Supplementary material

Alkalinity loss and limited ecological responses in a trio of tropical coastal ocean alkalinity enhancement experiments

Wang et al.

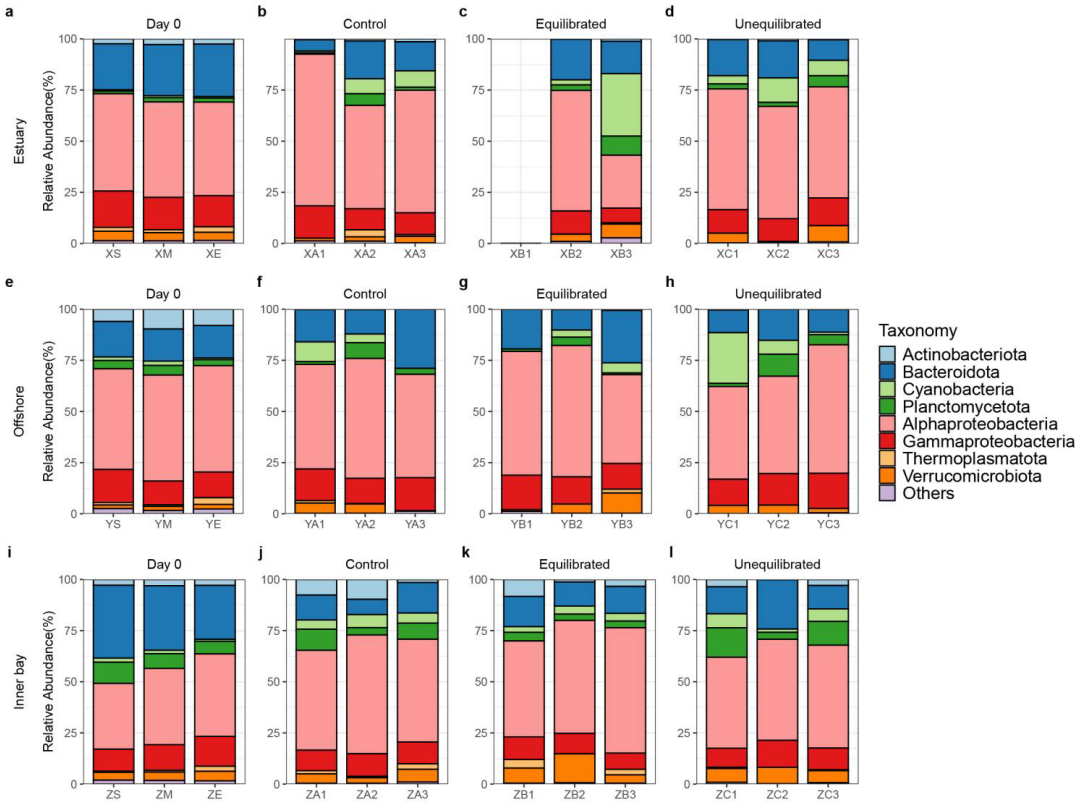


Figure S1. Prokaryotic community structure based on 16S rRNA gene sequences. Relative abundances are shown at phylum and class level for the three source waters and the control, equilibrated and unequilibrated treatments. XB1, without data, refers to the incubator which was withdrawn from the experiment due to a faulty aquarium heater.

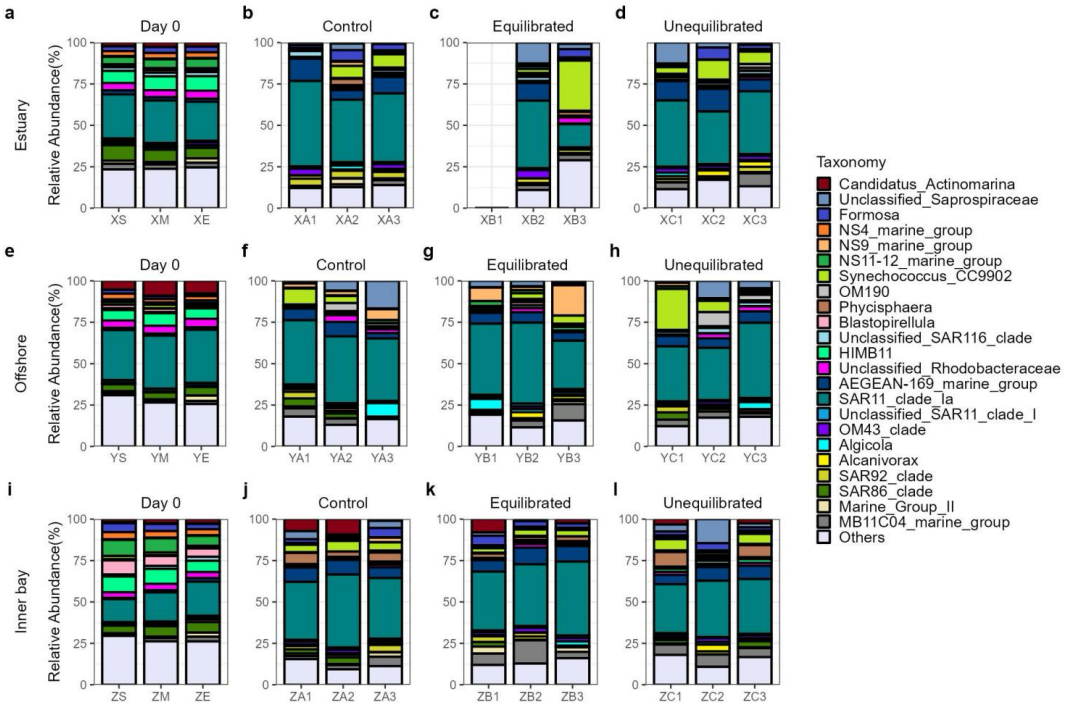


Figure S2. Prokaryotic community structure based on 16S rRNA gene sequences. Relative abundances are shown at finer taxonomy levels for the three source waters and the control, equilibrated and unequilibrated treatments. XB1, without data, refers to the incubator which was withdrawn from the experiment due to a faulty aquarium heater.

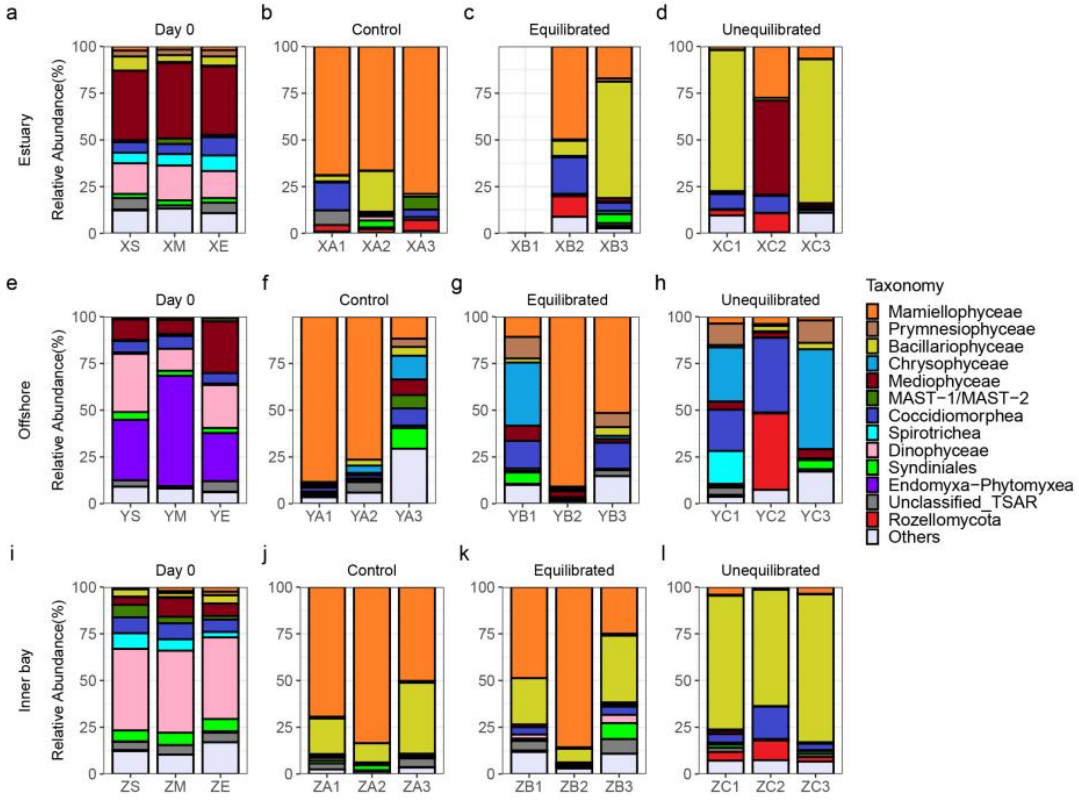


Figure S3. Eukaryotic microbial community structure based on 18S rRNA gene sequences annotated with PR2. Relative abundances are shown at class level for the three source waters and the control, equilibrated and unequilibrated treatments. Samples were rarefied to 408 reads; patterns are therefore interpreted as exploratory relative-abundance responses. XB1 refers to the incubator which was withdrawn from the experiment due to a faulty aquarium heater.

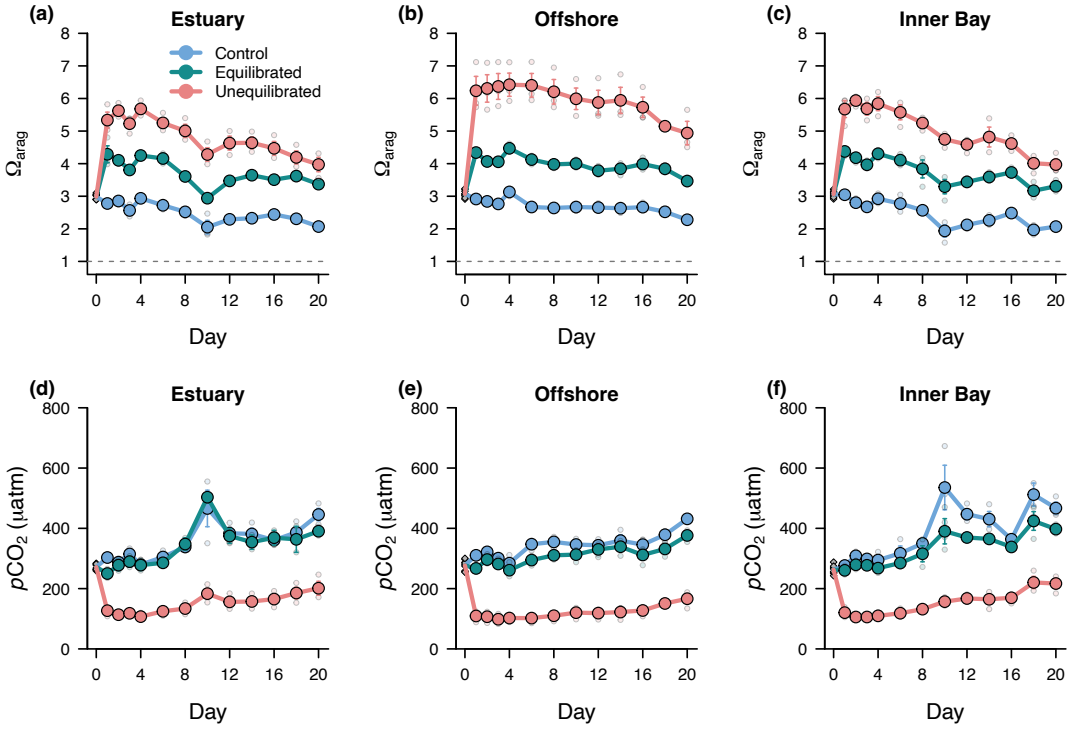


Figure S4. Temporal changes in Ω_{arag} and pCO_2. (a-c) Ω_{arag} for Estuary, Offshore, and Inner Bay source waters (d-f) pCO_2 for Estuary, Offshore, and Inner Bay source waters. Points indicate individual biologically independent microcosms, lines show treatment means, and error bars show standard errors where at least two replicate measurements were available.