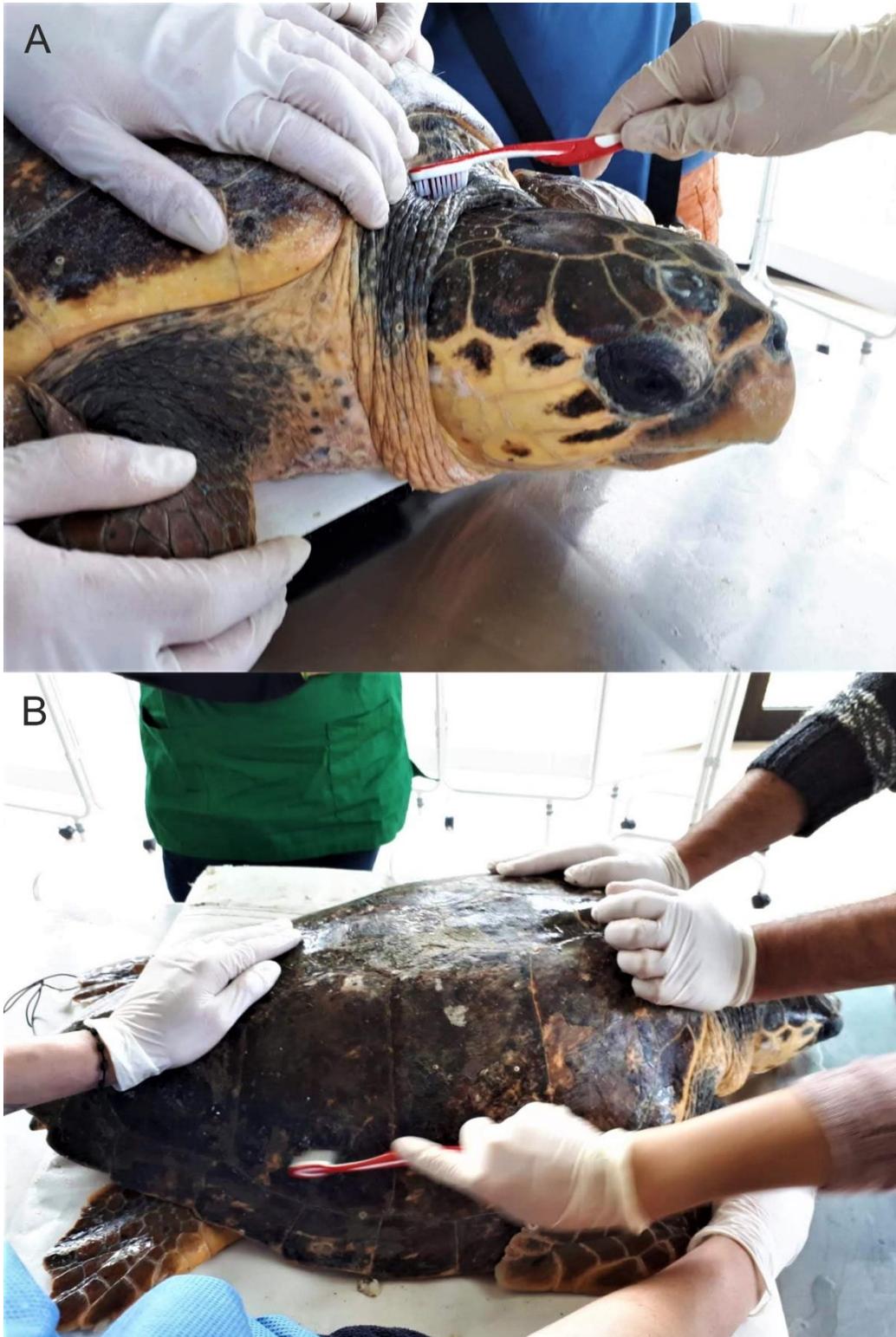
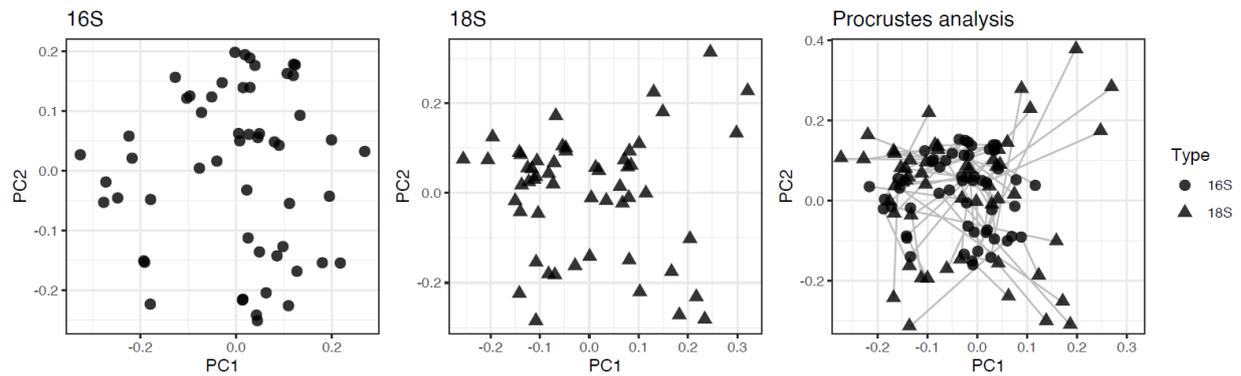


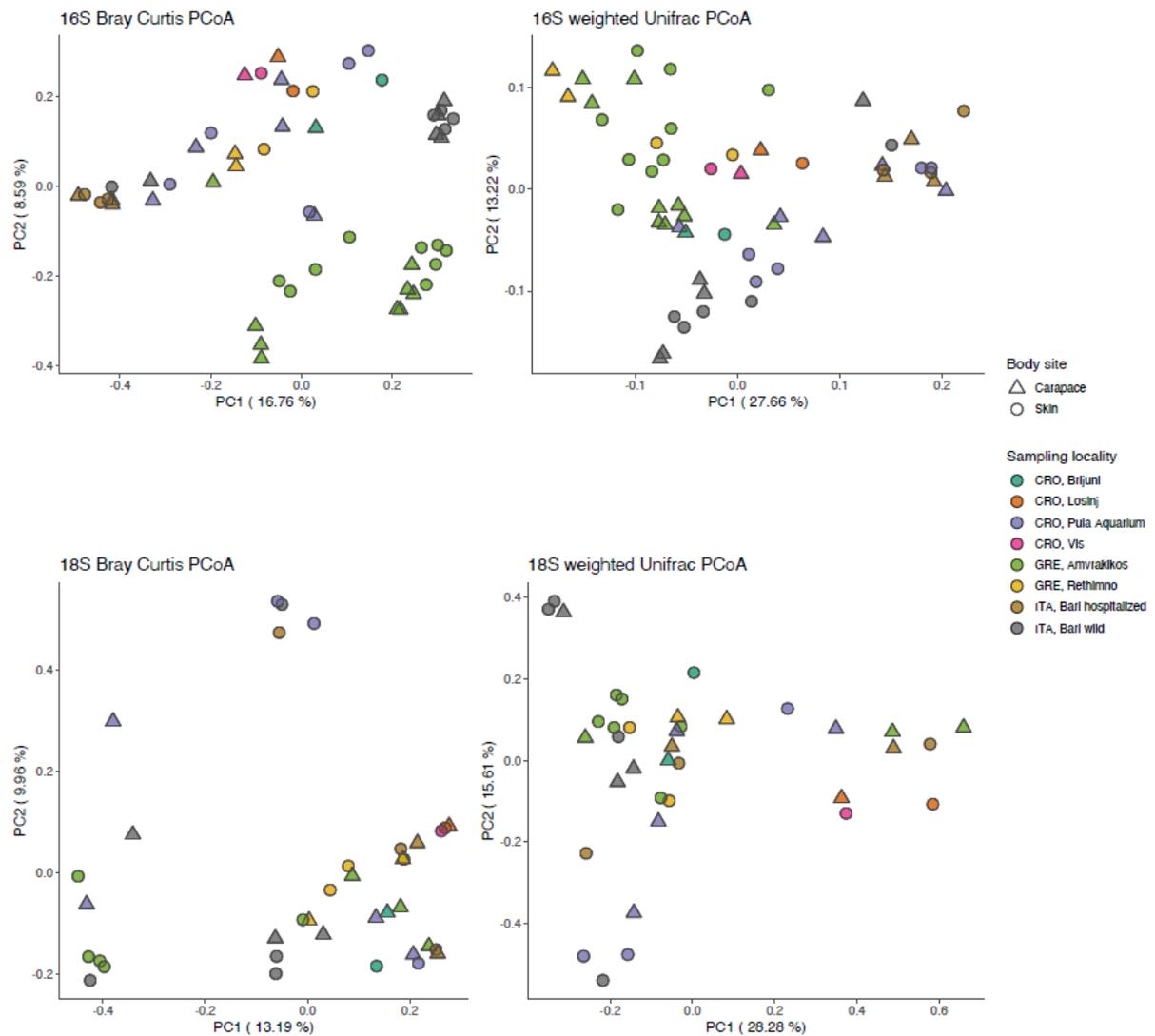
*Supplementary Material*



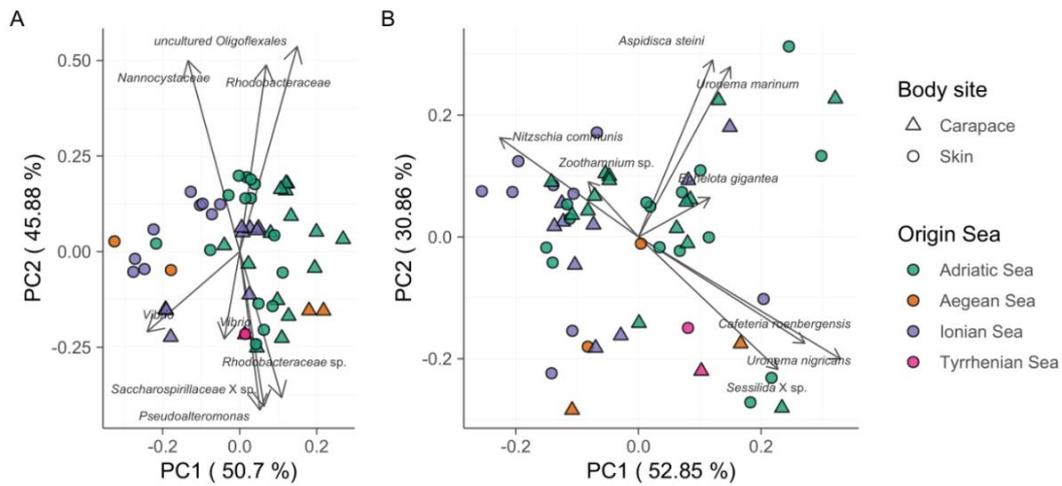
**Figure S1.** Collection of epibiotic biofilm scraping from skin (A) and carapace (B) of loggerhead sea turtles.



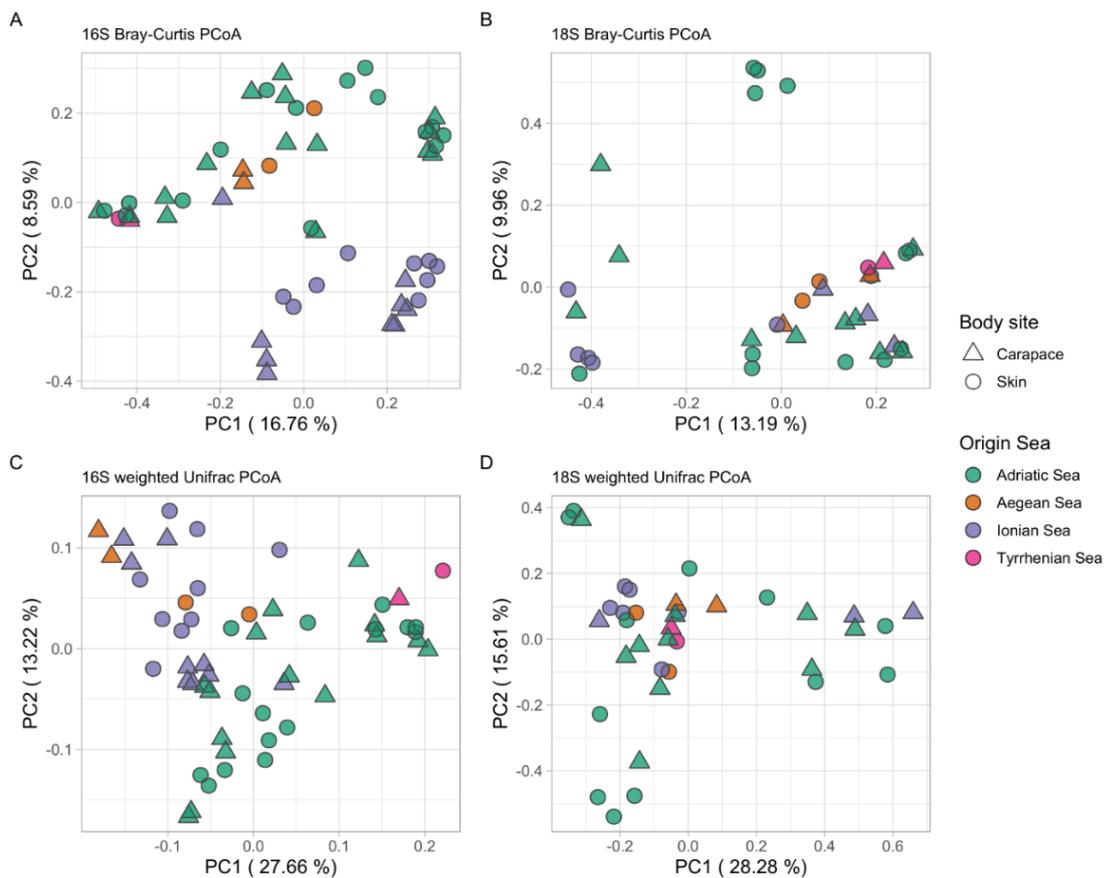
**Figure S2.** Robust Aitchison PCA for prokaryotes / 16S rRNA gene (left) and eukaryotes / 18S rRNA gene (middle). Robust Aitchison PCA results were used for the procrustes analysis (right) as to compare prokaryotes (left) and eukaryotes (middle) samples positioning in the ordination spaces; the distances between each sample positions are indicated by a connecting line. Prokaryotic community samples are indicated by a full circle, while eukaryotic community samples are indicated by a full triangle. Significance ( $m^2$  value) and p-values were calculated by 999 series of MonteCarlo permutations.



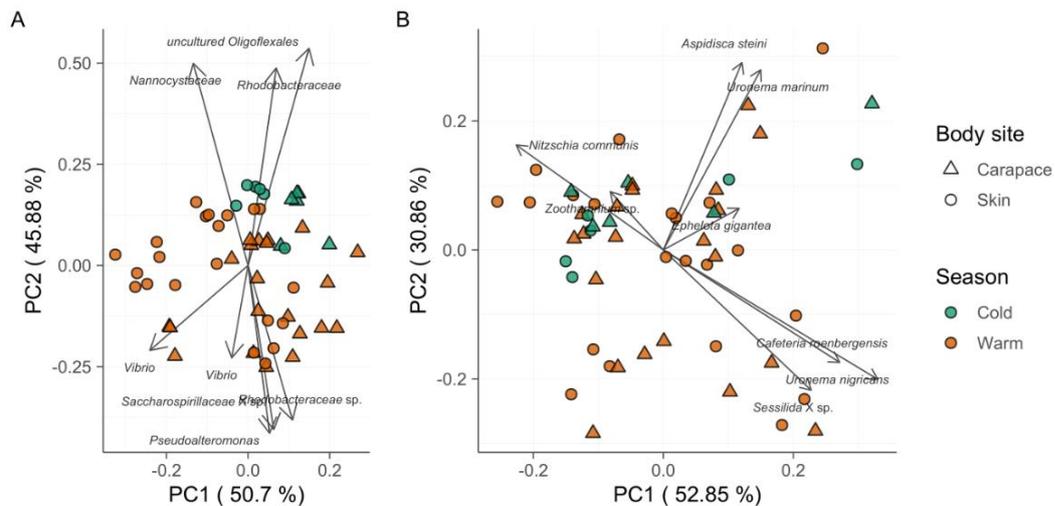
**Figure S3.** Principal coordinate analysis (PCoA) biplot of Bray-Curtis and weighted UniFrac distance for prokaryotic (16S, up) and eukaryotic diversity (18S, down). Sampling locality are indicated by color, body sites are indicated by shape for all four plots.



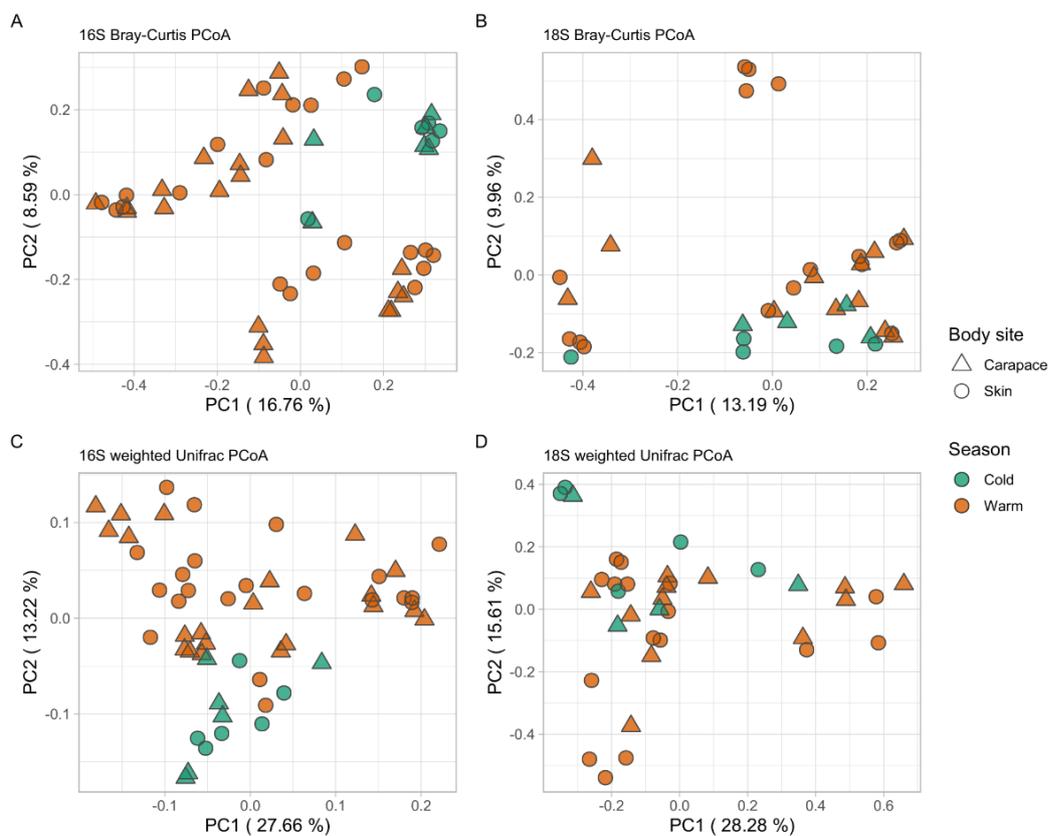
**Figure S4.** Principal component analysis (PCA) biplot of robust Aitchison distance for prokaryotic (16S, left) and eukaryotic diversity (18S, right); arrows indicate individual highly ranked ASVs that contribute to the displayed positions of the samples; lowest taxonomic assignment of each ASV is written in textboxes at the end of each arrow. Origin seas are indicated by color, body sites are indicated by shape for both plots.



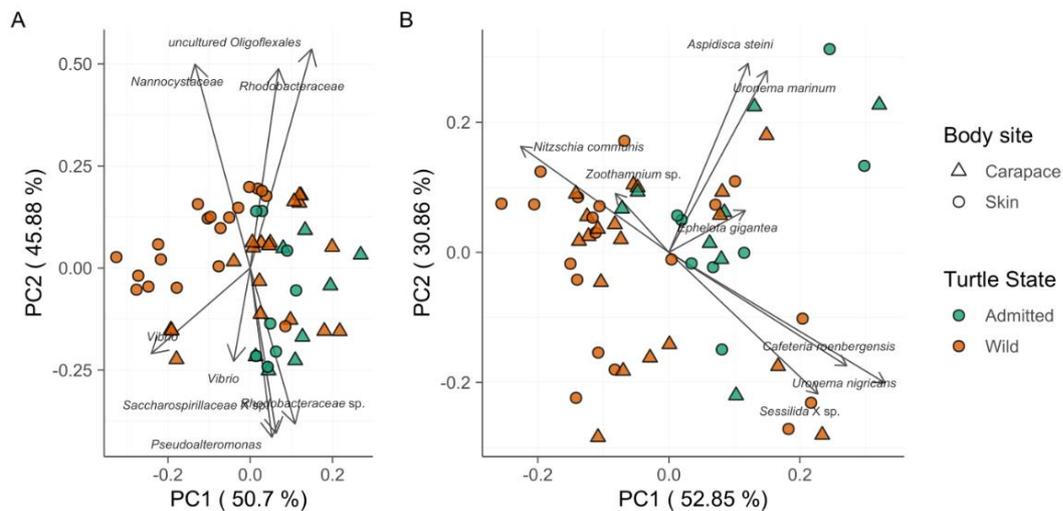
**Figure S5.** Principal coordinate analysis (PCoA) biplot of Bray-Curtis and weighted UniFrac distance for prokaryotic (16S, up) and eukaryotic diversity (18S, down). Origin seas are indicated by color, body sites are indicated by shape for all four plots.



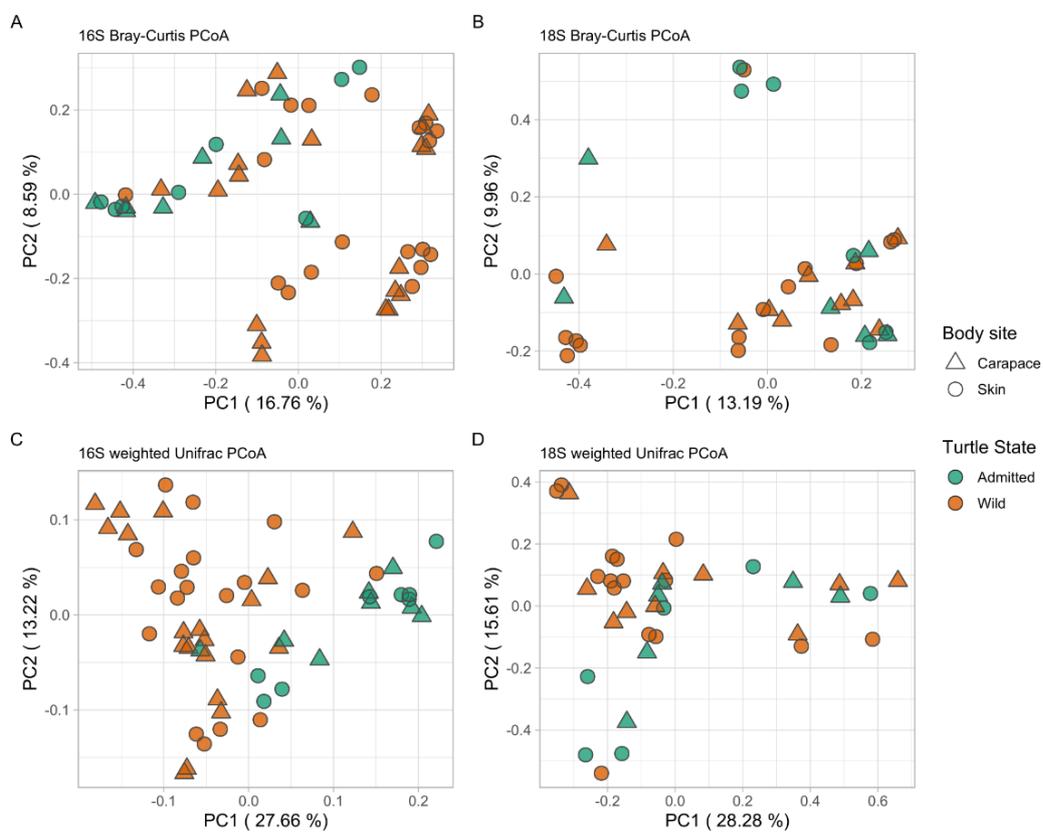
**Figure S6.** Principal component analysis (PCA) biplot of robust Aitchison distance for prokaryotic (16S, left) and eukaryotic diversity (18S, right); arrows indicate individual highly ranked ASVs that contribute to the displayed positions of the samples; lowest taxonomic assignment of each ASV is written in textboxes at the end of each arrow. Seasons are indicated by color, body sites are indicated by shape for both plots.



**Figure S7.** Principal coordinate analysis (PCoA) biplot of Bray-Curtis and weighted UniFrac distance for prokaryotic (16S, up) and eukaryotic diversity (18S, down). Seasons are indicated by color, body sites are indicated by shape for all four plots.



**Figure S8.** Principal component analysis (PCA) biplot of robust Aitchison distance for prokaryotic (16S, left) and eukaryotic diversity (18S, right); arrows indicate individual highly ranked ASVs that contribute to the displayed positions of the samples; lowest taxonomic assignment of each ASV is written in textboxes at the end of each arrow. Turtle states are indicated by color, body sites are indicated by shape for both plots.



**Figure S9.** Principal coordinate analysis (PCoA) biplot of Bray-Curtis and weighted UniFrac distance for prokaryotic (16S, up) and eukaryotic diversity (18S, down). Turtle states are indicated by color, body sites are indicated by shape for all four plots.