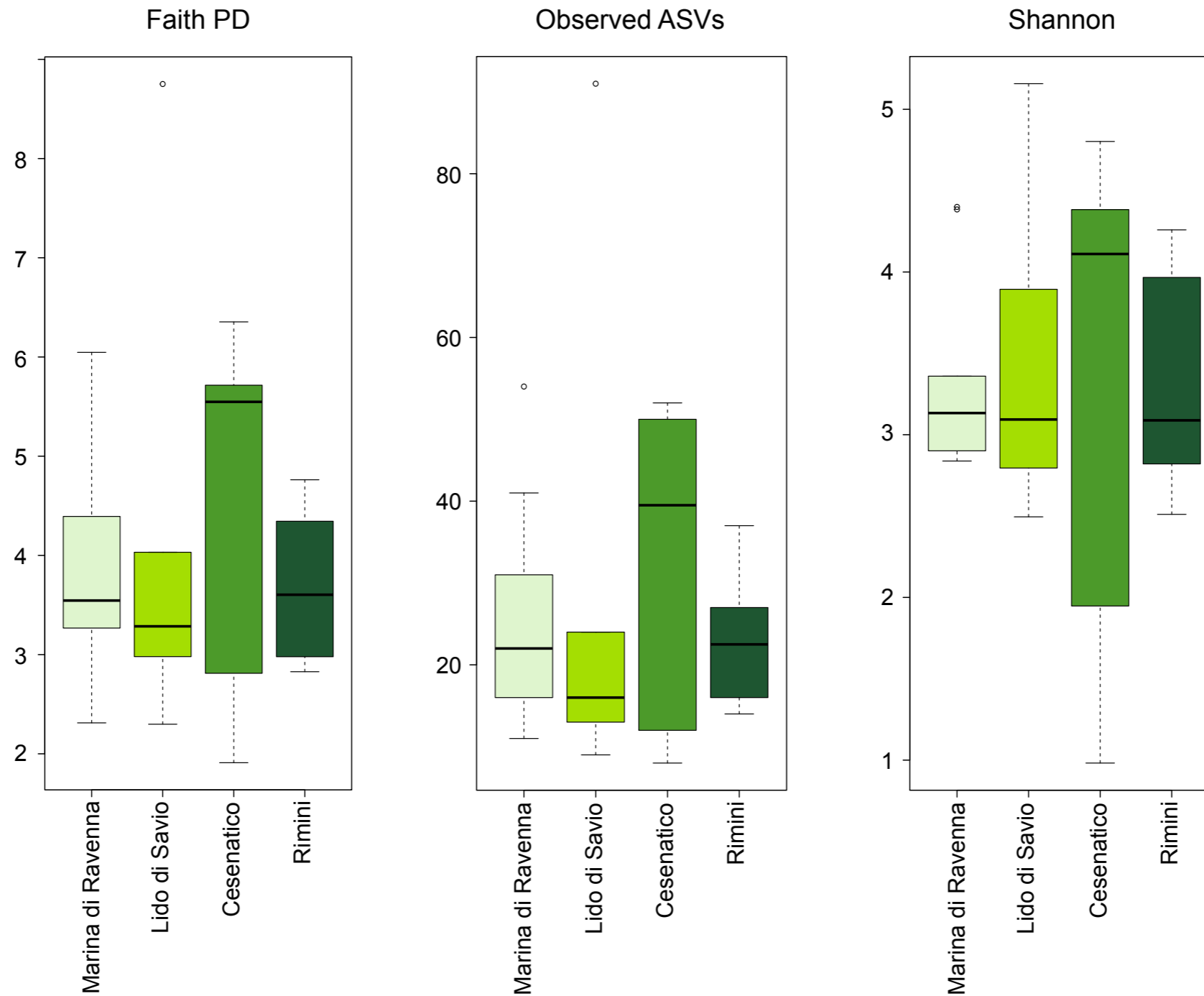
B)



Supplementary Figure S1 - Microbial communities associated with clam digestive glands, sediment and seawater in the North Adriatic Sea at phylum and family level. Barplots summarizing the overall phylum (A) and family (B) level microbial composition of the different ecosystems, namely clam, sediment, and seawater. Phyla with relative abundance > 2% and families with relative abundance > 5% in at least 1 sample are represented. NA = not assigned.



Supplementary Figure S2 - Microbial communities associated with clam digestive glands from 4 production sites in the North Adriatic Sea at family level. Boxplot summarizing the DG-associated microbial composition at the family level at the different sampling sites. Families with mean relative abundance (r.a.) > 0.5%, 0.4%, 0.5% and 0.6% for Marina di Ravenna, Lido di Savio, Cesenatico and Rimini, respectively, are represented. Different r.a. values were selected for representation purposes.



Supplementary Figure S3 - Box-and-whiskers distribution of alpha diversity of *C. gallina* digestive gland-associated microbiome in the different sampling sites. Faith's phylogenetic diversity (PD), the number of observed ASVs, and the Shannon index are represented. No significant p-values (Wilcoxon rank-sum test controlled for multiple testing using FDR) were found.

