

Supplemental Figures

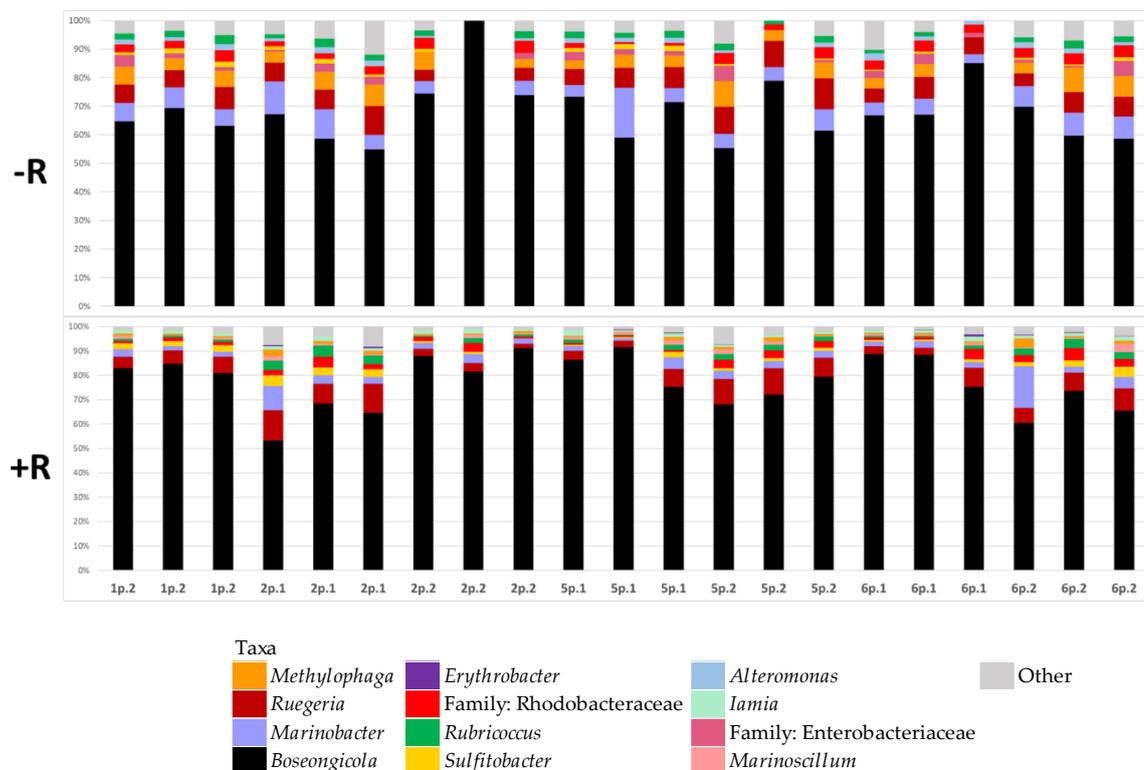


Figure S1: Stacked bar graph of the bacterial OTUs consisting of 99% of the total abundance present in every culture in the 40ret fraction. Bacterial OTUs shown represent bacteria associated with *B. plicatilis* in the absence (top, -R) and presence (bottom, +R) of *B. plicatilis*. Taxonomy is shown at the genus level unless otherwise stated. Bacterial OTUs less than 1% of the total abundance is categorized in ‘Other’ (grey).

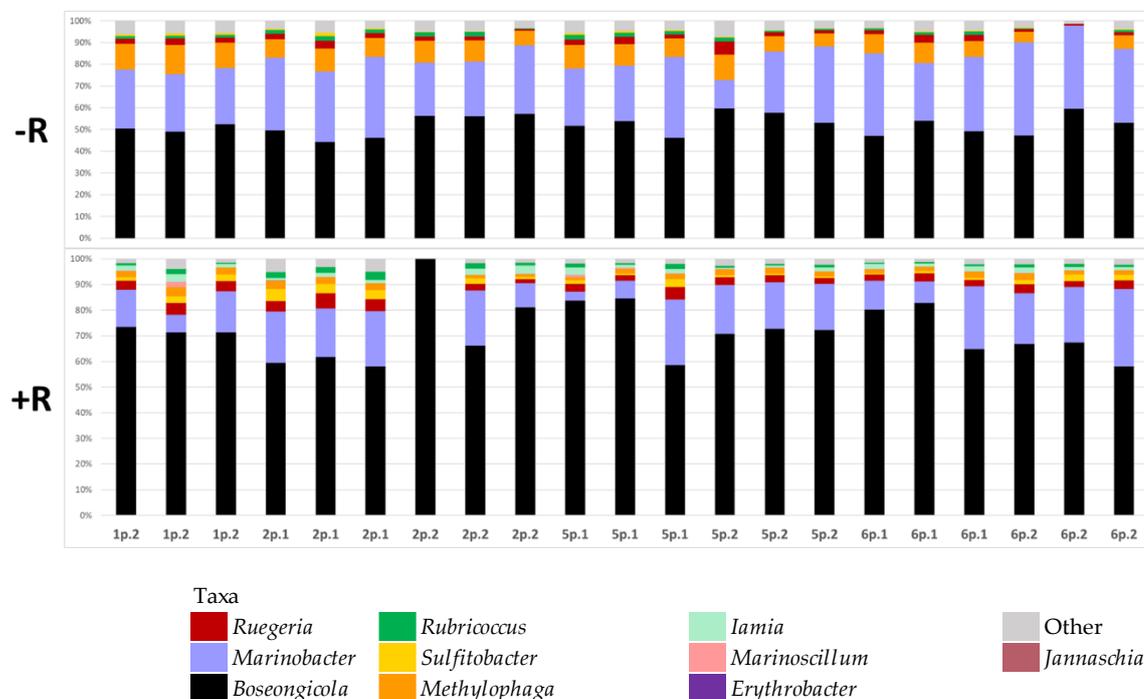


Figure S2: Stacked bar graph of the bacterial OTUs consisting of 99% of the total abundance present in every culture in the 0.8ret fraction. Bacterial OTUs shown represent bacteria associated with *B. plicatilis* in the absence (top, -R) and presence (bottom, +R) of *B. plicatilis*.

(bottom, +R) of *B. plicatilis*. Taxonomy is shown at the genus level unless otherwise stated. Bacterial OTUs less than 1% of the total abundance is categorized in ‘Other’ (grey).

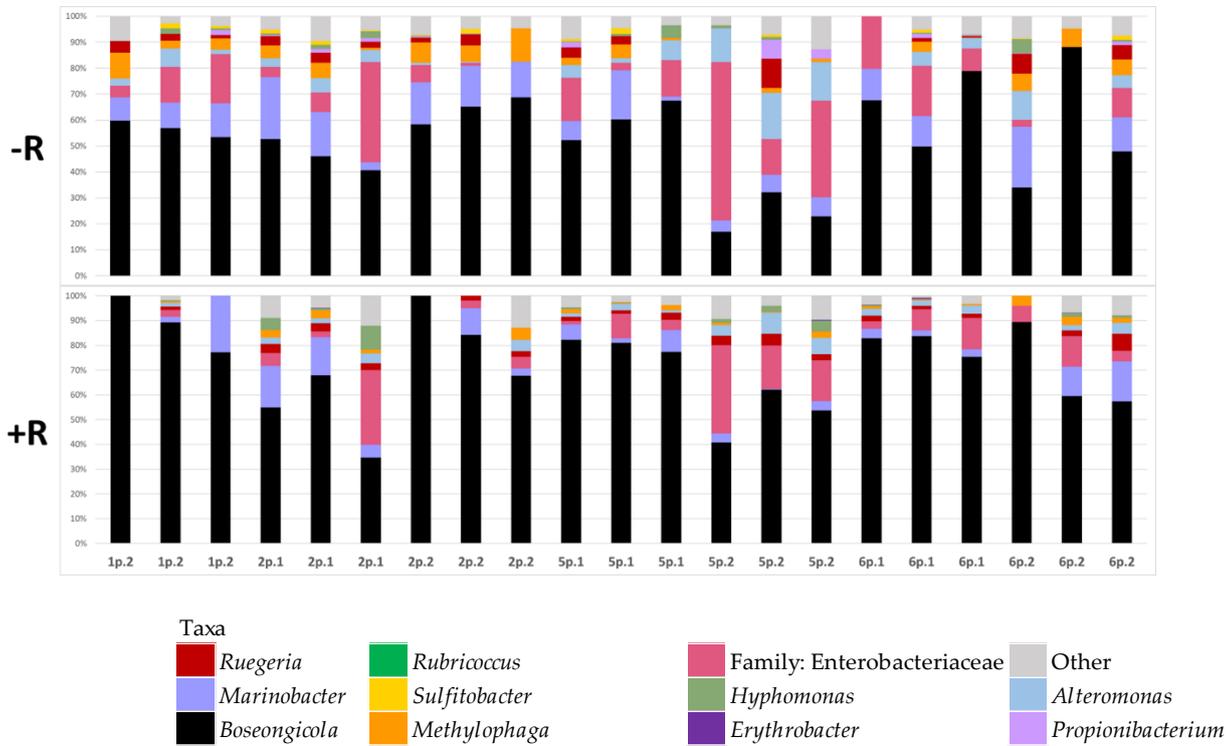


Figure S3: Stacked bar graph of the bacterial OTUs consisting of 99% of the total abundance present in every culture in the 0.22ret fraction. Bacterial OTUs shown represent bacteria associated with *B. plicatilis* in the absence (top, -R) and presence (bottom, +R) of *B. plicatilis*. Taxonomy is shown at the genus level unless otherwise stated. Bacterial OTUs less than 1% of the total abundance is categorized in ‘Other’ (grey).