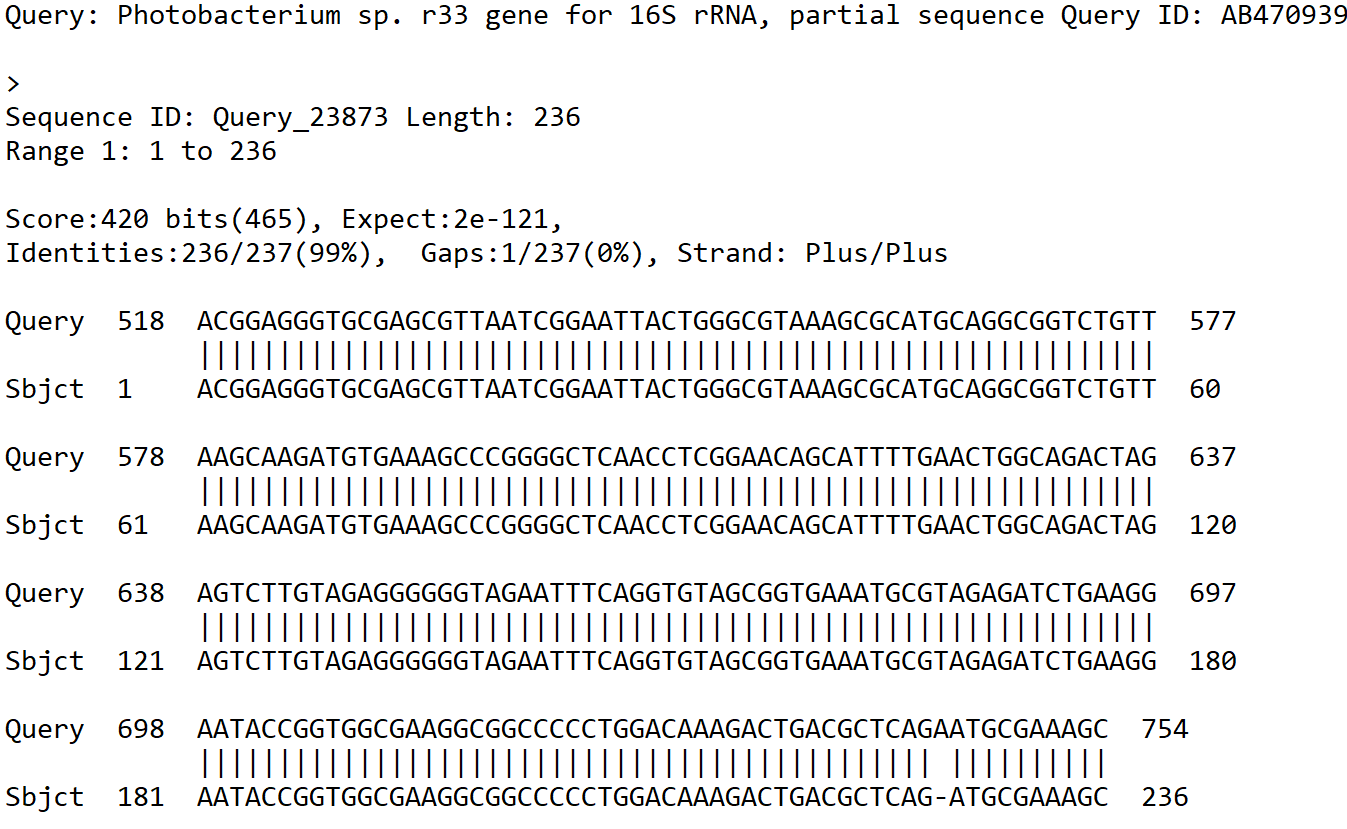
Supplementary Material

# Supplementary Data

**Supplementary Figure 1.** Map of collection sites for samples used in this study.



**Supplementary Figure 2.** BLAST alignment of recorded *Photobacterium sp. r33* from NCBI and sequence of *Photobacterium* pulled from the 16S rRNA analysis.



**Supplementary Figure 3.** Relative abundance of bacterial taxa (at the species level) across different samples. Columns 1 – 3 represent microbiomes derived from tunicate specimens preserved under different conditions. The next ten samples show bacterial distributions in seawater samples from the same location.

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**Supplementary Figure 4.** Phylogeny based on mitochondrial cytochrome oxidase I (COI) amino acid sequences using the PhyML method (Guindon and Gascuel, 2003). All taxa were subphylum Tunicata except for two outgroup mammals. The topology indicates a clear ingroup of only tunicates, with the pelagic tunicates more closely grouping. The following parameters were used to construct the tree: Substitution model - WAG; Gamma shape parameter - 0.543 Number of categories- 4; Proportion of invariant: 0.155. The following COI sequences were retrieved from NCBI and aligned with MUSCLE - *Rhodosoma turcicum* [YP\_008083018.1], *Doliolum nationalis* [BAD86512.1]; *Ascidiella aspersa* [YP\_008083028.1]; *Ciona intestinalis* [YP\_006341036.1], *Ciona savignyi* [QDO67183.1]. *Aplidium conicum* [YP\_003331401.1], *Herdmania momus* [YP\_003331094.1], *Polyandrocarpa misakiensis* [BAJ21359.1]. *Halocynthia papillosa* [CAQ68496.1], *Botryllus schlosseri* [CAQ68352.2], *Botrylloides leachii* YP\_009029811.1, *Styela plicata* YP\_003331150.1; *Mustela sibirica* [BAX03304.1]; *Perognathus longimembris* [ABO84893.1].