



Supplemental Figure 1. Predicted functional profiles of two symbionts. Bars show predicted relative abundances of KEGG pathways in each OTU based on sequenced relatives generated using the PICRUSt software (Methods). (A) Functional profile of Endozoicomonas. (B) Functional profile of Synechococcus. Note that only genes in KEGG Orthology groups can be predicted using this method; most genomes will contain a substantial proportion of orphan genes lacking orthologs and for which no functional predictions can be made.