



Supplementary data Figure S1 Alignment of the 16S–23S rRNA internal transcribed spacer (ITS) region from *Plectolyngbya hodgsonii*, *P. terrestris*, *P. koreana*, and *P. salina*. Different conserved domains (D1–D5), tRNA genes, major variable stem V3, and antiterminator (Box-B and Box-A) are indicated by boxes and names. *Plectolyngbya terrestris*, *P. koreana*, and *P. salina* contain both tRNA^{Ile} and tRNA^{Ala}. All compared sequences contain important structural elements of the ITS as described by Taton *et al.* [9].