

Table S1. Morphological comparison among the genera to which different clade B cyanobacteria were formerly attributed by the authors of the corresponding 16S rRNA and ITS region sequences, plus the genus *Tapinothrix*

Genus	General appearance	Trichomes	Sheath	Branching	Intercalary cells	Apical cells	References
<i>Heteroleibleinia</i> (Gottler) Hoffmann	filaments attached to the substrate with one end, solitary or in loose groups, rarely forming membranaceous tuft-like layers	uniseriate, cylindrical, with or without constrictions at cross-walls, less than 4 µm wide, heteropolar, not attenuated towards ends	firm, thin, colorless	false branching rarely present	± isodiametric or slightly shorter or longer than wide	rounded, without calyptra or thickened outer cell wall	Komárek & Anagnostidis, 2005
<i>Leptolungbya</i> Anagnostidis & Komárek	filaments rarely solitary, usually forming flaky clusters, floating or attached to the substrate, rarely forming compact thalli or crusts	uniseriate, ± flexuous, finely waved, rarely almost straight, 0.5-3.5 µm wide, isopolar	firm, thin, colorless or colored, hyaline or opaque, homogeneous or lamellated	false branching rarely or very rarely present	± isodiametric or shorter or longer than wide	usually rounded, in some species truncate elongated narrowed or conical, generally without calyptra or thickened outer cell wall	Komárek & Anagnostidis, 2005
<i>Phormidesmis</i> Turicchia <i>et al.</i>	filaments rarely solitary, usually aggregated in mats or clusters	uniseriate, cylindrical, ± straight or slightly coiled, constricted at cross-walls, 2.4-4 µm wide, isopolar	facultative, thin, colorless or slightly yellowish-brownish, usually one trichome per sheath but occasionally two or few trichomes per sheath	not present	± isodiametric or slightly shorter or longer than wide	not differentiated or rounded, without calyptra	Turicchia <i>et al.</i> , 2009; Komárek <i>et al.</i> , 2009
<i>Plectonema</i> Thuret <i>ex</i> Gomont	filaments usually forming tufty thalli, expanded, ± compact, up to 2 cm high, attached to the substrate, or in free-floating clusters	uniseriate, usually waved, 8-25 µm wide, isopolar	firm, thin to thick, up to 4 µm wide, initially colorless, later mostly yellow-brown, homogeneous or lamellated	false branching obligatorily present; branches copious to sparse, single or geminate, tolypotrichoid or scytonematoid type	short, discoid	always rounded, without or rarely with calyptra	Komárek & Anagnostidis, 2005
<i>Pseudophormidium</i> (Forti) Anagnostidis & Komárek	long or short filaments, aggregated to ± expanded, forming mats, tufts or clusters	uniseriate, mostly distinctly constricted at cross-walls, up to 10 µm wide, isopolar	firm, colorless or colored, unlamellated or lamellated	false branching obligatorily present; branches copious, single, geminate or overlapping with common sheath	± isodiametric or shorter or longer than wide	rounded to obtuse-conical, without calyptra or thickened outer cell wall	Komárek & Anagnostidis, 2005
<i>Tapinothrix</i> Sauvageau	filaments attached to the substrate with one end, solitary or in loose fascicles	thin, cylindrical, straight or coiled, with or without constrictions at cross-walls, generally up to 3 µm wide, heteropolar, narrowing towards one or both the ends	firm, thin, colorless or yellowish-colored, hyaline, lamellated	false branching rarely present	± isodiametric or shorter or longer than wide	elongated, tapered, hair-like	Komárek & Anagnostidis, 2005; Bohunická <i>et al.</i> , 2011



◀ Fig. S1. Phylogenetic reconstruction of Leptolyngbyaceae based on 16S rRNA gene analyses. The NJ topology is depicted and the numbers associated with nodes indicate support values for NJ, MP, ML, and BI analyses, respectively. Only bootstrap supports $\geq 50\%$ and posterior probabilities ≥ 0.70 are reported. Values for nodes that obtained support in only one of the performed phylogenetic analyses were omitted. Horizontal bar represents expected number of nucleotide substitutions per site. Genera are indicated by vertical bars and clades A and B are highlighted by gray boxes. Inside clades A and B, a symbol near each considered strain indicates if it was isolated from a mountain habitat (black triangle), from Antarctica (black circle), from the Arctic (white circle), or from a different environment (black square).

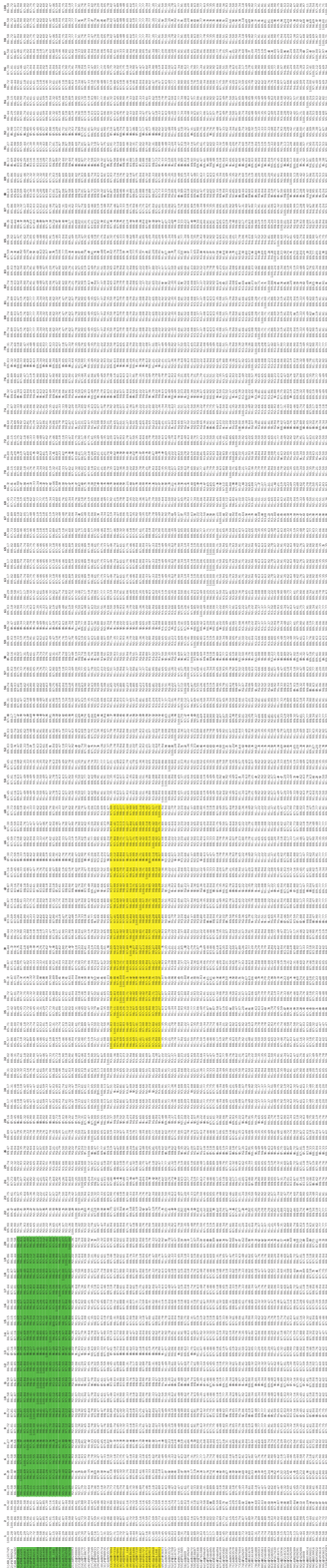


Fig. S2. Matrix showing percent identities of 16S rRNA gene sequences of the considered taxa, based on the alignment used in phylogenetic analyses (713 aligned positions). Clade A is highlighted by a yellow box, clade B by a green box.

100 713
 NR_121745 ACGAA--ACCTGACGGTACCTGACGAATAAGCATCGGCTAACTCCGTGCC
 FR798924 ACGAA--ACCTGACGGTACCTGACGAATAAGCATCGGCTAACTCCGTGCC
 NR_074282 ACGAA--ACCTGACGGTACCTGACGAATAAGCATCGGCTAACTCCGTGCC
 AY493586 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 FN811229 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AY493587 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 GQ162216 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AF091110 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 KX818210 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AY493584 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 GQ162217 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 DQ181690 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AY250881 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AY250870 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 GR2_16S AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 KM462586 AAGAA-GAACTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AY493585 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
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 KF264596 AAGAA-GTTCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AF170758 AAGAA-ATTCTGACCGTTCCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 AF320093 AAGAA-GTACTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 DQ058860 AAGAA-GTACTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
 DQ058890 AAGAA-GTACTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
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 KF307598 AAGAA-GAACTGACGGTACCAGAGGAATAAGCCTCGGCTAACTCCGTGCC
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 JQ687334 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 JX887891 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 HQ189046 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 HQ189044 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 GR13_16S AAGAAGACAGTGACGGTACCGATCGAATCAGCCTCGGCTAACTCCGTGCC
 HM018691 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 DQ181686 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 JQ687330 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 DQ181682 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 AY151727 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 KU219710 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 KM052813 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 GQ324968 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
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 HQ188993 AAGAAGACAGTGACGGTACCTATCGAATCAGCCTCGGCTAACTCCGTGCC
 AY493603 AAGAA-GATCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 AY493607 AAGAA-GATCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 AY493572 AAGAA-GATCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
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 FM210757 AAGAA-GCTCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 KF417431 AAGAACACAATGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 KF761585 AAGAACACAATGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 X84809 AAGAAGCAAGTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 KP739262 AAGAAGCAAGTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 EU528672 AAGAACACAATGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
 HM018687 AAGAA-GTTCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC

Fig. S3. 16S rRNA alignment used for the phylogenetic analyses.

DQ786166 AAGAA-GTTCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
KF761588 AAGAA-GTTCTGACGGTACCTATCGAATCAGCATCGGCTAACTCCGTGCC
GQ859645 NNNAAGATAATGACGGTACCTAATGAATCAGCATCGGCTAACTCCGTGCC
KF246497 AAGAA-GATCTGACGGTACCTAATGAATCAGCATCGGCTAACTCCGTGCC
KF246495 AAGAA-GATCTGACGGTACCTAATGAATCAGCATCGGCTAACTCCGTGCC
KF246496 AAGAA-GATCTGACGGTACCTAATGAATCAGCATCGGCTAACTCCGTGCC
KF246494 AAGAA-GATCTGACGGTACCTAATGAATCAGCATCGGCTAACTCCGTGCC
KJ469129 NNNNN-NNGCTGACGGTACCTGAGGAATCAGCATCGGCTAACTCCGTGCC
AY493582 AAGAAAAAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493581 AAGAACAACAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493578 AAGAACAACAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493579 AAGAACAACAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493580 AAGAACAACAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
KF307604 AAGAAGACAGTGACGGTACCTTGAGGAATCAGCATCGGCTAACTCCGTGCC
EF429297 AAGAAGACAGTGACGGTACCTTGAGGAATCAGCATCGGCTAACTCCGTGCC
KP688589 AAGAACAACAATGACGGTACCTGACGAATCAGCATCGGCTAACTCCGTGCC
KU161670 AAGAA-GATCTGACGGTACCGAATGAATCAGCATCGGCTAACTCCGTGCC
KU161669 AAGAA-GATCTGACGGTACCGAATGAATCAGCATCGGCTAACTCCGTGCC
KF246488 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
KF246503 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
HM105583 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
KF246484 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
KF246483 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
KF246501 AAGAAGACAGTGACGGTACCGATCGAATCAGCATCGGCTAACTCCGTGCC
KF417430 AAGAA-GTTCTGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AF218371 AAGAA-GATCTGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
HQ132936 AAGAA-GATCTGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AF218372 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AF218368 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
EF429299 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
EF429289 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
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EF429288 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
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KM019914 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
KJ939021 AAGAA-AAGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
KM019916 AAGAA-AAGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
KJ939022 AAGAA-TCGATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493618 AAGAA-AGAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493615 AAGAA-AGAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC
AY493583 AAGAA-TCGAATGACGGTACCTGATGAATCAGCATCGGCTAACTCCGTGCC

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CGG

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34 787

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 AY493636 AGGGAGACC-TACTAAGTTAGTA--CTTGAAAGCAATTA-----
 AY493637 AAGGAGACC-TACTAAGTTAATA--CCTGAAAGCGATTT-----
 GQ162323 NAGGAGACC-TACTAAGTTAATA--CTGAAAGCGATTT-----
 KF264597 AAAGAGACC-CACTAA-TCATTC--ACTGAAAGCGATTT-----
 GR2 ITS AAGGAGACC-TACTAGGTAATAC--TTTGAAAGCACATT-----
 AY493644 AAGGAGACC-TACCCCTTTGATTTTCTTAAT-----
 AY493646 NNNNNNNCC--CCCTTTGACTT--TCTTAAT-----
 EF429299 AAGGAGACC-TACCTCTCCCTAATTTTAA-----
 EF429288 AAGGAGACC-TACCTCTCACTT--AGCTAAAGC-----
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 AY493642 AGGGAGACC-TACCTACTCAA--GTTGAACGTGAGTT-----
 AY493643 AGGGAGACC-TACCTACTCAA--GTTGAACGTGAGTT-----
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 KM052813 AGGGAGACC-TACCTGTTGAATA--ACTGAAAGCGCTTG-----
 JX887894 AGGGAGACC-TACCTGTTGAATA--ACTGAAAGCGCTTG-----
 JX887891 AGGGAGACC-TACCTGTTGAATA--ACTGAAAGCGCTTG-----
 GR4 ITS AGGGAGACC-TACCTATTCCCT--ATGGAAGCAACGA-----
 GR13 ITS AGGGAGACC-TACCTGTTTCGAT--ATTGAAAGCAGCAG-----
 KU219710 AGGGAGACC-TACCTGTTGAAT--CAGGAAAGTAAATC-----
 AY493640 AGGGAGACC-TACCCGTTTCTC---CTGAAACGTTCAAGTCTCCAGTGAA
 AY493641 AGGGAGACC-TACCCGTTTCTA--CTTAAACGCTTACTTTCT-----
 KF307604 AGGGAGACC-TACCTATCGGAT--ACCGAACCCAA-----
 EF429297 AGGGAGACC-TACCTATCGAAT--ACCGAACCCACATTG-----
 KU161670 AGGGAGACC-TACCCACTCTTAA--GCTGAACGCACACT-----
 KU161669 AGGGAGACC-TACCCACTCTTAA--GCTGAACGCACACT-----
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 EU528672 AGGGAGACC-TACCCGCTCAAAT--TCTGAAAGCAATGT-----
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 -----TAGGATGAGAA--AGG
 -----TAGGATGAGAA--AGG
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 -----GACAAGTAAAAAAGAGC--AGG
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 -----AGAAATAACGAGCTGGTAAGCTAAGAGT--TGG
 -----GCGAAAAGGGAGATGAT--TGG
 -----CGCGATTAGGCTATCAAC--TGG
 -----CGCAATTGAAGGTATCAACTGG
 -----CGCAATTAGGGTATCAAC--TGG
 -----GAAGTCAAGAGACTCAACGCTGTGATTAGATAGAGAAC--AGG
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 -----GGCAACGATGAGCGAGTAATGAAACAAC--TGG
 TCAATTAACTCGGTTGATTGATTGGTTAGAGGATTGGGCTATTAGAGAAGAAGC--TGG
 -----ACTATTCAACCTGGTTGAGTGAGGAAAAGATTATCAGAGTAGAGAT--TGG

Fig. S4. 16S-23S ITS alignment used for the phylogenetic analyses.

-----GTGAACTAGGTAACGATAAGG
-----AATTAGGTAACGATAAGG
-----GTTATTAAGCAAGAGTC--GG
-----GATATTAAGCAAGAGTC--GG
-----GCAAATAGGAAGTGGAT-TGG
-----GCAAATAGGGAAGTGAAT-TGG
-----GCAAATAAGGATTGAGT-TGG
-----GCAAATAAGGATTGAGT-TGG
-----TATAGGAGAATTGAGAGG
-----AATTAGGAGTATTGAGTGG

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TCACCT--AAGGTCGTTGAGGGTTTTGTTTTTACTGC-----
TCACCT--AAGGTCGTTGAGGGTTTGTGTTAGTCTCTGGT-----
TCACCT--AAGGTCGTTGAGGGTTTGTGTTAGTCTCTCT-----
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TCACCT--AAGGTCGTTGAGGGTTTCGATAGTTAAAGTCAACAAGCGACCAGAGAAAACCT
TCAACTT--AGGTCGTTCCGAGCTTTCGCGCGGATTATTTATATT-----
TCAACCT--AGGTCGTTCCGAGCTTTCGCGCAGATTATTTATATT-----
TCAACT--AGGTCGTTCCGAAGCTTTC-----
TCAACT--AGGTCGTTCCGAAGCTTTC-----
TCAACT--AGGTCGTTCCGAAGCTTTC-----
TCATCTC--AAGGTCGTTCCAGGAATA-----
TCATCTC--AAGGTCGTTCCAGGAATG-----
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CCATCCCAAAGGTCGTTTCG-GATAT-----
TCATCCCAAAGGTCGTTTCGGAATT-----
TCATCCCAAAGGTCGTTTCG-GATTT-----
TCATCCCAAAGGTCGTTTCG-GATTT-----
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-----CATAAATTTTCGATGTGCT-----
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-----TAGTG-----TTGGTT-----
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-----AGAAG-----TTAGGCT-----
-----AGAAG-----TTAGGCT-----
-----AGAAG-----TTAGGCT-----
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-----TGATG-----TTGACT-----
-----GAGTG-----TTGACT-----
-----GAGTG-----TTGACT-----
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-----GGGTAGAACTAAATGGCT-----
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-----AGATG-----TTGGTT-----
-----GAGTG-----TTCGTGGCT-----
-----GAGTG-----TAAGGCT-----
-----GAGTG-----TCGGGCT-----
-----GAGTG-----TAAGGCT-----
-----GAGGA-----AGAGTT-----
-----GAGTA-----GAGTT-----

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-----TCCAAA-TTATTCAGG---TGTT-----ACGAC
-----TCCAAG-TTATTCGG---TGTT-----ATGAC
-----TCCAAG-TTATTCGG---TGTT-----ATGAC
-----TTCAAA-TTATCGTG---TGTT-----ACGCC
-----TTCAAA-TTATCGTG---TGTT-----ACGAC
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-----TCTAAA-CTATCCC---GGTT-----CAGGG
-----TCTAAA-CTATCCC---GGTT-----CAGGG
-----TCTAAA-CTATCCC---GGTT-----CAGGG
-----TCCAAG-CTGTCT---GGTC-----TGGGT
-----TCCAAG-CTGTCT---GGTC-----TGGGT
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-----TCCAAG-CTATTT---GGTT-----CGGTT
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-----TTCAAAGCTATATAGAGACTGGTT-----CGG--
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-----TTCAAAGCTATATT---GGTT-----CGGGT
-----TCTAGA-CTATGTAAGATT---GGTT-----CGGGC
-----TCTAAA-CTATGTAAGATT---GGTT-----CGGGT
-----TTCAAA-CTAACTA---GGTG-----AGGGA
-----TTCAAA-CTAACTA---GGTG-----AGGGA
-----TTCAAA-CTATTTA---GGTT-----CGGTT
-----TTCAAA-CTATTTA---GGTT-----CGGTT
-----TTCAAA-CTATTACA---GGTT-----CGGTA
-----TTCAAA-CTATTAAA---GGTT-----CGGA-
-----TTCAAA-CTATTAAA---GGTT-----CGGT-
-----TCTAAA-CTAAGTCGA---GGTTAATCGGTCTGAGGCA
-----TCTAGA-CTAT---GGTT-----GAGGT

ACCACT-----CGAAAGATAAGGGCTATT
GACAGT-----TAATACACCGAGAGAGACGGGCTATT
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AATGGT-----TGAGA-AACCGAGTCAAAGCATCAATCAAACGGGCTATT

```

ATCATGTTACGCCATGAATAGAGGCAC-CGACTAAATAACGGGCTTAATAACGGGCTATT
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A-TGT-----GGGCTATT
A-TGG-----GGGCTATT
A-TGG-----GGGCTATT
A-TGG-----GGGCTATT
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TTTCAA-----CCAGTATGGGCTATT
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--CAT-----GGGCTATT
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T-TAT-----GGGCTATT
--TGT-----GGGCTATT
--TAT-----GGGCTATT
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T-TATTTCTCACCTTTTGTCTTGATAGAGAAGGGTAGAGGAACAAACCCGGGCTATT

[illegible]

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-----TGGAGAGGGGGTTTAGCTC
-----TGAGGGGGTTTAGCTC
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-----TCAAACGATTGATGGGGGTTTAGCTC
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[illegible]

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CCACGCCAGCCGCTA-----AGCGAAACGGAACATA--
CCACAAGAAACGCT-----AAGGAAACGGAACGAA--
CTGAGT-----TCACGCTCAGACATGAA--
CTGAGT-----TCACGCTCAGACATGAA--
CCAACCGCTTAATTGACGATTTTT-----ATTGAATTGAGCG--

CCAACCGATTGATTGAATCACTCTGTTGAATTTTTT-----GTTGAATTGAGCG----
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 CTGAGTGATTT-----ATTCACCTCTAAAA----
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 CTGAG-----
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 CTGGGTAATAGCAAATTGT-----TATTAGCCAAATT----
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 CTGG-----AGTTGATAGAGCA--AG
 CTGG-----AGTTGATAGAGCG----
 CTGG-----AGTTAATAGAAC-----
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 CCACGA-----AAGCATGGGATTG----

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 -----ACG---GTAAAAATCAGCAACCA-----GGGATGTGAGCATTAGGTT--
 -----AAATCAGCAACCA--GGAAGTGAGCATTAGGTTCAA--
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 CCGATTTTTG---GAACAACACAGCAATTC-----ATTTGATTTTACAGAAAC
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 ---ATTGAGG---ATATGCGACAGCAACTC-----ATCTGCGAGAT-----
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 -----GTGT---TAACAATTTAGCAACTTTATTGTTGACAGATTTAATCTGT-----
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 -----CATTTTCAGCAACTG-----ATCTAGCGAAGATTCAAT
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 -----GAAGATATCAGCAACTT-----ATCTAGATGAA-----
 -----TCAACTTCAGCAACTT-----GTCTAACTAGGTCTTCAC
 -----ATTCCAGCAACTC-----ATCTAATCT-----
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 -----TTA---GAAGGATTTCAGCAACTG-----TTCTAGTTTTCCAA-----
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 -----GC---GGAGAGTTTCAGCAACTT-----ATCTAACCAATTCATCAA
 ---AGAGGTA---GGAAAGTTTCAGCAACTT-----ATCTAGGTTTAG-----
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 ---AGAG---GAAGAATACAGCAACTT-----ATCTAGGTTTTG-----
 ---AGAGTTA---GGAAGATTTCAGCAACTT-----ATCTAGGTTTTG-----
 TAGGTTGTTTCATCGAAGAGATGGGTGACGT-----AT-----
 -----AATTACAGCACGGT-----GTGTTTTGGTGATAG-----

-----CATCAT---AGCTTGCTGGTCTATCTAGACTAGTAAAAGAA
-----CAACATCGTAGATGCTGGTCTTTTCGGGACTAGC--TAGAA
-----CAACATCATGGCTGCTGGTCTTTCAAGACTAGC--GAGAA
-----CATCAT---GGGCTGCTGGTCTTTTCAGCACTAGC--GAGAA
AACGTTCTG-----ATACACCATAGCGTGTCTGGTCACTAAAGACCAGT--AAGAA
AAGTTCTG-----ATACAACATAGTGTGCTGGTCACTAAAGGCCAGT--AAGAA
TGGA-----TCAAAG--AGCCTGTCTGGG--GTTAGTCCCAGACAGAGAA
TGGA-----TCAAAG--AGCCTGTCTGGG--TTAGTCCCAGACAGAGAA
-----GCAGAG--AGTCTGTCTGGA---TTATATCCAGTGCGAGAA
-----GTAGAG--AGCCTGTCTGGA---TTATGTCCAGTACAAGAA
-----GTAGAG--AGCCTGTCTGGA---TTATGTCCAGTACAAGAA
-----TTAGCAATCAGTCTGCTGGA-TTGTATTACAGT--CAGAA
-----TTAGCAATCAGTCTGCTGGA-TTGTATTACAGT--CAGAA
-----CAAGAG--TATCTGTCTGGA---TTTAGATTCAGC-GAAGAA
-----CAAGAG--TATCTGTCTGGA---TTTAGATTCAGC-GAAGAA
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TATCTTCAA-----CTAGAG--AGCCTGTCTGAG--GAAGTCTCAGT--GAGAA
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GATTGAGTTTGGGAATAAGATAGAG--AGCCTGTCTGAG--GAAGTCTCAGT--AAGAA
TAACCTTCCT-----CTAGAG--AGCCTGTCTGAG--GTTAGCCTCAGT--GAGAA
TAAA-----TTAGAG--AGCCTGTCTGAG--GTAAAGCTCAGT--GAGAA
-----CTAGAG--AGCCTGTCTGAG--ATTAGTCTCAGT--GAGAA
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-----TTAGAG--AGCCTACTGGA---CTTGTTCAGT--CAGAA
-----CTAGAG--AGCCTGTCTGGA--TGCGAGTCCAGT--CAGAA
-----CTAGAG--AGCCTGTCTGGA---TTTAGTCCAGT--CAGAA
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G-----TTAGAG--AGCCTGTCTGGA---GTAATCCAGT--CAGAA
-----CTAGAG--AGCCTGTCTGGA---GATGTCCAGC--CAGAA
-----CTAGAG--AGCCTGTCTGGG---ATTGTCCAGC--CAGAA
-----CTAGAG--AGCCTGTCTGGA---TTTAGTCCAGT--CAGAA
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-----AGTCTGTCTAGG--TGAGAGCCTAGT--GAAGAA
-----CCAAGGCATAGTCTGCTGGG--TGAGAACTTACG--AAAGAA

[illegible]

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CCTTGAAAAC TG CATAG
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CCTTGAAAAC TG CATAG
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CCATGAAAAC TG CATAG
CCATGAAAAC TG CATAG
CCTAGACAAC TG AATAC
CCTTGAAAAC TG AATAC

	1.	2.	3.	4.	5.	6.	7.	8.	9.	10.	11.	12.	13.	14.	15.
1.AF218372_L_angustata	100.00	98.47	98.32	99.10	99.01	90.56	90.47	88.33	88.42	89.94	90.31	90.04	90.04	89.77	89.77
2.EF429299_L_corticola	98.47	100.00	99.01	99.19	99.10	90.83	90.74	88.69	88.87	90.39	90.57	90.31	90.31	90.04	90.04
3.AF218368_L_tenerima	98.92	99.01	100.00	99.64	99.55	90.91	90.82	88.68	88.77	90.20	90.57	90.30	90.30	90.03	90.03
4.X84808_L_foveolarum	99.10	99.19	99.64	100.00	99.73	91.10	91.01	88.96	88.96	90.39	90.75	90.48	90.48	90.31	90.31
5.EF429291_L_boryana	99.01	99.10	99.55	99.73	100.00	91.00	90.91	88.77	88.86	90.29	90.66	90.39	90.39	90.12	90.12
6.FM210757_T_albertanoae	90.56	90.83	90.91	91.10	91.00	100.00	99.46	93.17	93.79	93.25	94.06	93.88	92.99	93.44	93.17
7.FM210758_T_oregonensis	90.47	90.74	90.82	91.01	90.91	99.46	100.00	93.08	93.71	93.16	93.88	93.79	92.99	93.35	93.17
8.GR4_168	88.33	88.69	88.68	88.96	88.77	93.17	93.08	100.00	98.65	94.79	94.17	94.34	93.81	93.45	94.08
9.GR13_168	88.42	88.87	88.77	88.96	88.86	93.79	93.71	98.65	100.00	94.34	93.90	94.08	93.36	93.00	93.45
10.EU528672_O_neakamenienis	89.94	90.39	90.20	90.39	90.29	93.25	93.16	94.79	94.34	100.00	98.47	98.65	97.22	97.04	97.40
11.KF761588_O_atacamensis	90.31	90.57	90.57	90.75	90.66	94.06	93.88	94.17	93.90	98.47	100.00	99.10	97.31	96.95	97.49
12.HM018687_O_coburnii	90.04	90.31	90.30	90.48	90.39	93.88	93.79	94.34	94.08	98.65	99.10	100.00	97.49	96.95	97.31
13.X84809_O_subterranea	90.04	90.31	90.30	90.48	90.39	92.99	92.99	93.81	93.36	97.22	97.31	97.49	100.00	97.40	97.85
14.KF417431_O_kauaiensis	89.77	90.04	90.03	90.31	90.12	93.44	93.35	93.45	93.00	97.04	96.95	96.95	97.40	100.00	97.85
15.KF761585_O_cataractarum	89.77	90.04	90.03	90.31	90.12	93.17	93.17	94.08	93.45	97.40	97.49	97.31	97.85	97.85	100.00

Fig. S5. Matrix showing percent identities of 16S rRNA gene sequences of strain GR4, GR13 and some focus taxa (representatives of the genera *Leptolyngbya*, *Oculatella*, and *Thermoleptolyngbya*) based on an alignment of 1119 positions. The different clades are highlighted by gray boxes.

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

-----TGCAAGTCGAACGAACCTATTTCGTAGGTAAAGT
GATGAACGCTGGCGCGTGTAAACACATGCAAGTCGAACGAACACTTCGGGTGAGT

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

GGCGGACGGGTGAGTAACCGCTGAGGATCTGCCTACAGGATCGGGATAACAGCGAGAAAT
GGCGGACGGGTGAGTAACCGCTGAGGATCTGCCTACAGGATCGGGATAACAGCTGGGAAAC

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

TCTACTATAAACCCAAATGTGCCGAGAGGTGAAATATTTATAGCCTGTAGATGACCTCGCG
TGCTCTATAAACCCGATGTGCCGAGAGGTGAAATATTTATAGCCTGTAGATGAACTCGCG

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

GGGGAATTTTCCGCAATGGGCGAAGCGCTGACGGAGCAACGCCGCGTGAGGGAGGAAGGC
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GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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-----AAGAAGTTCTGACGGTACTGAGGAATCAGC

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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TATTGGGCGTAAAGCGTCCGTAGGCGGTTTCAAAAGTCTGTTGTTAAATCCACAGCTCA

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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ACTGTGGATGGCAATGGAACTATGAGACTAGAGCGTGGTAGGGGTAGAGGGAATTCCT

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

AGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGCGCTCTACTG
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AGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGGCGAAGCGCTCTACTG

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

GGCCATTAAGTACGCTGATGGACGAAAGCTAGGGGAGCGAAAGGGATTAGATACCCCTGT
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GGCCATTAAGTACGCTGATGGACGAAAGCTAGGGGAGCGAAAGGGATTAGATACCCCTGT

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

AGTCCTAGCTGTAACAGATGGATACTAGGTGTTGGCCGTATCGACCCGGTCAGTATCGAA
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AGTCCTAGCTGTAACAGATGGATACTAGGTGTTGGCCGTATCGACCCGGTCAGTATCGAA

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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GCAACGCGTTAAGTATCCCGCTGGGGAGTACGCACGCAAGTGTGAACTCAAAGGAAT
GCAACGCGTTAAGTATCCCGCTGGGGAGTACGCACGCAAGTGTGAACTCAAAGGAAT

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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TGACGGGGGCCCGCACAAAGCGGTGGAGTATGTGGTTTAATTCGATGCAACGCGAAGAACC

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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TTACACAGGATTGACATCTACGAACTTTCTGAAGCAGAGTGGTGCCTTCGGGAGCGTA
TTACACAGGATTGACATCTACGAACTTTCTGAAGCAGAGTGGTGCCTTCGGGAGCGTA

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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GAGACAGGTGGTGCATGGCTGCTGCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGC
GAGACAGGTGGTGCATGGCTGCTGCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGC

GR2_16S
AY493585_Phormidesmis_priestleyi
KF264596_Heteroleibleinia_fontan

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AACGAGCGCAACCCCTCGTCTTAGTTGCCATCATTAAGTTGGGCACCTTTAAGGAGACTGC
AACGAGCGCAACCCCTCGTCTTAGTTGCCATCATTAAGTTGGGCACCTTTAAGGAGACTGC

GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	CGGTGACAAACCGAGGAAGGTGGGGATGACGTCAAGTCATCATGCCCTTACATCCTGG CGGTGACAAACCGAGGAAGGTGGGGATGACGTCAAGTCATCATGCCCTTACATCCTGG CGG----- ***
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	GCTACACACGTACTACAATGCAACGGACAAAGGGCAGCCAAGTACGATAGTGC ^{AAAT} GCTACACACGTACTACAATGCAACGGACAAAGGGCAGCCAAGTACGATAGTGA ^{GCT} AAAT -----
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	CCCATAAACCGTTGC ^A CAGTTCAGATTGCAGGCTGCAACTCGCCTGCATGAAGGCGGAAT CCCATAAACCGTTGC ^T CAGTTCAGATTGCAGGCTGCAACTCGCCTGCATGAAGGCGGAAT -----
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	CGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATACGTTCCCGGGCCTTGTACACACCG CGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATACGTTCCCGGGCCTTGTACACACCG -----
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	CCCGTCACACCATGGAAGTTGGCCACGCCCGAAGTCGTTACCCCAACCGTT----- CCCGTCACACCATGGAAGTTGGCCACGCCCGAAGTCGTTACCCCAACCGTTACGGAGGG -----
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	----- GGACCCGAAGGCAGGGCTGATGACTGGGGTGAAGTCGTAACAAGGTAGCCGTACCGGAA -----
GR2_16S AY493585_Phormidesmis_priestleyi KF264596_Heteroleibleinia_fontan	----- GGTGTGGCTGGATCACCTCCTTA -----

Fig. S6. 16S rRNA alignment among the sequences of strain GR2, *Heteroleibleinia fontana* UCFM_HF, and *Phormidesmis priestleyi* ANT.LPR2.6. The nucleotide differences are highlighted in yellow color.

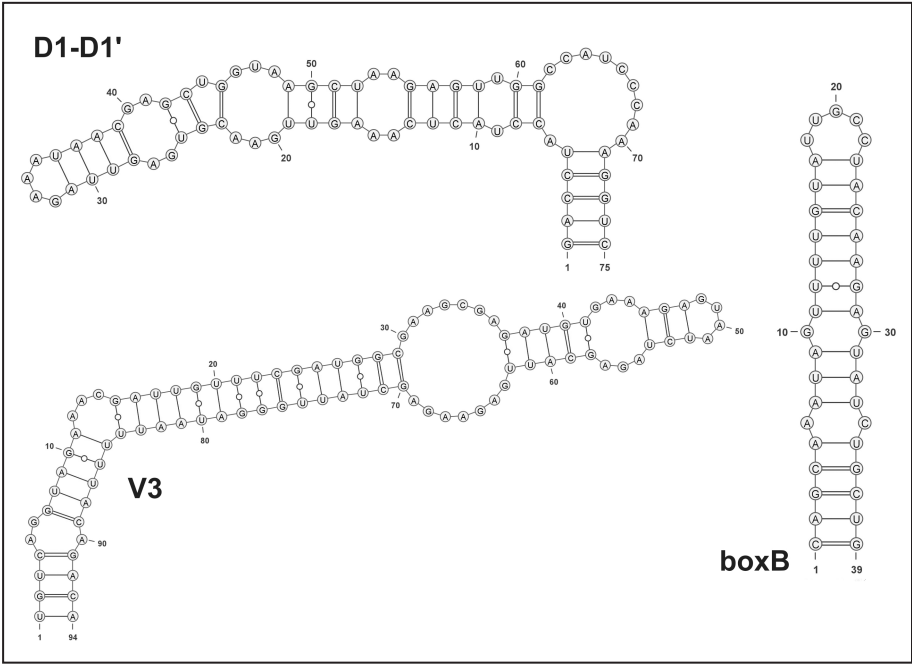


Fig. S7. Hypothetical secondary structures of the 16S-23S ITS region domains (D1-D1', boxB, V3) for "*Leptolyngbya frigida*" clade.