

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 1CSAR: Barcode-1a

SAG 211-9a

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•||| | | | | C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||| | | | | |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31683134-----44-4813883485428316-3361-3262248

BC

CAG---- G C C C U G U
GAU-GAGC CC C-AG -GC GCU GAU GGUA GUUUUC C
||•||| || | || | •|| | | •|| | | •|| |
CUG-CUCG GG G-UC -CG UGA CUG CCGU CAGAAG C
UCAACCA G - A A - A G

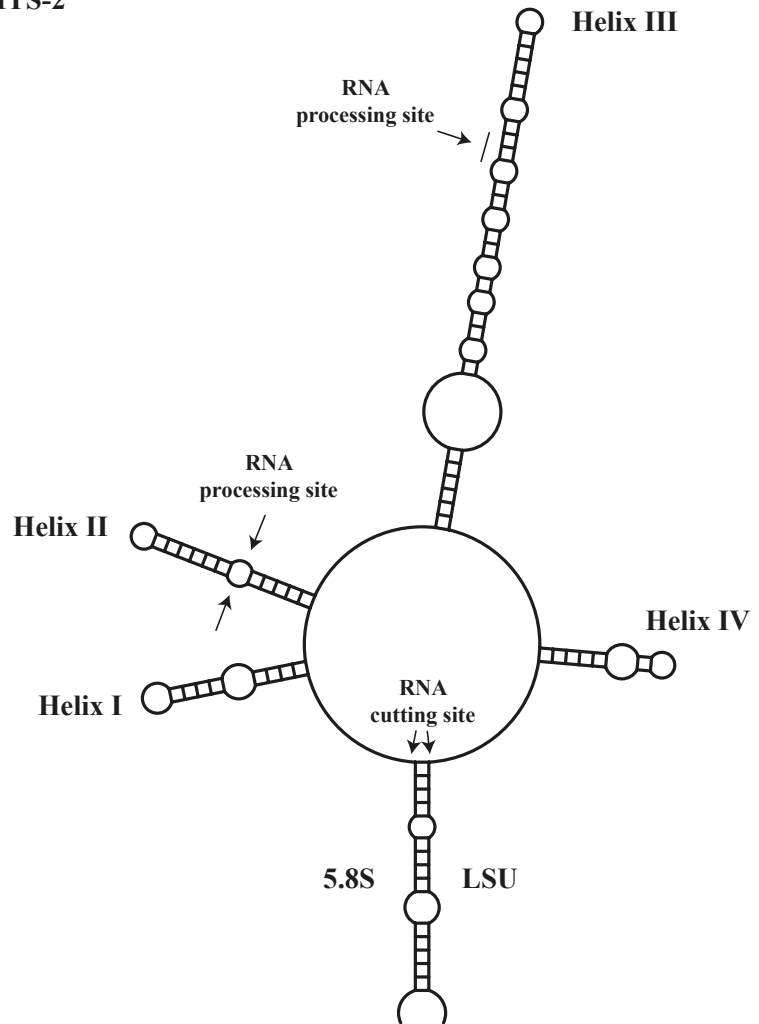
CUACUAACGAC

Helix IV

GC G
GGGGGA GC C
||| | | |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium saccharophilum
Haplotype 6CSAR: Barcode-1b

SAG 2055
Fall/B-1b

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•|||| | C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••|||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31683134-----44-4813883485424316-3361-3262248

BC

CAG---- G C C U G U
GAU-GAGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||• |||| | | | | • ||||| • ||• ||• ||| |
CUG-CUCG GG G-UC -CG UGAGCUG CCGU CAGAAG C
UCAACCA G - A - A G

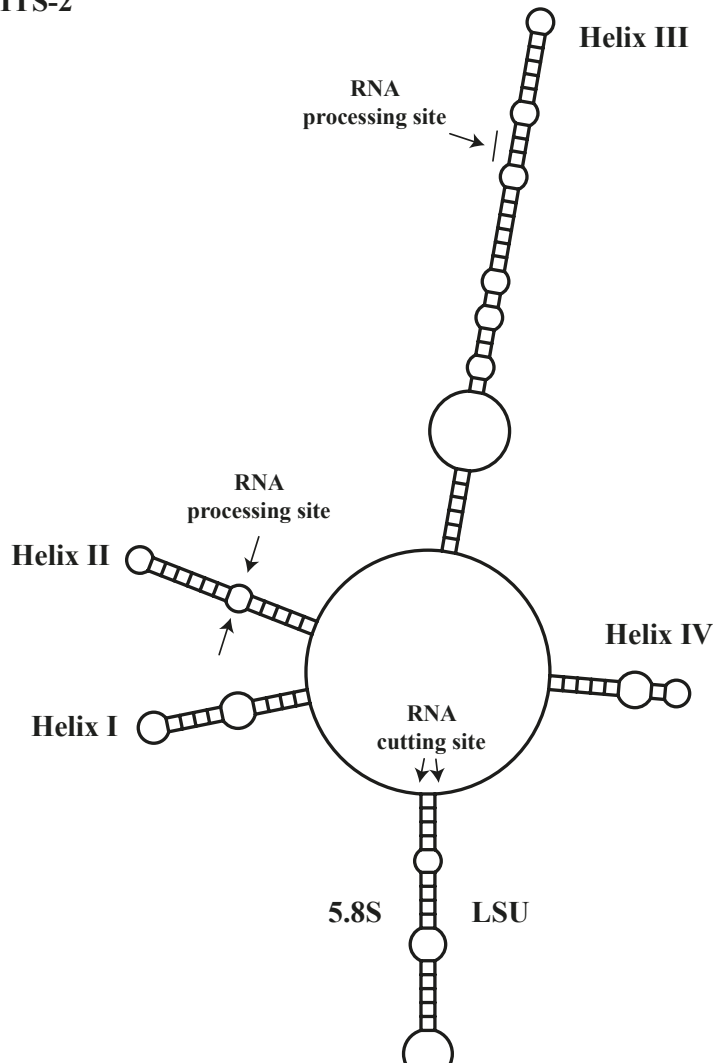
CUACUAACGAC

Helix IV

GC G
GGGGGA GC C
||||| || |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 2CSAR: Barcode-1c

SAG 211-1c
SAG 2197
CCAP 211/27
CCAP 211/32
CCAP 211/34
CCAP 211/40

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•|||| |||| C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••|||| |||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483134-----44-4813883485424316-3361-3262248

BC

CAG---- G C C U G U
GAC-GAGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| ||| || | || | •|||• ||• ||•||| |
CUG-CUCG GG G-UC -CG UGAGCUG CCGU CAGAAG C
UCAACCA G - A - A G

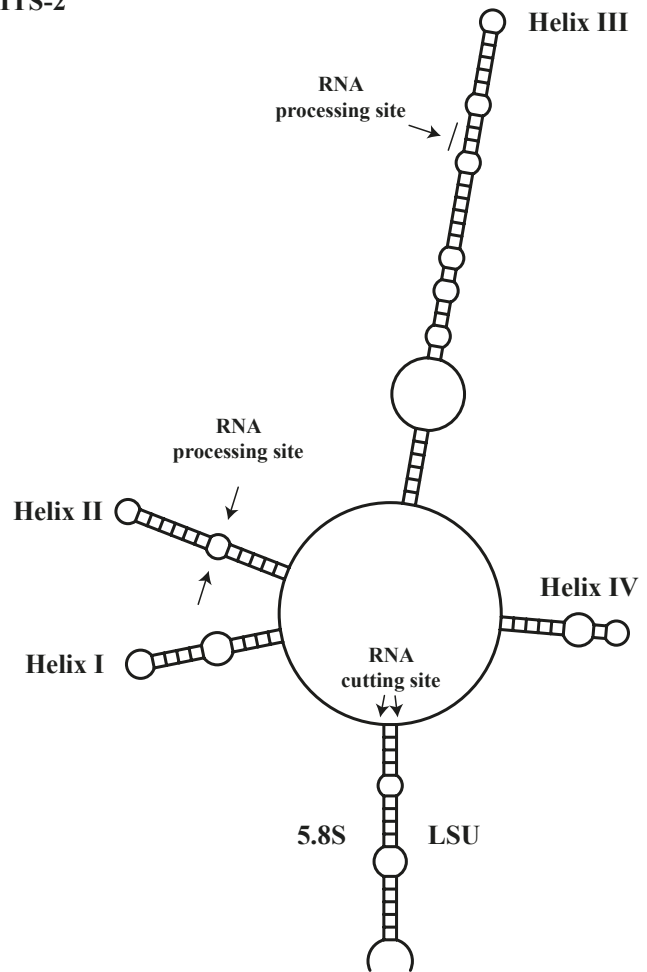
CUACUAACGAC

Helix IV

GC G
GGGGGA GC C
||||| || |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 4CSAR: Barcode-1c

CCAP 211/36

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

CAA CU
UCGUC UUC \
•||| | | | | C
GGCAG AAGG /
ACG UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||| | | | | |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483134-----44-4813883485424316-3361-3262248

BC

CAG---- G C C U G U
GAC-GAGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| ||| || | || | •||| | • ||• ||•||| |
CUG-CUCG GG G-UC -CG UGAGCUG CCGU CAGAAG C
UCAACCA G - A - A G

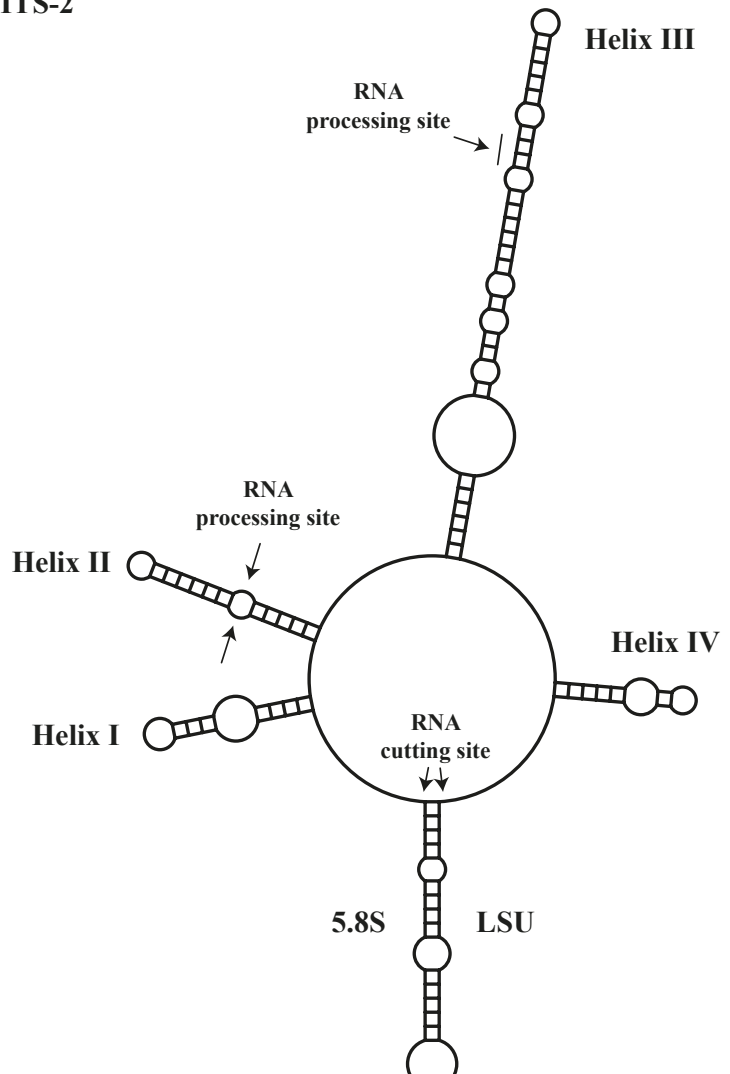
CUACCAACGAA

Helix IV

GC G
GGGGGA GC C
||| | | | |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 5CSAR: Barcode-1c

CCAP 211/42
SAG 2120
SAG 2149

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•||||| ||||| C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||||| ||||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483134-----44-4813883485424316-3361-3262248

BC

CAG---- G C C U G U
GAC-GAGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| |||| || | || || •|||||• ||• ||•||| |
CUG-CUCG GG G-UC -CG UGAGCUG CCGU CAGAAG C
UCAACCA G - A - A G

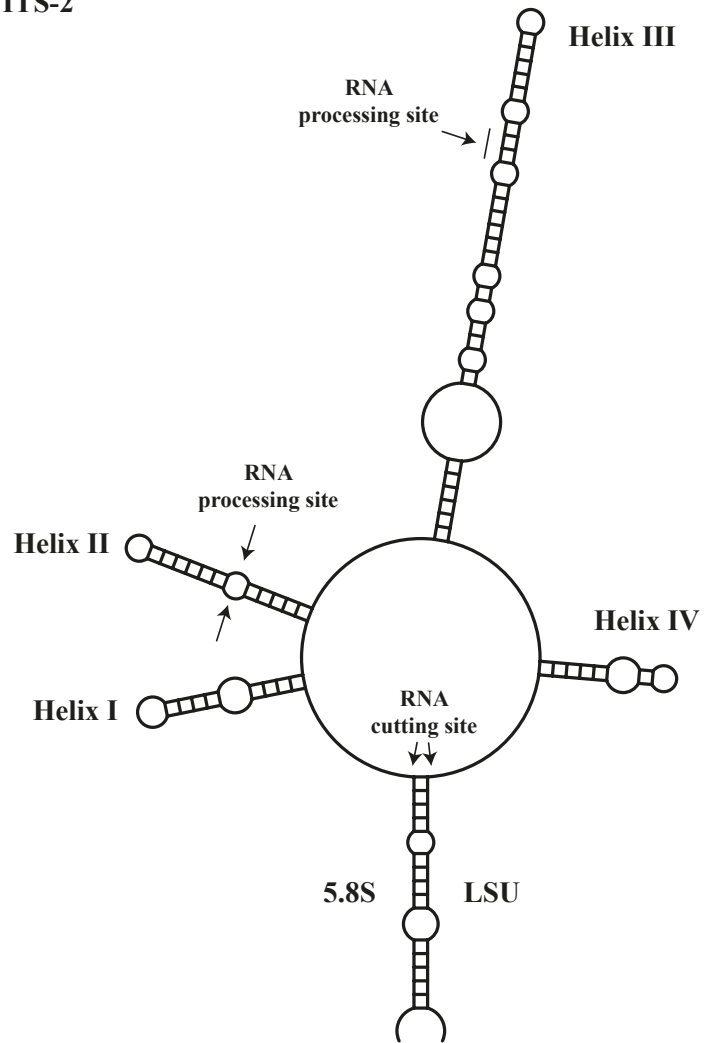
CUACCAACGAC

Helix IV

GC G
GGGGGA GC C
||||| || |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 7CSAR: Barcode-1c

SAG 211-1b
SAG 211-1d

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•||| ||||| C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||| ||||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483134-----44-4813883485424316-3361-3262248

BC

CAG---- G C C U G U
GAC-GAGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| ||| || | || | •||| • ||• ||•||| |
CUG-CUCG GG G-UC -CG UGAGCUG CCGU CAGAAG C
UCAACCA G - A - A G

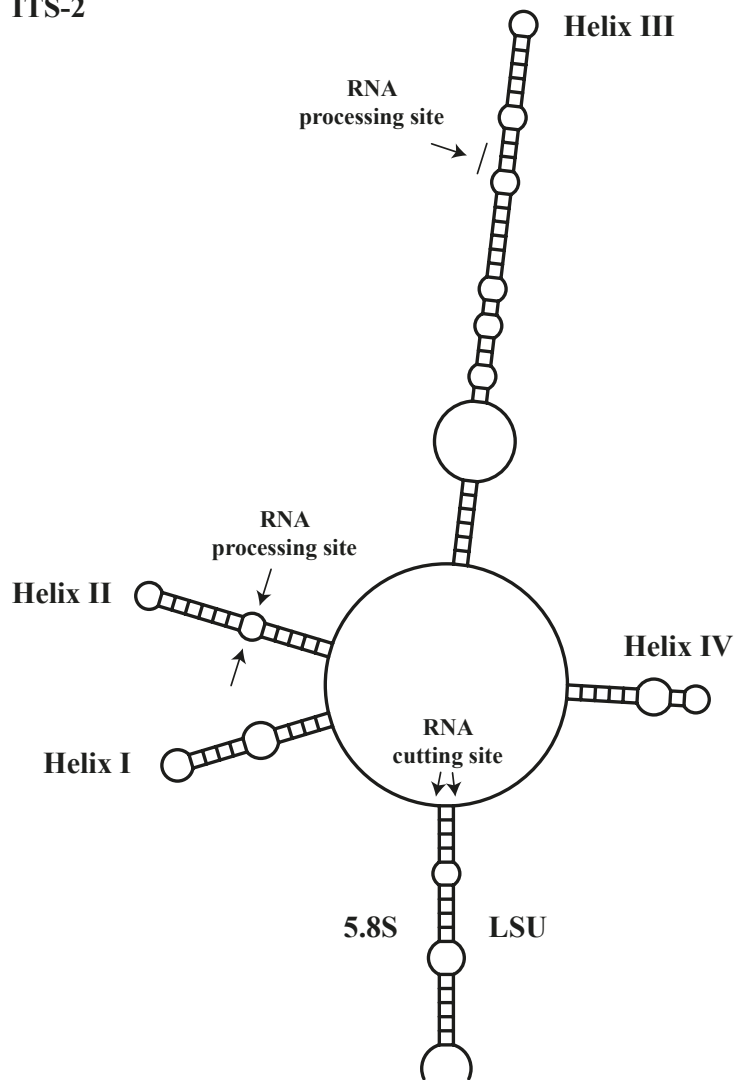
CUACUAACGAC

Helix IV

GC G
GGGGGA GC C
||| || |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium saccharophilum
Haplotype 3CSAR: Barcode-1d

ISBAL-007

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

CAA CU
UCGUC UUC \
•||| |||| C
GGCAG AAGG /
ACG UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||| ||||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483834-----44-4813883485424316-3361-3262248

BC

A CAG---- G C C U G U
GAC-G GC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| | || || | || •||| • ||• ||•||| |
CUG-C CG GG G-UC -CG UGAGCUG CCGU CAGAAG C
C UCAACCA G - A - A G

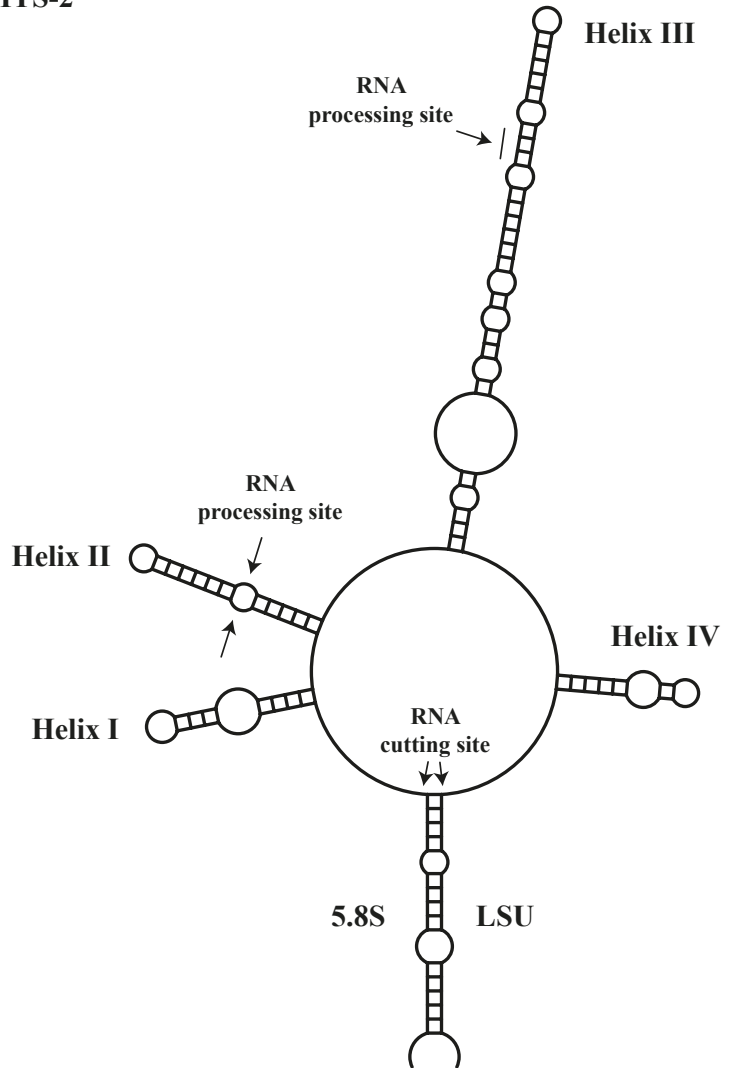
CUACCAACGAC

Helix IV

GC G
GGGGGA GC C
||| || |
CCCCCU CG A
AC A

UGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium saccharophilum
Haplotype 9CSAR: Barcode-1e

CCAP 264/2

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•||||| ||||| C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||||| ||||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483534-----44-4813883885424316-3361-3262248

BC

CAG---- U C CC U G U
GAC-GGGC CC C-AG -G GCUCGAU GGUA GUUUUC C
||| |•|| | | | | •|||||• ||• ||•||| |
CUG-CUCG GG G-UC -C UGAGCUG CCGU CAGAAG C
UCAACCA C - AA - A G

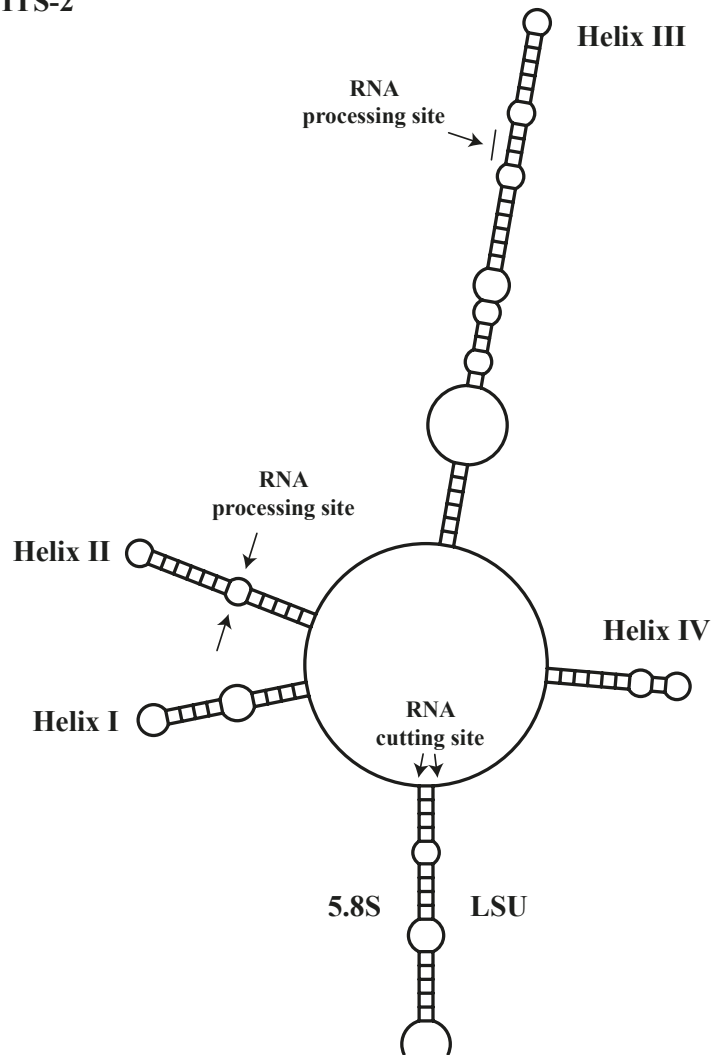
CUACCAACGAC

Helix IV

C G
GGGGGAG GC C
||||||| || |
CCCCCUC CG A
- A

CGACUCUCAUU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium saccharophilum
Haplotype 8CSAR: Barcode-1f

CCAP 211/58

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

CA CU
UCGUC CUUCC \
•|||| | C
GGCAG GAAGG /
AC UG

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••|||| |
GUCGUC GGGCGAC G
U A

CAGAACAGAC

Helix III

33333334-----44-4444444555555555-5666-6666666
34567890-----12-3456789012345678-9012-3456789

31483534-----44-4813883485424312-3361-3262248

BC

CAG---- A C C U G U
GAC-GGGC CC C-AG -GC GCUCGAU GGUA GUUUUC C
||| |•|| | | | | •|||| | |•| |•||| |
CUG-CUCG GG G-UC -CG UGAGCUA CCGU CAGAAG C
UCAACCA C - A - A G

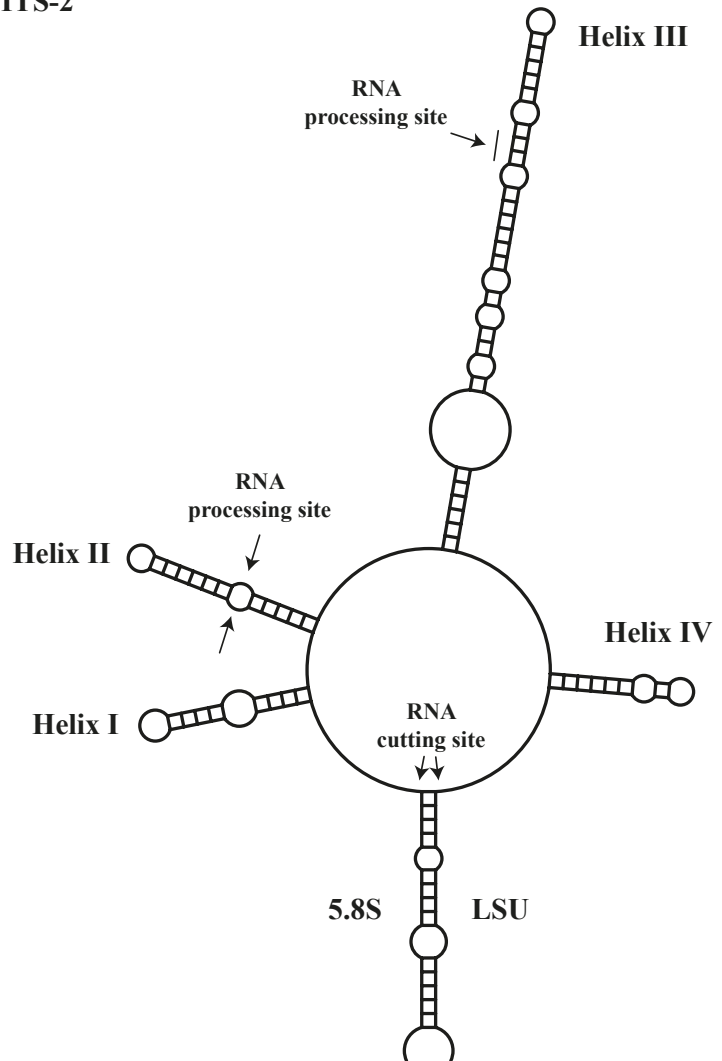
CUACCAACGAC

Helix IV

U G
GGGGGAG GC C
|||||| |
CCCCCUC CG A
- A

CGACUCUCAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium engadinense
Haplotype CENG: Barcode-2

SAG 812-1

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64144

BC

GC CU
UCACCC CUCC C
•||||| ||||| |
GGUGGG GAGG A
AA AC

AUC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG A
••||||| ||||| |
GUCGUC GGGCGAC A
U A

CAGACCAGAC

Helix III

3333333444-----444-44---44555555555-5666-6666666
3456789012-----345-67---89012345678-9012-3456789

5148323413-----261-34---53445428312-3361-3284448

BC

CCUCGC U AAA G U G U CU
GAC-GUGCAG UUA GC GGCCGCU GAU GGUA GU CCC A
•|| ||||| |•|| •|||•|| ||| ||•|| ||||| |
UUG-CACGUC AGU CG UCGGUGA CUA CCGU CA GGG G
AAC--- C GG- G C A U AC

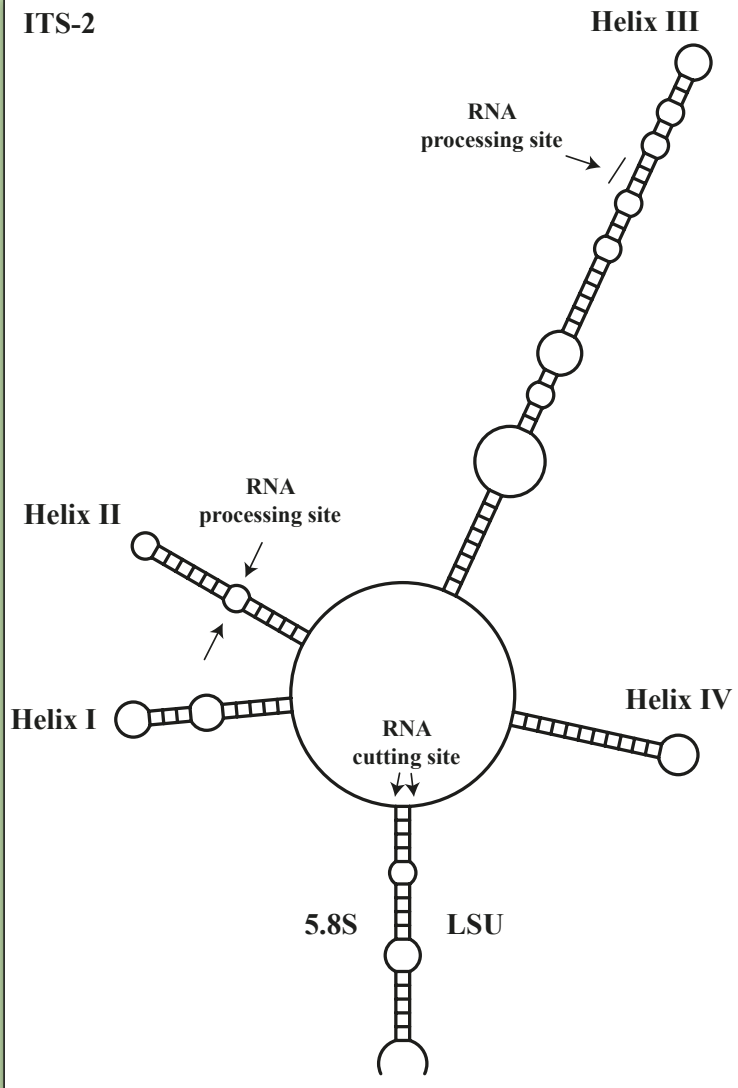
UCCAACCAC

Helix IV

CUA
GAGGGCAGUGGG \
||•||||||| C
CUUCCGUCACCC /
UCU

CUUCUCAGU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium viscosum
Haplotype CVIS: Barcode-3

SAG 56.87
MG-2

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64224

BC

AA CU
UCUUC CUC U
•||||| ||||| |
GGAAG GAGG A
CG CC

ACC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||||| ||||| |
GUCGUC GGGCGAC A
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

3148343413-----428--34---53445428312-3361-3284448

BC

- CCUCG UAU AAA G U G U CU
GAC GCGCAG CU GC GGCCGCU GAU GGUA GU CCC U
||| ||||| || || •|||•|| ||| ||•|| ||| |
CUG CGCGUC GA CG UCGGUGA CUA CCGU CA GGG G
C ACCA- C-- GG- G C A U AC

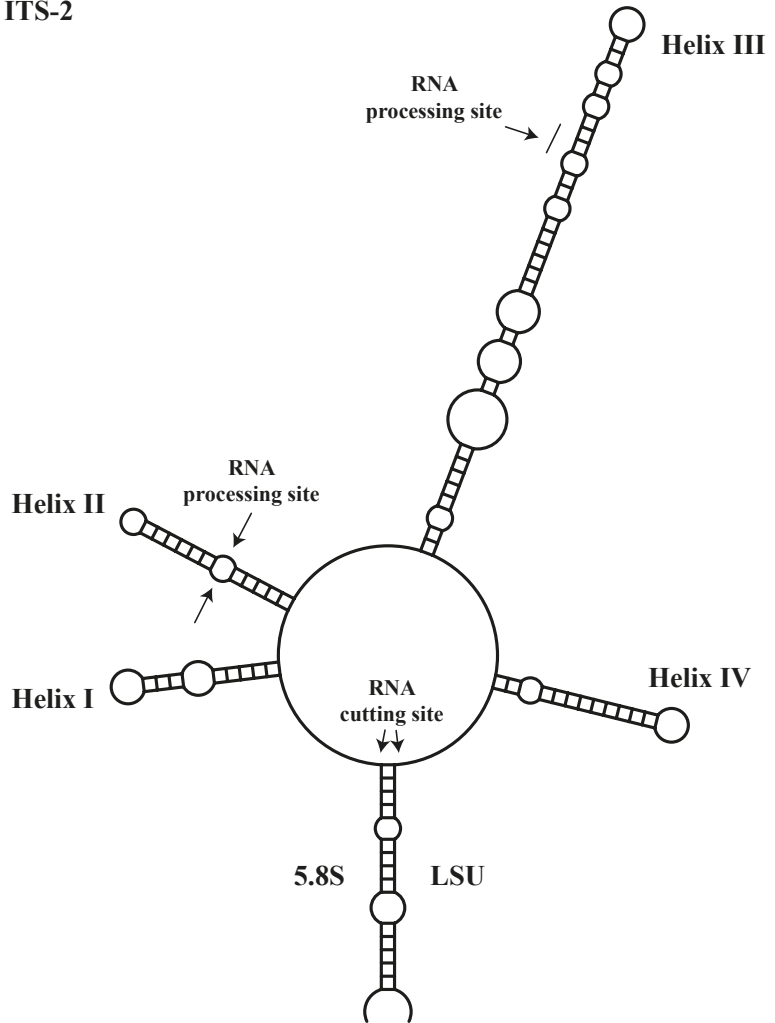
CAAACCAACC

Helix IV

C UU
GAG GGGCGAGGGG A
||| ||•|||||• |
CUC CCUGCUCCCU C
- CU

UCUCUCAGU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium ellipsoideum
Haplotype 1CELL: Barcode-4a

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

C
UCGUCUUUC U
•||||•||| |
GGCAGGAAG C
G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••|||| | ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

3148323413-----422--34---53234328314-3361-3224388

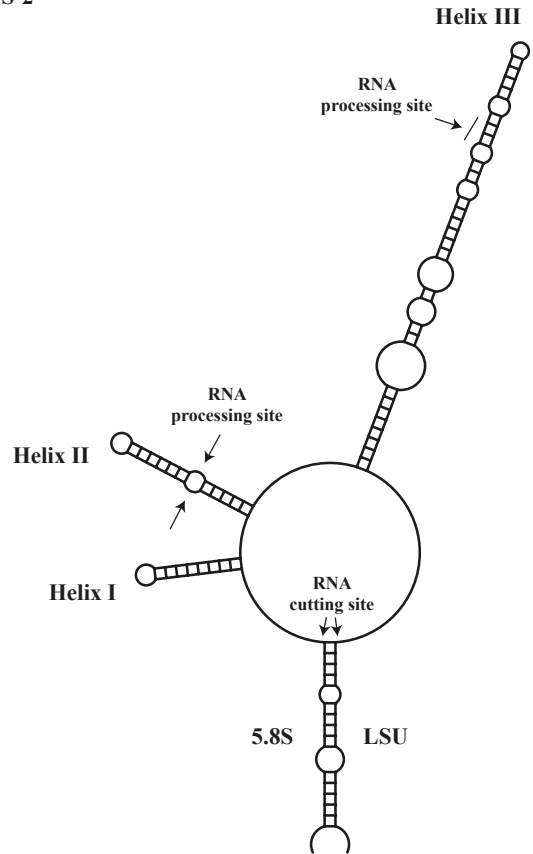
BC

CCUCG AC AGA G U G U
GAC-GUGCAG CUU GC GGUCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||||| ||| ||• ||||| U
CUG-CACGUC GAA CG UCAGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A U

CCGACCACACUCACUCAUAUU->

SAG 3.95
ISBAL-004
ISBAL-010
SAG 2143
CAUP H1949
SAG 2061
SAG 2142
SAG 2111
Fall/W-8

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium ellipsoideum
Haplotype 2CELL: Barcode-4b

SAG 2140
CCAP 211/76
ISBAL-005
ISBAL-006
ISBAL-009
CCAP 211/101

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

C
UCGUCUUUC U
•||||•||| |
GGCAGGAAG C
G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••|||| | ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---445555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

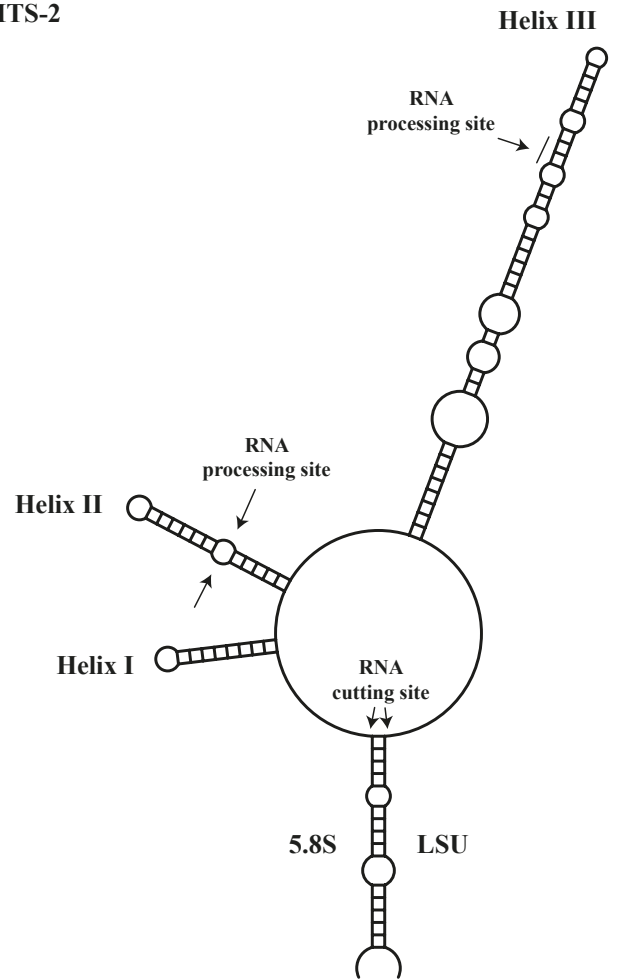
3148323413-----422--34---53263428314-3361-3224388

BC

CCUCG AC AGA G U G U
GAC-GUGCAG CUU GC GGUUGCU GAC GGUA GUUCG \
||| ||||| ||| || •||•||| ||| ||• ||||| U
CUG-CACGUC GAA CG UCAGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A U

CCGACCACACUCACUCAUAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium lichenum
Haplotype 1CLIC: Barcode-5a

SAG 2115
SAG 2144
CCAP 211/108
BII/B-9
BII/C-1
MG-4

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64384

BC

A C
UCG CCUUC U
•|| ||||| |
GGC GGAAG C
A G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||| ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

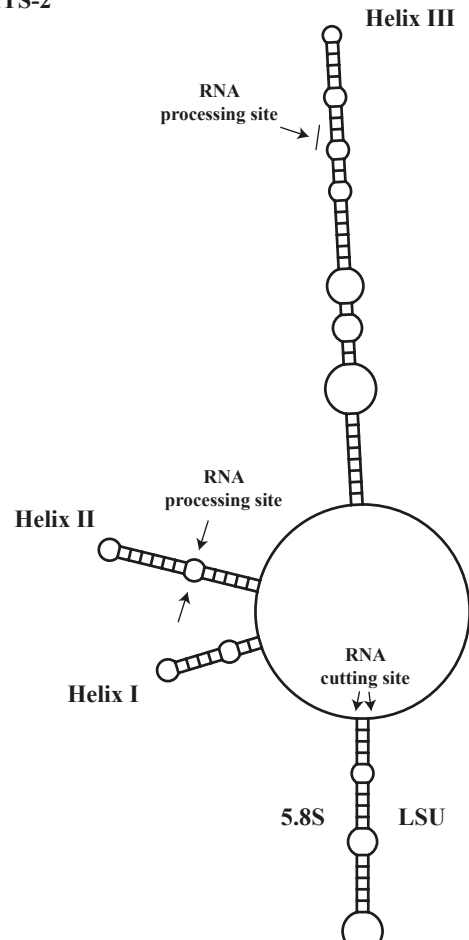
3148323413-----422--34---53443428314-3361-3264388

BC

CCUCG AC AGA G U G U
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||| ||| ||• ||•|| U
CUG-CACGUC GAA CG UCGGCGA CUG CCGU CAGGC /
AACAA- -- GG- G - A C

CUCCAAACACACUCACUCACAUCACAUU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 2CLIC: Barcode-5b

QII/C-5b

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

G A
UCGUCUC CUCCC \
•||||| ||||| C
GGCAGAG GAGGG /
G U

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||||| ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

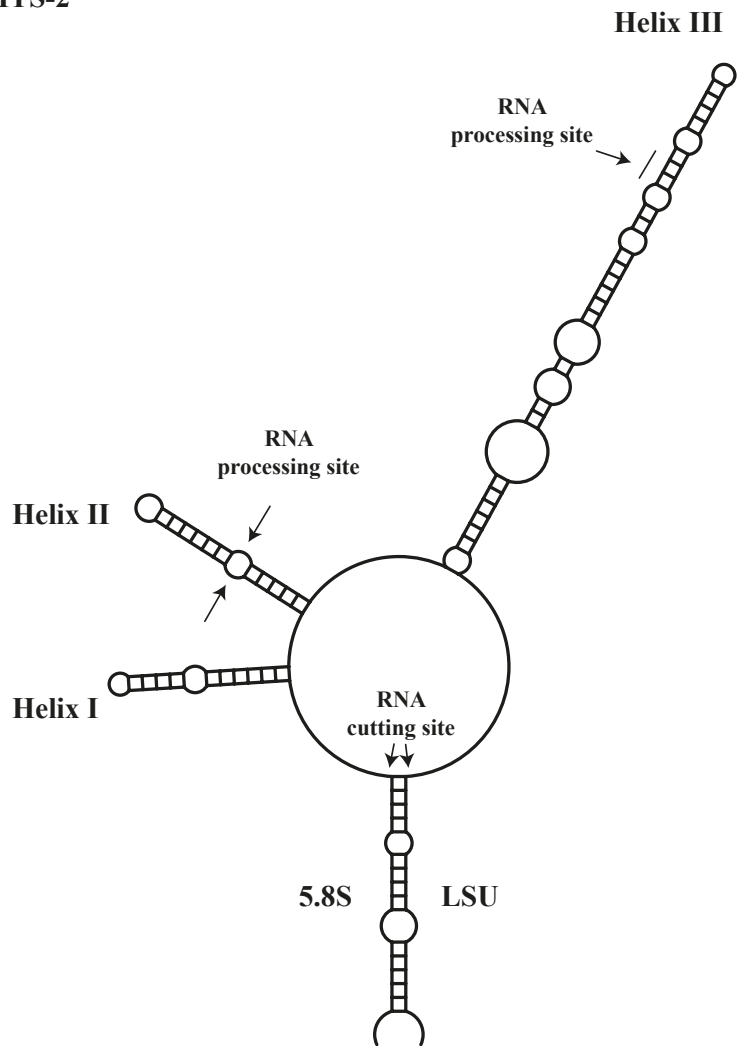
3848323413-----422--34---53443428314-3361-3224388

BC

A CCUCG AC AGA G U G U
G C-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
| | ||||| ||| || •||||| ||| ||• ||||| U
C G-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
C CACA- -- GG- G - A C

UCAUCCACUCACUCAAUU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 4CLIC: Barcode-5c

SAG 2293
SAG 2294

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64384

BC

C U
UCG CUUUCU U
•|| ||•||| |
GGC GAGAGGG C
A G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||| ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

3848323413-----422--34---53443428314-3361-3224388

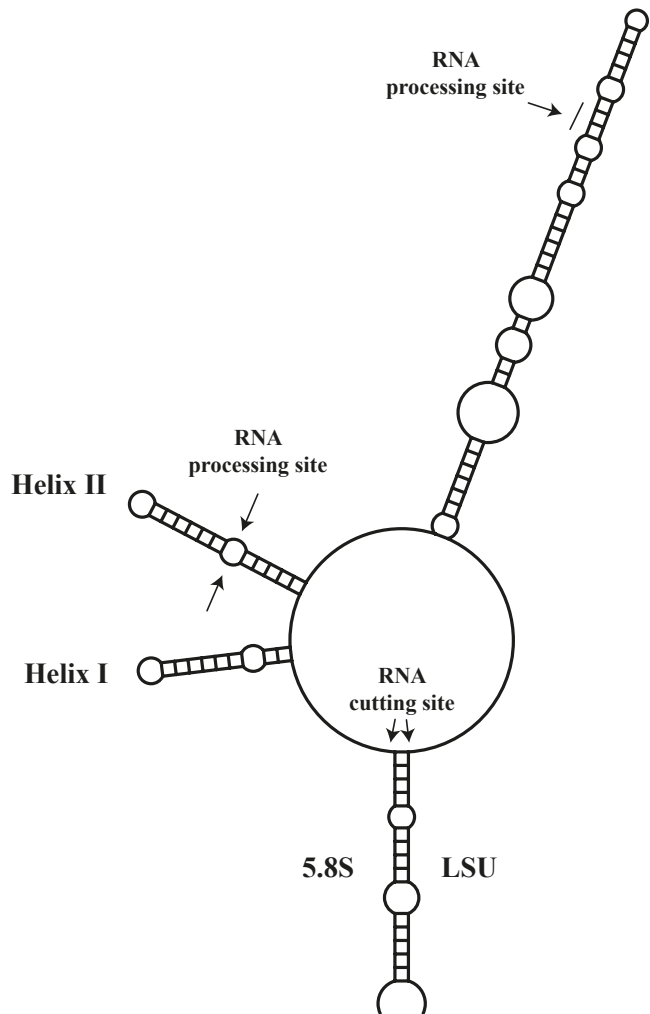
BC

A CCUCG AC AGA G U G U
G C-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
| | ||||| ||| || •||| ||| ||• |||| U
C G-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
G AACAC- -- GG- G - A C

UUCCAAACACUCACUCACAUU->

ITS-2

Helix III



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 3CLIC: Barcode-5d

AB-98017

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64324

BC

C C
UCGUCU UC U
•||||| • |||
GGCAGG AG C
A G

ACC

Helix II

22222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||||| ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

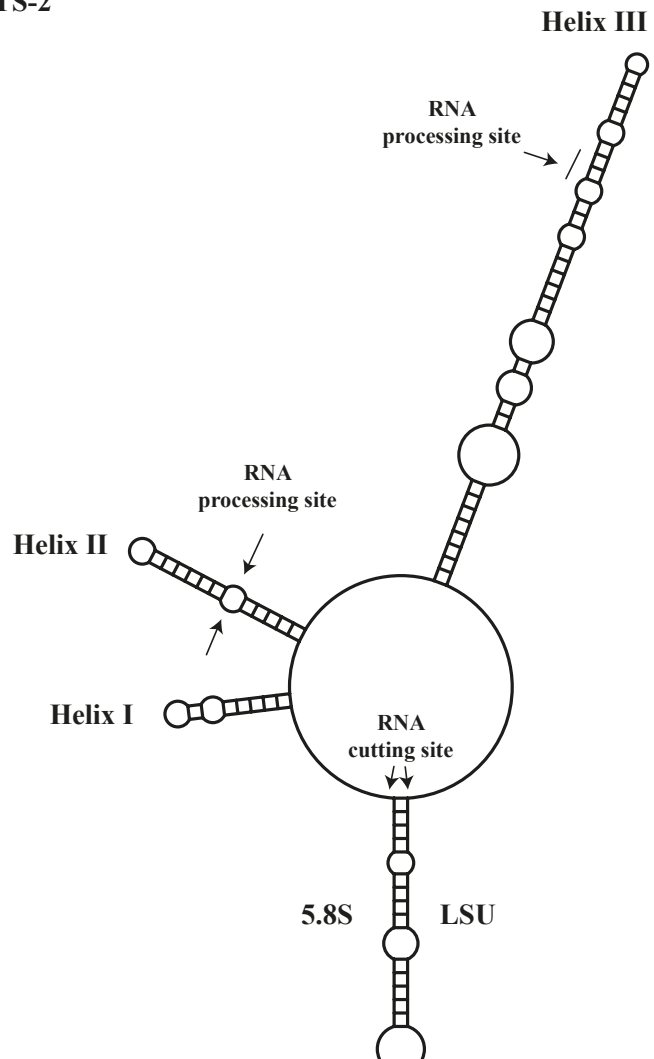
3148323413-----422--34---53443428314-3361-3224388

BC

CCUCG AC AGA G C G U
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||||| ||| |||• ||||| U
CUG-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A C

CCGACCACAACCACUCACAUU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 5CLIC: Barcode-5e

SAG 2141

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

C
UCGUCCUCCU U
•||||||| |
GGCAGGAAGGA C
G

ACC

Helix II

2222222333
23456789012

65343574443

BC

U G
UGGCGG CCCGCUG A
••|||• ||||| |
GUCGCU GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

3148323413-----422--34---53443428314-3361-3224388

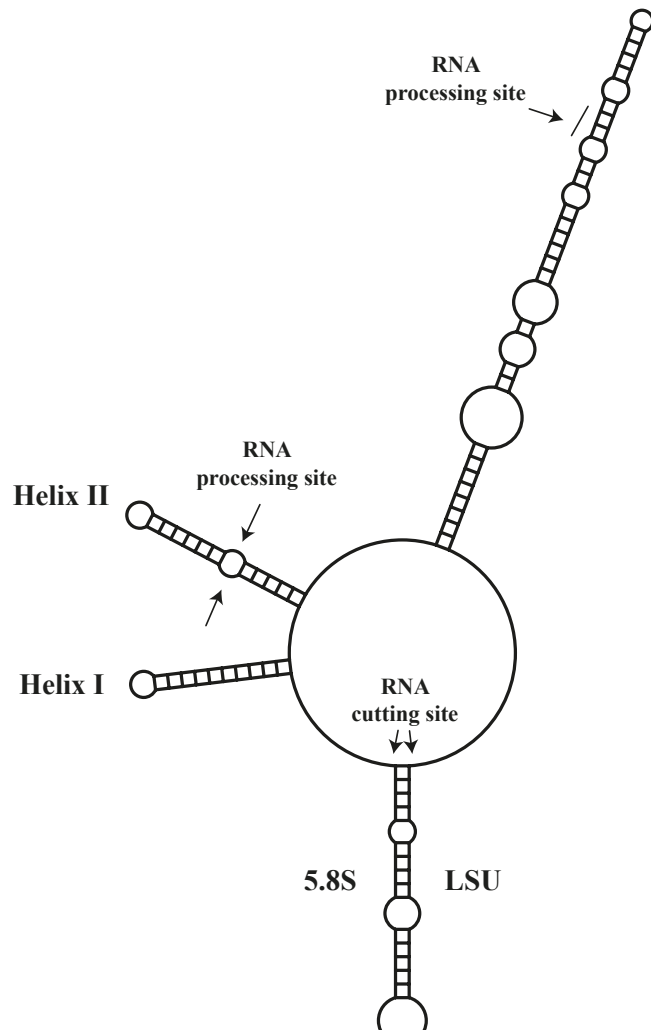
BC

CCUCG AC AGA G U G A
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||||| ||| ||• ||||| U
CUG-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A U

CAACCCACACUCACUCAU-->

ITS-2

Helix III



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 6CLIC: Barcode-5f

SAG 2041
CCAP 464/1
CAUP H1999-1
ISBAL-008

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCCUC

Helix I

11122
78901

64326

BC

C
UCGUUUUUC U
•|||••||| |
GGCAGGAAG C
G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||| | | | | | | |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---445555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

3148323413-----422--34---53443428314-3361-3224388

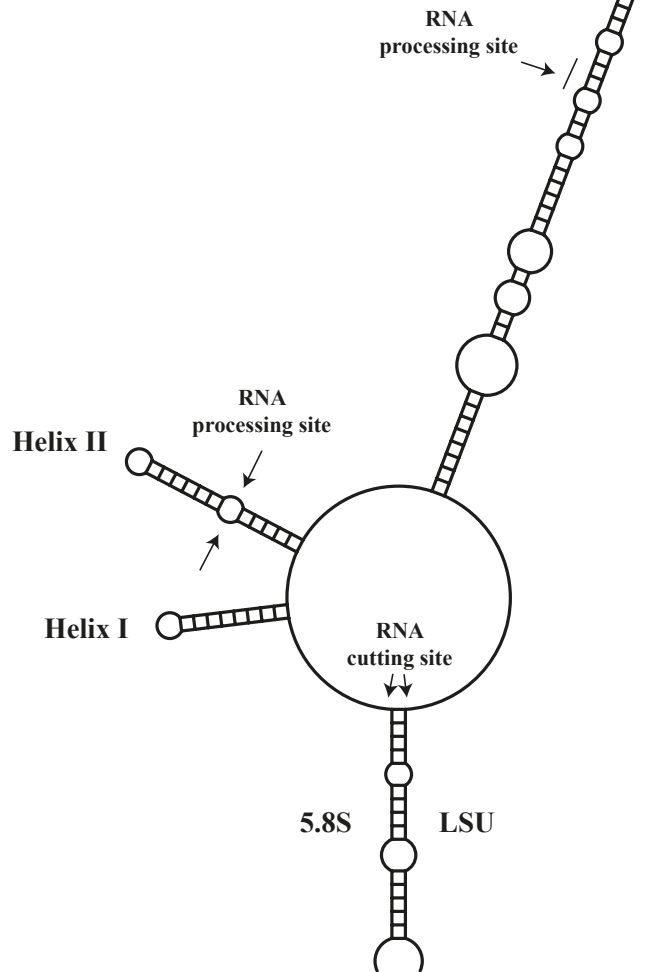
BC

CCUCG AC AGA G U G U
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||| ||| ||• |||| U
CUG-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
AACA- -- GG- G - A U

CCAACCACACUCACUCAUAUU->

ITS-2

Helix III



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 7CLIC: Barcode-5g

SAG 2295

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

C
UCGUCUUUC U
•||||•||| |
GGCAGGAAG C
G

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••|||| | ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

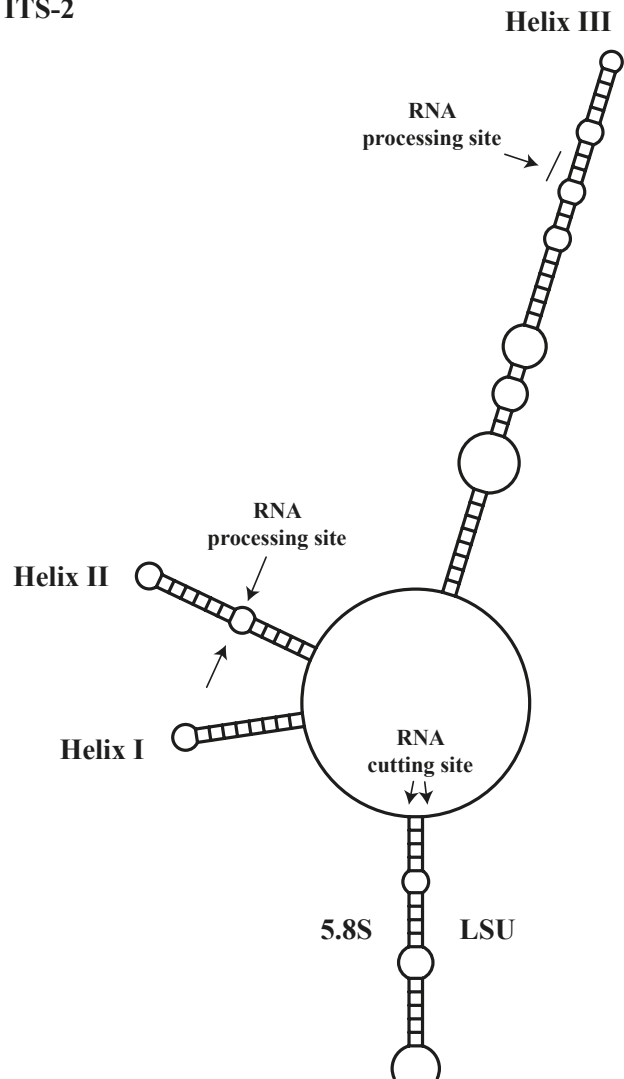
3148323413-----422--34---53443428314-3361-3224388

BC

CCUCG AC AGA G U G U
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
||| ||||| ||| || •||||| ||| ||• ||||| U
CUG-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A C

CCAACCCACACUCACUCAUAUU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium lichenum
Haplotype 8CLIC: Barcode-5h

CCAP 211/33

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| |||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64324

BC

U
UCGUCCUUCU C
•|||||||• |
GGCAGGAAGG A
C

ACC

Helix II

2222222333
23456789012

65343374443

BC

U G
UGGCGG CCCGCUG A
••||||| ||||| |
GUCGCC GGGCGAC G
U A

CAGAGCAGAC

Helix III

3333333444-----444--44---44555555555-5666-6666666
3456789012-----345--67---89012345678-9012-3456789

5148323413-----422--34---53443428314-3361-3224388

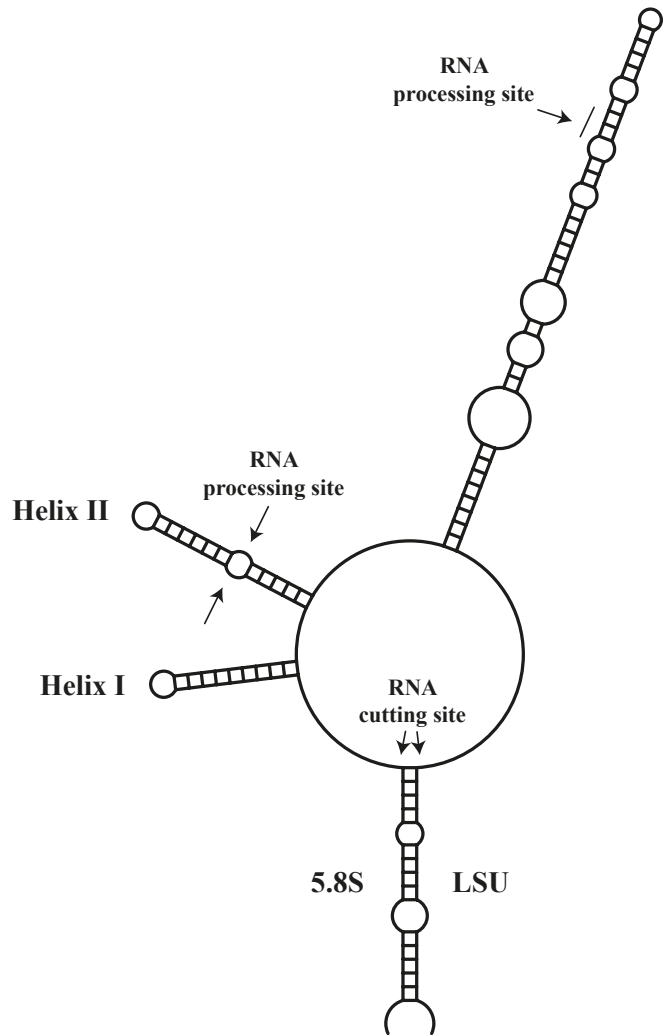
BC

CCUCG AC AGA G U G A
GAC-GUGCAG CUU GC GGCCGCU GAC GGUA GUUCG \
•|| ||||| ||| || •||||| ||| ||• ||||| U
UUG-CACGUC GAA CG UCGGCGA CUG CCGU CAAGC /
AACAA- -- GG- G - A U

CCAACCACACUCACUCAAUU->

ITS-2

Helix III



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium antarcticum
Haplotype CANT: Barcode-6

ISBAL-1013

5.8S/LSU stem

---000000--00011-11111
---123456--78901-23456

---234423--42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACCCUC

Helix I

11122
78901

64248

BC

C G
UCUC UCCUUC A
•||| ||||| |
GGAG AGGAAG A
A A

AUC

Helix II

2222222333
23456789012

65341374443

BC

U G
UGGCAG CCCGCUG C
••||| ||||| |
GUCGUC GGGCGAC G
U A

CAGACCAGAC

Helix III

333333-344-4444444-----4555555555-5666-6666666
345678-901-2345678-----9012345678-9012-3456789

814832-343-2311348-----3865423312-3361-3242688

BC

C G GCUCCC U G UA
-AC-GU GCG UGAAGC G-UGCUGGAU GGUA GUCUU \
|| || || ||||| | ••||| ||• | |||• C
-UG-CA CGC ACUUCG C-GUGACCUA CCGU CAGAG /
- G A----- U A CU

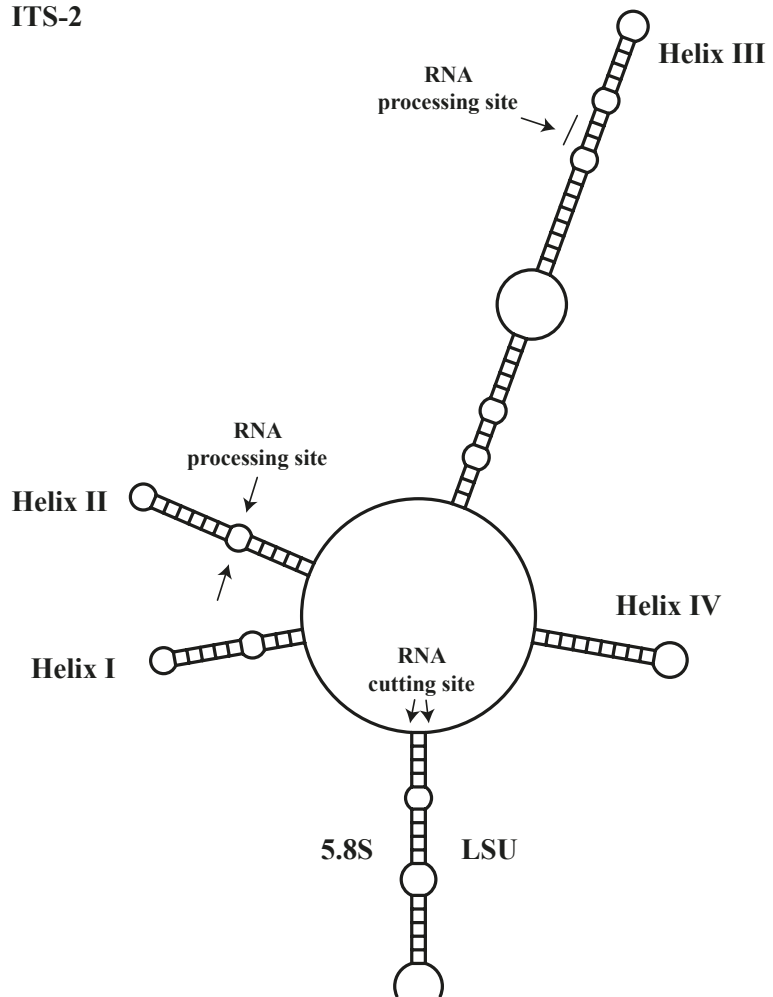
GAACAACCAA

Helix IV

GU
CCUGGGUCGU A
|||•|•||• |
GGACUCGGCG A
AA

CUUUCUCAGU->

ITS-2



Barcode legend:

- 1 = A-U
- 2 = U-A
- 3 = G-C
- 4 = C-G
- 5 = G•U
- 6 = U•G
- 7 = mismatch
- 8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloroidium arboriculum
Haplotype CARB: Barcode-7

MG-1
MG-3

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUUACCCCU

Helix I

11122
78901

64884

BC

UU -- U
UC CUGU CCUCGU C
•| |||| |||||•|
GG GACA GGAGCG A
CU UC G

ACC

Helix II

2222222333
23456789012

65364374483

BC

U A G
UGGUCG CC GCUG A
••|•|| || |||||
GUCGGC GG CGAC A
U G A

CAGCGCAGAGA

Helix III

333-3333444444444-----4555555555-5666-6666666
345-6789012345678-----9012345678-9012-3456789

312-4435446244324-----3488441318-3361-3651243

BC

G GACAGAC GG UU G A
GAU CCGGCCUCCGUC GC CCAGA GGUA GUGAUCG C
||| |||•||•||| || |||| ||•| |••||| |
CUA GGCUGGGAGGCAG CG GGUCU CCGU CGUAGC C
- AU----- AA UC A A

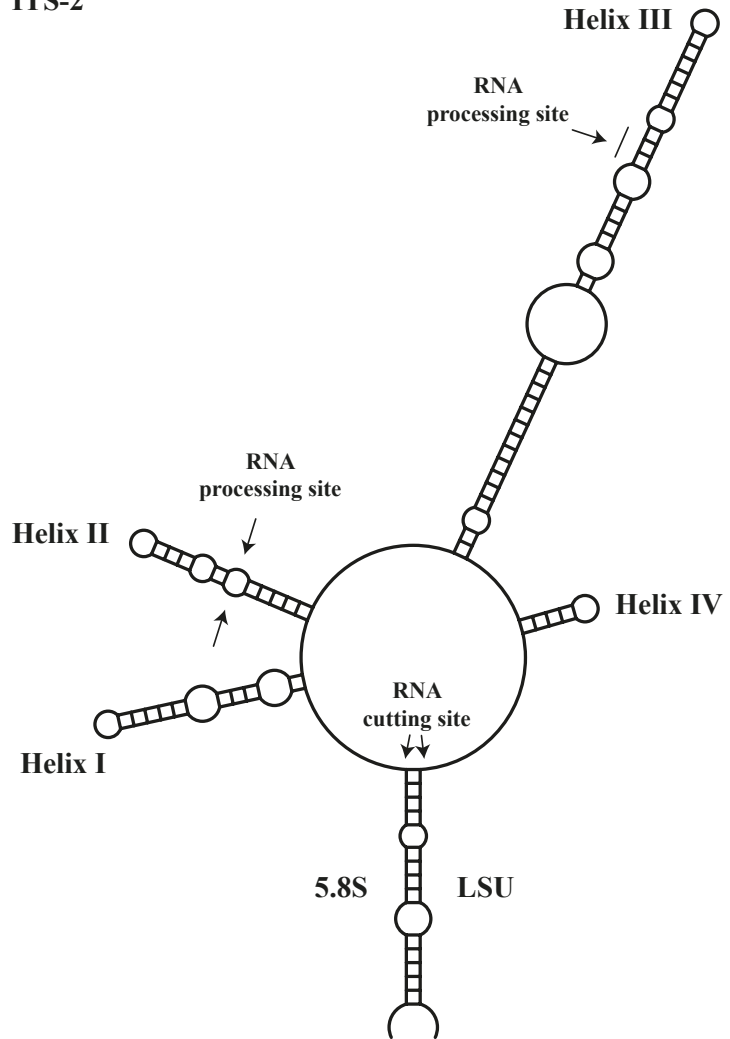
CCCUC

Helix IV

C
GAACC U
|||| |
CUUGG C
G

ACCCAUUCUCAGU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium laureanum
Haplotype CLAU: Barcode-8

CAUP H8501

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---234423---42413-32435

BC

GCA C- C
UGCCUG CUCAG GUCGG->
||||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UUGACUCCA

Helix I

11122
78901

64324

BC

UCG CU
UCGUC CUUCC \
•|||| ||||| C
GGCAG GAAGG /
UUG CG

AUC

Helix II

2222222333
23456789012

65364374443

BC

U G
UGGUCG CCCGCUG A
••|•| ||||| |
GUCGGC GGGCGAC G
U A

CAGCGCAGAGU

Helix III

33333334--44444444-----455555555-55666-6666666
34567890--12345678-----901234567-89012-3456789

31288435--43424324-----348844131-83361-3615243

BC

A- A- GACAGAC GG UU G C
GAU -CGG CGCUCGUC GC CCAGA GGUA GUAGUCG U
||| ||• ||||| || ||||| ||• |•|•||| |
CUA -GCU GCGAGCAG CG GGUCU CCGU CGUUAGC C
-- AA AC----- AA U- A A

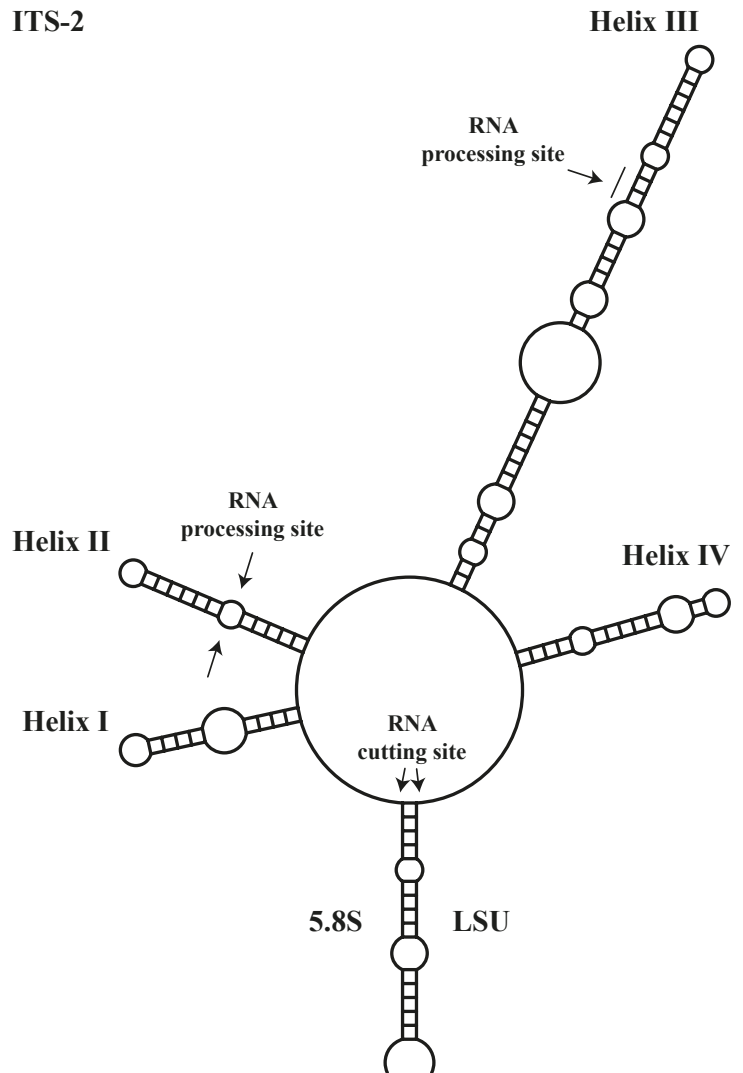
CAGCA

Helix IV

- C
GGGCG GGGGACUGGC A
|•||| |•|||••|| |
CUCGC CUCCUGGUCG C
U G

AAACCUUCUCAGU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases

ITS-2 rRNA secondary structure model of
Chloridium lobatum
Haplotype CLOB: Barcode-9

CAUP H8502

5.8S/LSU stem

---000000---00011-11111
---123456---78901-23456

---236423---42413-32435

BC

GCA C- C
UGUCUG CUCAG GUCGG->
||•||| ||||| ||||•
ACGGAC GAGUC CAGCU<-
AGA UU -

->UCGACAUUC

Helix I

11122
78901

64524

BC

CCU C C
UCGUCC GCG CCGC C
•|•||| ||| |||||
GGUAGG CGC GGCG C
CCU A G

AUC

Helix II

2222222333
23456789012

65344374443

BC

U CA
UGGCCG CCCGCU C
••||| ||||| |
GUCGGC GGGCGA U
U CC

CAGCACAGAGU

Helix III

33333334444444---44-----4555555555-5666-6666666
34567890123456---78-----9012345678-9012-3456789

31485435435246---44-----3428441318-3361-3255243

BC

GUU GACAGC G UU G A
GAC-GCGGCGGUCU CC GCU CCAGA GGUA GUGGUCG A
||| •||•||•||• || ||| ||||| ||•| ||••||| |
CUG-UGCUGCUAGG GG CGA GGUCU CCGU CAUAGC U
--- AC--- G UC A C

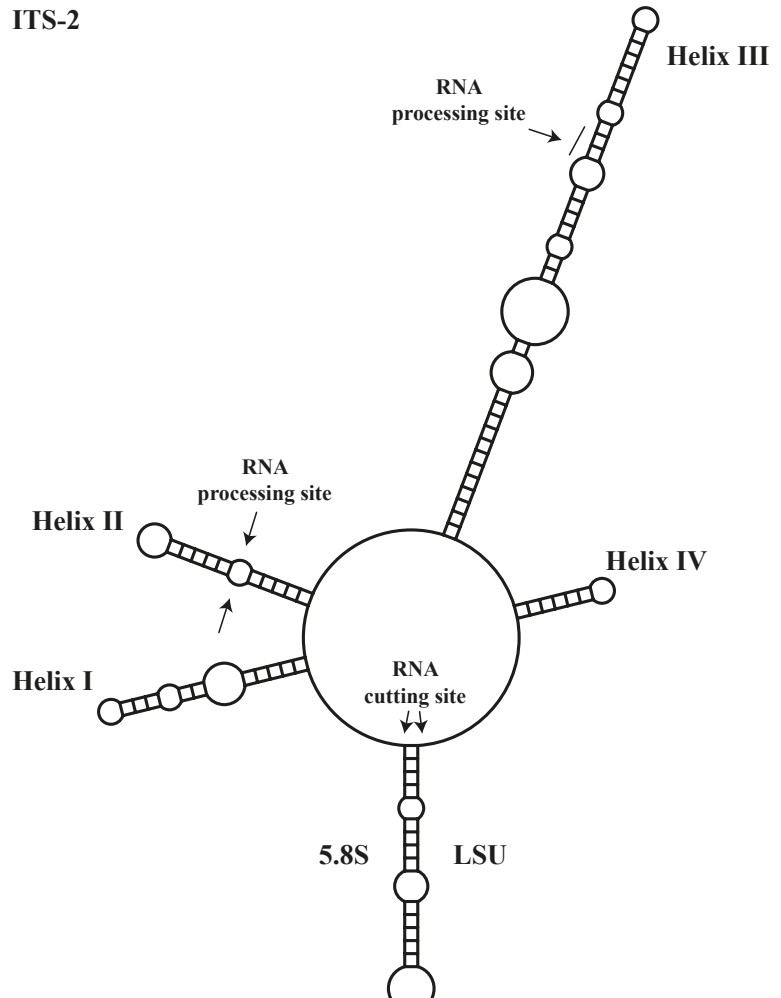
CGCUCG

Helix IV

U
GAGGGAG C
||| ||| |
CUCCUC C
G

ACUCUUUCUCAAU->

ITS-2



Barcode legend:

1 = A-U

2 = U-A

3 = G-C

4 = C-G

5 = G•U

6 = U•G

7 = mismatch

8 = deletion, single or unpaired bases