



Supplementary Figure S3: Coverage estimation and *alpha* diversity indices for the 18S rRNA gene OTUs from seawater at tide sites (TS-sw), landing *Sargassum* (TS-sarg), *Sargassum* from inland storage sites (ISS-sarg) samples. (A) Good's coverage estimator. The *alpha* diversity of each sample was estimated using (B) the observed OTU richness, (C) the Shannon diversity index, and (D) the inverse of Simpson diversity index. To compare the *alpha* diversity indices between compartments, we used Kruskal-Wallis tests and corrected our P-values for multiple comparisons with the Benjamini-Hochberg method. Significant differences ($P < 0.05$) are indicated by the different letters.