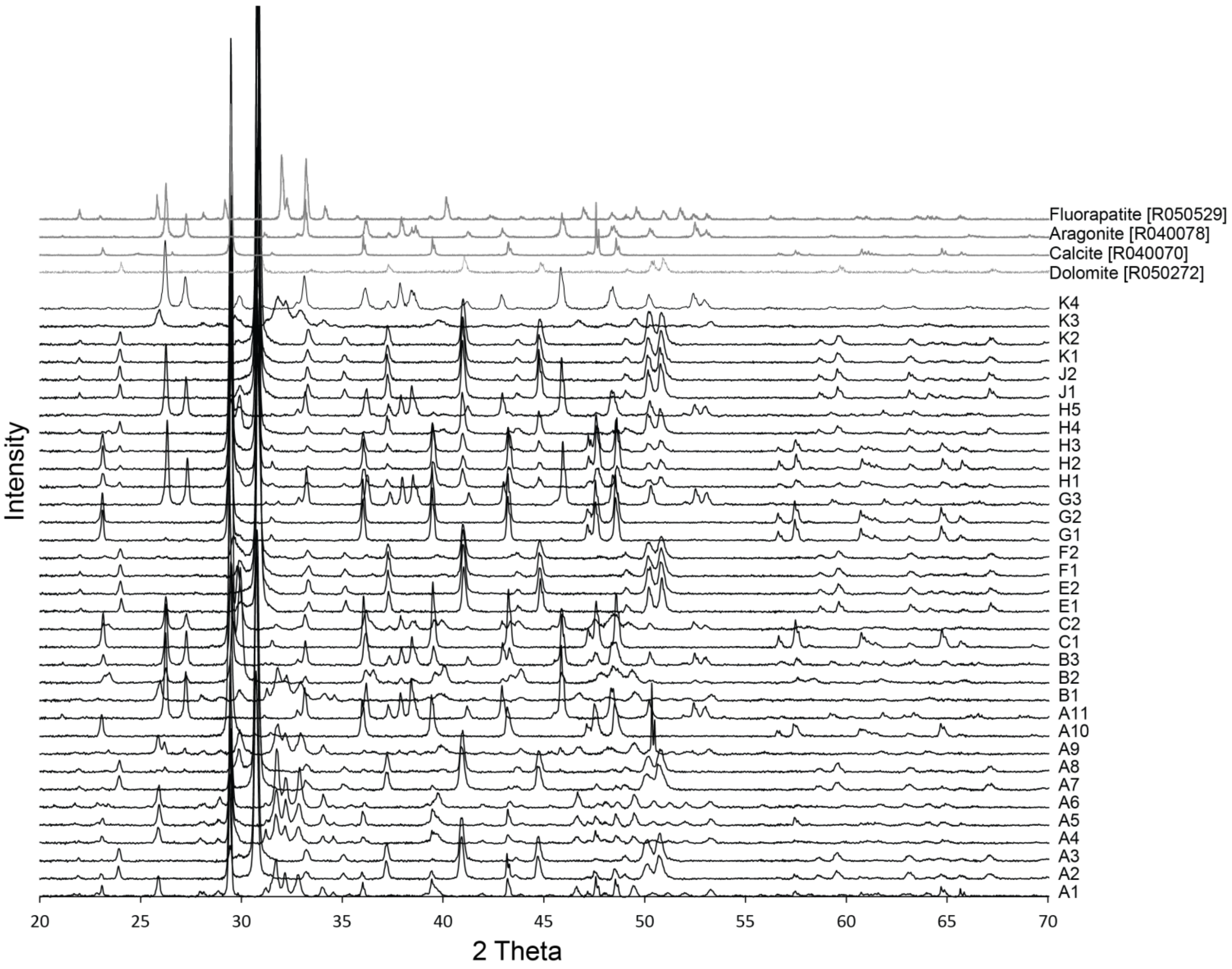

**Figure S1: X Ray diffraction patterns of Isla de Mona sample set** (black) **compared to mineral references retrieved from the RUFF database** (grey)**, the RUFF ID is displayed between brackets**

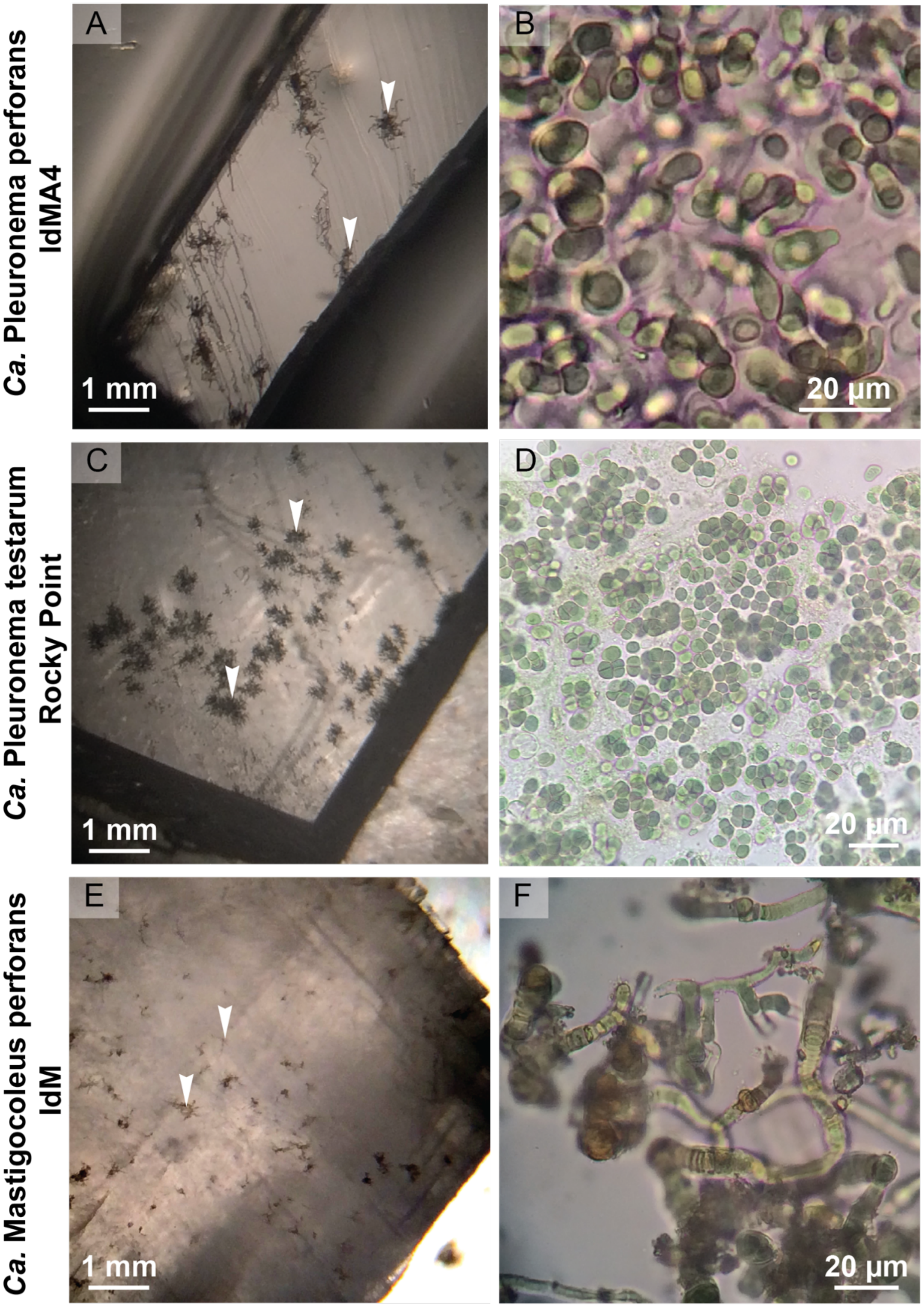

**Figure S2: Macro- (A-C-E) and microscopic (B-D-F) pictures of euendolithic strains boring in Iceland spar calcite chips in laboratory conditions.** Macropictures illustrate bored chips where clear euendolithic colonies are visible (e.g. white arrows). Micropictures illustrate strains morphology. (A-B) show the unialgal strain *Ca*. Pleuronema perforans IdMA4 from Isla de Mona (PR), (C-D) show the unialgal strain *Ca.* Pleuronema testarum from Rocky Point (MX), (E-F) show the unialgal strain *Ca.* Mastigocoleus perforans IdM from Isla de Mona (PR)

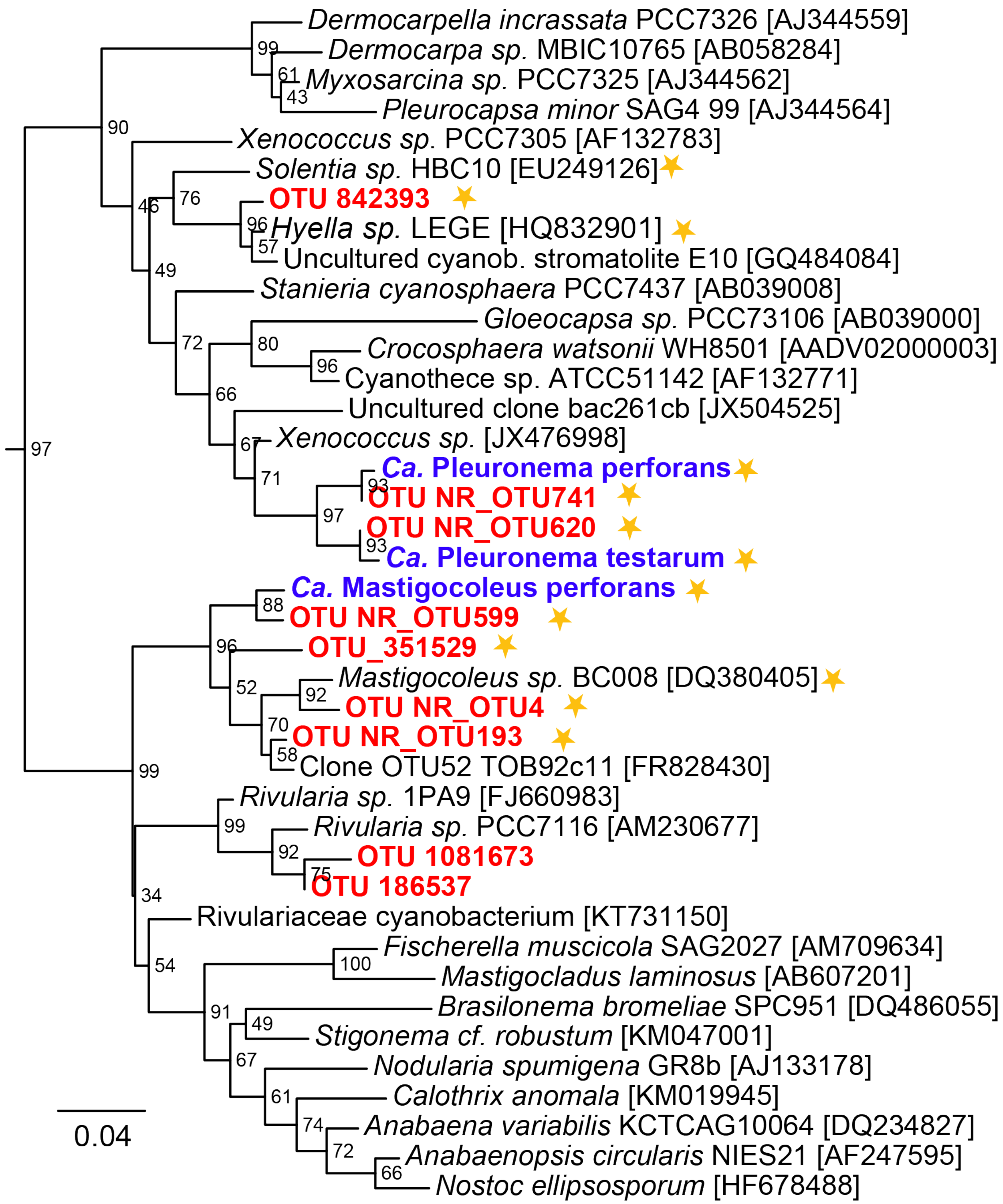

**Figure S3: Maximum likelihood (ML) phylogenetic tree of SSU rDNA of selected cyanobacteria OTUs from Isla de Mona (in red) compared to boring cultures isolated in the present study (in blue) and reference sequences.** Numbers at nodes indicate bootstrap values. Asterisks indicate OTUs tagged as possible or proven euendoliths (see Table 1). The scale bar indicates the number of substitutions per site for a unit branch length.

**Table S1: Physico-chemical analysis of Isla de Mona intertidal sea water and major elements composition of a sub-set of 10 representatives rock samples**

| | **sample** | **Sea water** | **A2** | **A4** | **B1** | **B2** | **C1** | **E2** | **F1** | **H3** | **H5** | **K3** |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | unit | mg/L | mg per g of powdered rock sample | | | | | | | | | |
| Concentration of major elements | Al | - | 3.2E-02 | 2.0E+00 | 4.1E-02 | 4.4E-02 | 1.3E-02 | 1.3E-02 | 1.9E-02 | 2.8E-02 | 2.6E-02 | 2.1E-02 |
| | B | 5.6E+00 | - | - | - | - | - | - | - | - | - | - |
| | Ca | 5.1E+02 | 9.8E+01 | 2.1E+02 | 1.1E+02 | 8.0E+01 | 2.9E+01 | 9.8E+01 | 9.7E+01 | 8.2E+01 | 4.0E+01 | 5.5E+01 |
| | Fe | ND | 2.2E-02 | 2.9E+00 | 2.9E-01 | 6.7E-03 | 1.1E-02 | 1.1E-02 | 1.2E-02 | 2.0E-02 | 1.2E-02 | 5.0E-02 |
| | K | 5.4E+02 | - | - | - | - | - | - | - | - | - | - |
| | Mg | 1.6E+03 | 2.5E+01 | 8.1E+00 | 1.0E+01 | 1.8E+01 | 1.5E+00 | 4.2E+01 | 3.3E+01 | 1.8E+01 | 3.1E+00 | 5.7E+00 |
| | Na | 2.9E+03 | 4.5E-01 | 3.5E+00 | 5.7E+00 | 1.3E+00 | 4.6E-01 | 6.2E-01 | 1.2E+00 | 1.2E+00 | 3.2E+00 | 4.5E+00 |
| | P | 2.2E-02 | 1.6E+00 | 1.0E+02 | 1.4E+02 | 5.5E-01 | 1.7E-01 | 2.3E-01 | 1.2E-01 | 1.4E-01 | 1.7E-01 | 1.4E+02 |
| | S | 1.0E+03 | 9.8E-01 | 3.5E+00 | 3.6E+00 | 1.9E+00 | 5.8E-01 | 1.0E+00 | 1.6E+00 | 1.2E+00 | 2.6E+00 | 5.0E+00 |
| | Sr | 6.1E+00 | - | - | - | - | - | - | - | - | - | - |
| | Si | - | 1.7E+00 | 8.3E+00 | 2.6E+00 | 9.8E-01 | 7.2E-01 | 7.2E-01 | 6.6E-01 | 4.1E-01 | 3.6E-01 | 5.6E-01 |
| | pH | 8.1E+00 | - | - | - | - | - | - | - | - | - | - |
| | salinity | 35 ‰ | - | - | - | - | - | - | - | - | - | - |

**Table S2: 16S rDNA libraries description, including sequencing depth and coverage.**

| | good's coverage | % of sequences kept through filtering | % of OTUs kept through filtering | Total number of sequences analyzed | Total number of OTUs |
|---|---|---|---|---|---|
| **A001** | 94.2 | 85.3 | 37.7 | 58536 | 2925 |
| **A002** | 95.9 | 93.5 | 46.9 | 94453 | 3453 |
| **A003** | 97.8 | 92.7 | 39.9 | 139143 | 2795 |
| **A004** | 97.6 | 91.1 | 34.9 | 127498 | 2444 |
| **A005** | 98.0 | 94.5 | 38.3 | 164343 | 2626 |
| **A006** | 97.7 | 91.0 | 32.7 | 141722 | 2470 |
| **A007** | 98.7 | 98.7 | 67.7 | 59603 | 840 |
| **A008** | 97.6 | 92.2 | 34.1 | 113913 | 1993 |
| **A009** | 96.4 | 87.9 | 33.9 | 98359 | 2766 |
| **A010** | 97.5 | 89.8 | 42.9 | 126036 | 3258 |
| **A011** | 97.4 | 94.6 | 50.6 | 82546 | 2086 |
| **B001** | 96.5 | 89.5 | 35.9 | 166886 | 4959 |
| **B002** | 98.2 | 94.3 | 54.2 | 93794 | 1931 |
| **B003** | 97.4 | 88.0 | 32.9 | 154321 | 3432 |
| **C001** | 96.7 | 81.4 | 35.4 | 102725 | 3887 |
| **C002** | 92.9 | 82.4 | 50.0 | 26933 | 2537 |
| **E001** | 97.1 | 96.4 | 63.4 | 54264 | 1875 |
| **E002** | 97.9 | 94.6 | 39.4 | 94107 | 1547 |
| **F001** | 96.8 | 96.8 | 62.9 | 60175 | 2142 |
| **F002** | 96.6 | 97.5 | 66.0 | 37342 | 1400 |
| **G001** | 98.5 | 90.5 | 30.0 | 165147 | 2002 |
| **G002** | 97.7 | 87.6 | 30.8 | 162738 | 2948 |
| **G003** | 95.2 | 85.0 | 33.5 | 97434 | 3829 |
| **H001** | 96.0 | 92.1 | 42.3 | 123104 | 4284 |
| **H002** | 96.7 | 93.1 | 49.3 | 105394 | 3569 |
| **H003** | 96.1 | 93.3 | 66.6 | 13860 | 830 |
| **H004** | 97.5 | 84.0 | 39.6 | 131407 | 3755 |
| **H005** | 93.7 | 94.1 | 60.6 | 27726 | 1816 |
| **J001** | 92.0 | 90.8 | 56.3 | 32476 | 2791 |
| **J002** | 91.7 | 83.3 | 54.6 | 16375 | 1946 |
| **K001** | 97.6 | 87.6 | 48.6 | 69994 | 2199 |
| **K002** | 98.5 | 94.8 | 69.3 | 41162 | 940 |
| **K003** | 98.0 | 83.5 | 37.5 | 134505 | 3341 |
| **K004** | 98.5 | 96.0 | 70.1 | 41723 | 957 |