Supplemental Material S2, Zhang et al. (2009)

Sequence of fragments corresponding to *Cucurbita sp.* 5S (n=116) and 5.8S (n=1) ribosomal RNA*:*

Blue, green, magenta: identical; red: mismatch

Corresponding to 5S ribosomal RNA:

```
>85_17_2s             1-81   AAGGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>II_85_30_F8_2s       1-80   AAGGGTGCGATCATACCAGCACTAATGCACCGGG--ATCCCC-ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_15_1s             1-79     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>85_41_3s             1-79     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>II_85_11_II_2s       1-79     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTCGGGCGAGAGT---AGTACT
>85_14_2s             1-79     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCATGCTTGGGCGAGAGT---AGTACT
>II_85_12_2s          1-79     GGGTGCGATCAGACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTCGGGCGAGAGT---AGTACT
>85_20_3s             1-79     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>85_35_4s             1-79     GGGTGCGATCATACCAGCACTAGTGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>85_36_2s             1-79     GGGTGCGATCATACCAGCACTAAAGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACT
>II_85_27_II_3s       1-79     GGGTGGGATCAAGCCAGCACTAATGCTCCGG---ATCCC-TACAGAACTCCGC---CATTAAGCTTGATTTGGCCAGAGT---AGTAAT
>II_85_33_F10_2s      1-79     GGGGTGCGATCATACCCAGCACTAATGCACCGGGATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_6_E6_2s        1-79     GGGTGCGATCATACCGGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAGGCGTGCTTGGGCGAGAGT---AGTACT
>85_14_2s             1-77     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCATGCTTGGGCGAGAGT---AGTACT
>85_45_4s             1-77     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTA
>II_85_4_E4_2s        1-77     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_15_E12_3s      1-77    AGGGTGCGATCATACCAGCACTAATGCACCGG---ATCCA--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_45_G7_2s       1-77     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAAACTCCCGCAGTTTAAGCGTGCTTGGGGCGAG----AGT
>II_85_15_E12_4s      1-76     GGGGTGCGATCATACCAGCACTAATGCACCGG--ATCC---ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_4_4s              1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_15_3s176          1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_35_1s176          1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_16_F1__1s      1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_28_2s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_1_4s176           1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_43_II_2s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_16_4s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_38_1s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_1_E2__2s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_51_3s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCGTGGGCGAGAGT---AGT
>85_4_3s              1-76     GGGTGCGATCATACCAGCACAAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_3_E3_1s        1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_3_II_4s        1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_30_F8_1s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_16_F1_2s       1-76     GGGTGCGATCATAGCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_95_4_2s           1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCTC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_38_3s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>I_85_72_H12_1s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_24_F5_1s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_33_F10_1s      1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_29_2s             1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_22_F4_2s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_51_1s             1-76     GGGTGCGATCATACCAGCACTAATGCACCAG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>85_46_2s             1-76     GGGTGCGATCATACCAGCACTAAAGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_27_II_4s       1-76     GGGTGCGATCATACCAGCACTAATGCTCCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_43_II_3s       1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGC
>II_85_43_G5__1s      1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGC
>II-85-49_G9_2S       1-76     GGGTGCGATCATACCAACACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGTGAGT---ACC
>II-85-50_G10_2s      1-76     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGTGAGT---ACA
>85_19_2s             1-75     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AG
>85_21_2s             1-75     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AG
>85_22_2s             1-75     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AG
>85_26_1s             1-74     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--ATGTTAAGCGTGCTTGGGCGAGAG---T
>85_6_3s              1-73     GGGTGCGATCATACCAGCCCTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTCCCCCCCCTTGGGCGAGAGT
>85_1_2s              1-73     GGGTGCGATCATACCAGCACTAAAGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>I_85_62_II_2s        1-73     GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGCTAAGCGTGCTTGGGCGAGAGT
>I_85_62_H9_2s        1-73     GGGTGCAATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_33_3s             1-73     GGGTGCGATCATACCAGCACTAACGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
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>85_12_3s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_43_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_6_1s              1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_12_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_46_3s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_51_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_17_3s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCATGTTTGGGCGAGAGT
>II_85_13_E10_3s      1-73    GGGTGCGATCATACCACCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--ATTTAACCGTGCTTGGCCGAGAGT
>85_16_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85     13_II_2s   1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85_28_F7_1s       1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_9_4s              1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_42_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_42_1s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_40_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_37_2s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_28_1s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_14_3s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_1_1s              1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85_1_E2_1s        1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85_44_II_4S       1-73    GGGTGCGATCATACCAGCCCTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTCCCCCCCTTGGGCGAGAGT
>II_85_13_II_3s       1-73    GGGTGCGATCATACCAGCACTAAAGCACTGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>I_85_62_II_3s        1-73    GGGTGCAAGCAGTACAGCACTAATGCGGCGG---ATCCC--ATCAGAACTACGC--AGTTAAGCGTGGTTTGGCGAGAGT
>85_44_1s             1-73    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAAT
>II_85_13_E10__2s     1-72    GGGTGCGATCATACCAGCACTAAAGCACTGG---ATCCC--ATCAGA-CTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>85_7_3s              1-72    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAG-
>85_28_3s             1-72    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAG-
>85_50_2s             1-71    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGA--
>85_35_3s             1-71    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGA--
>II_85_35_F11_3s      1-74    AGGTGCGATCATACCAGCACTAAATGCACCC-GGATCCC--ATCAGACCTCCC---AGTTAACCGTGCTTGGCGAAGAAT
>85_95_5_1s           1-72    GGGTGCGATCAAACCAGCACTAAT-CACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85_37_F12_2s      1-71    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ACCAGAACTCCT---AGTTAAGCGTGCTTGGGCG-GAGT
>II_85_37_F12_3s      1-71    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ACCAGAACTCCT---AGTTAAGCGTGCTTGGGCG-GAGT
>85_30_3s             1-72    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATTAAAACTGCGC--ACCTAAGCGTGCTTGGGCTAGAG-
>I_85_62_H9_3s        1-70    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCG---A=TTAAGCGT-CTTGGGCGAGAGT
>85_31_1s             1-67    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGC------
>II_85_8_E7_3s        1-69    GGGTGCGAACATACCAGCACTAATGCATTTGT--ATTCCC-ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGC------
>II_85_50_II_1S       1-67    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTAAAGCGTGCATGGGC------
>II_85_27_II_1s       1-67    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCATGGGC------
>II_85_38_G1__2s      1-77    GGGTGCGATCATACCAGCACTAATGGATCCG--GTTCCAACATCACAACTCTC--AAGTTAAGCTTGCTTGGGCGAGAGTC
>II_85_14_E11_2s      1-74    GGGTGCGATCATACCAGCACTAATGCACCGG---AT-CC-AATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGTC
>I_85_60_II_3s        1-74    GGGTGCGATCATACCAGCACTAATGCACCGG---ATGCC--ACCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGTC
>I_85_67_H10_2s       1-83    GGTCGCGAACATAGCAGCACTAATGCACCGG---ATCCC--ATCAGACCTCCTC--AGTTAAACGGGCTTGGGCAATAGTC-TGTA-----GTCAC
>85_30_1s             1-83    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAG-C-TGTA-----TGCACC
>85_6_2s              1-138   GGGTGCGATCATACCAGCACTAACGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGTC----------ATACTGAGTCGGATGACAATTTATTGAGTCCTCGTTTACAACCCCTCTGTAGTCACTATTAATT
>II_85_40_G2__3s      1-82    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGATAGT--AG-------CACGTTC
>85_95_5_2s           1-88    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAG-GT-----------GTTTGCCGAAAGTAGT
>II_85_49_1s          1-84    GGGTGCGATCATACCAGCACTCAAGCTCCGG---ATTACC-ATCAGACCGGCCC--AGCTAAGCGTGTTTG--------------------TACCTCTAGGCCCCATCAA
>II_85_27_F6_2s       1-71    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGC------C----------TGA
>II_85_44_G6_2s       1-64    GGCCGCGACAATGCCAGCACTAATGCACCGG---ATCCC--ATGAGGACCTCCTC-AGCTTA-----------------------------TCGTGCGT
>II_85_38_II_3s       1-73    GGTTACGACCACACCAGCGCTAATGCTCCCG---ATACC--ACCAGA-C-------AGTTA------------------------------CACTTGAGTGTGCTTGAGTAAGACT
>II_85_41_G3__3s      1-68    GGGTGCGATCATACCAGCACTAAAGGCACCCGG-ATCCC-AATCA-AACTCCCC--AATTTA-----------------------------AGCGTGGCTTG
>II_85_49_3s          1-70    GATCAAGATTGGACCAGTACTAATGCACCCT---ATTCC--ATCACGCCATTGC--ACTTAAGCGTGCTTGGACCAT---
>85_19_5s             1-30    ------------------------------------------------TCCGGC--AGTTAAGCGTGCTTGGGCGAGAGT
>II_85_43_G5_2s       1-76    GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGT
>II_85_42_G4_2s       1-77    -GGTGCGATCA-ACCGGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAGGCGTGCTTGGGCGAGAGT---AGTACT-----------------------------------------
>85_3_3s              1-45    -------------------------------------CC--ATTAGAAATAAGA--AAATAAACGTGCTTGGGCGAGAGT---AGTACT-----------------------------------------
>II_8535_F11__2s      1-66    --------------------------------------------------------AGTTAAGCGTGCTTGGGCGAGAGT---AGTACTAAGTTGGGTGACCACTTGGGAAGTCCTCGTGTTGC------
>85_28_4s             1-71    --------------------------------------------------------AGTTAAGCGTGCTTGGGCGAGAGT---AGTACTAAGTTGGGTGACCACTTGGGAAGTCCTCGTGTTGCATCCCT
```

Reference sequence (assembled by the uncovered sequences):

```
5S RNA C. max         1-120   GGGTGCGATCATACCAGCACTAATGCACCGG---ATCCC--ATCAGAACTCCGC--AGTTAAGCGTGCTTGGGCGAGAGT---AGTACTAAGTTGGGTGACCACTTGGGAAGTCCTCGTGTTGCATCCCT
```

Corresponding to 5.8S ribosomal RNA

```
>85_2_1s              1-82       GTAGCGAAATGCGATACTTGGTGTGAATTGCAGGATCCCGCGAACCACCGAGTCTTTGAACGCAAGTTGCGCCCGGAGCCTT
```

Reference sequence: Cucumis pepo 5.8S ribosomal RNA (AJ488214) (163 bases):

```
caacgactctcggcaacggatatctcggctctcgcatcgatgaagaacgtagcgaaatgcgatacttggtgtgaattgcaggatcccgcgaaccaccgagtctttgaacgcaagttgcgcccggagccttctggccgagggcacgtctgcctgggcgtcacgc
```

Sequence of fragments (n=110) corresponding to *Cucurbita sp.* 18S ribosomal RNA*:*

Blue, green, magenta, orange, brown: identical; **red**: mismatch/not found.

Matching from 1 to 76 (note the 27 additional Arabidopsis 18S RNA nucleotides at 5` end, brown):

```
>85_38_2s             1-76       TACCTGGTTGATCC-TGCCAGTAGTCATATGCTT-GTCTCAAAGATTAAGCCATGCATGTGTAAGTATGAACTAATTC
>85_41_2s             1-72       TACCTGGTTGATCC-TGCCAGTAGTCATATGCTT-GTCTCAAAGATTAAGCCATGCATGTGTAAGTATGAACTA----
>85_45_3s             1-73       TACCTGGTTGATCC-TGCCAGTAGTCATATGCTT-GTCTCAAAGATTACGCCATGCATGTGTAAGTATGAACTAA---
>II_85_22_F4__3s      1-76       TACCTGGTTGATCCCTGCCAGTAGTCATATGCTTTGTCTCAAAGAATAAGCCATGCATGTGTAAGTTTGAACT-----(CTG)
```

Matching from 113 to 174:

```
>85_16_5s             1-62       ATAGTTTGTTTGATGGTATTTGCTACTCGGATAACCGTAGTAATTCTAGAGCTAATACGTGC
```

Matching from 203 to 258:

```
>85_9_3s              1-56       ATTTATTAGATAAAAGGTCGACGCGGGCTCTGCCCGTTGCTCTGATGATTCATGAT
```

Matching from 267 to 373:

```
>II_85_22_F4_1s       1-59       AACT-GACGGATCGCACGGCCATCGTGCCGGCGACGCATCATTCAAATTTCTGCCCTATC-------------------------------------------------------
>II_85_18_F2__2as     1-71       --------------------------------------------AAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACTATGGTGGTGACGGGTGACGGAGAATT
>II_85_19_F3__2s      1-68       -------------------------------------(TAA)--AAA-TTCTGCC-TATCAACTT-CGATGGTAGGATAGTGGCCTACTATG--GGGGACGGGTGA-GGAGAATT
```

Matching from 374 to 439:

```
>II-85-14_E11_1s      1-66       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCGC
>85_43_4s             1-66       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCGC
>85_14_4s             1-66       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCGC
>85_4_2s              1-66       AGGGTTCGATTCCGGAAAGGGAGCCTGACAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCGC
>I-85-67_H10_1s       1-66       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCAC
>85_43_1s             1-66       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAA-GGCAGCAGGCGCAC
>85_5_5s              1-62       --GGGTCGATTTCGGAGAGGGAGCCTAA-AAACGGCTACC-CATCCAAGGAA-GCCAGCAGGCGCGC
>II-85-15_E12_2s      1-68       AGGGTTCGATTCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAAGGCAGCAGGCGCGC--C
>I-85-67_H10_4s       1-68       AGGG-TCGAT-CCTGAAAGGGAGCCTGAGAAACG-C-AACACATCCAAGGAA-GGC-GCAGCGCGCC--(GTAGCAC)
```

Matching from 449 to 587:

```
>85_31_3s             1-60       AATCCTGACACGGGGAGGTAGTGACAATAAATAACAATACCGGGCTCTTCGAGTCTGGTA--------------------------------------------------------------------------------
>II-85-13_II_1s       1-67       ------------------------------------------------TCGAGTCTGGTAATTGGAATGAGTACAATCTAAATCCCTTAACGAGGATCAATTGGAGGGCAAGTCT-------------------------
>85_1_5s              1-60       -------------------------------------------------------------------------------AAATCCCTTAACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCC-GCGGTAATTCC
>I-85-70_H11_2s       1-60       -------------------------------------------------------------------------------AAATCCCTTAACGAGGATCAATTGGAGGGCAAGTCTGGT-CCAGCAGCCCGCGGTAATTCC
```

Matching from 633 to 707:

```
>85_23_2s             1-63       AGTTGGACCTT-GGGTTGGGTC-GATCGGTCCGCCTATGGTGAGCACCGATTGGCTCGTCCCTTC------------
>85_20_1s             1-64       AGTTGGACCTT-GGGTTGGGTC-GATCGGTCCGCCTATGGTGAGCACCGATTGGCTCGTCCCTTCT-----------
>85_4_5s              1-62       ------------TGGTTG-TTC-GATCGGTCCGCCTATGGAGAGCACCGATTGGCTCG-CCCTTCTGTCGGCGATGC
>85_35_2s             1-67       --------CTT-GGGTTGGGTC-GATCGGTCCGCCTATGGTGAGCACCGATTGGCTCGTCCCTTCTGTCGGCGATGC
>85_26_2s             1-66       ---------TT-GGGTTGGGTC-GATCGGTCCGCCTATGGTGAGCACCGATTGGCTCGTCCCTTCTGTCGGCGATGC
>42_28_2s             1-38       -------------------------------------TGGTGAGCACCGATTGGCTCGTCCCTTCTGTCGGCGAT--
>II-85-48_G8__3S      1-111      --------CTT-GGTTGGG-TCCGATCGGTCCGCCTATGGTGAGCACCGATTTGCTTGCCCCTTCCGTTAGCGATGC------------------(CTGTGGGCCCCATCAACATTGTAGGCACATTGACCTTTAAGAAA)
```

Matching from 720 to 796:

```
>85_19_1s             1-84       CCTCAAAAACTGGCCGGGTCGTGCCTCCGG-CGCTGTTACTTTGAAGAAATTAGAGTGCTCAAA-GCAAG-CCTACGCTCTGTATAC
>85_21_1s             1-84       CCTCAAAAACTGGCCGGGTCGTGCCTCCGG-CGCTGTTACTTTGAAGAAATTAGAGTGCTCAAA-GCAAG-CCTACGCTCTGTATAC
>85-22-1s             1-84       CCTCAAAAACTGGCCGGGTCGTGCCTCCGG-CGCTGTTACTTTGAAGAAATTAGAGTGCTCAAA-GCAAG-CCTACGCTCTGTATAC
>85_46_1s             1-73       -------AACTGGCCGGGTCGTGCCTCCGG-CGCTGTTACTTTGAAGAAATTAGAGTGCTCAAA-GCAAG-CCTACGCTCTGT----
>II-85-43_II_1S       1-69       -------AACTGGCCGGGTCGTGCCTCCGG-CGCTGTCACTTTGAAGAAATTAGAGTGCTCAAA-GCAAG-CCTACGCT--------
>II_85_43_G5__3s      1-72       -------ATCTGCCCGGATCGTGCGTCCGGGCGCTGTCACTTTGAACAAATCAGGGTGATCAAACGCAAGGCCTACGCT--------
```

```
Matching from 797 to 934:
>II-85-38_II_2S       1-71       -----------------------------------------------ATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATTAACAGGGACAGTCGGGGGCATT
>85_10_3s             1-69       -----------------------------------------------ATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATTAACAGGGGCAGTCGGGGGCA--
>85_1_3s              1-71       --------------------------------------------ATCATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATTAACAGGGACAGTCGGGGGC---
>85_8_3s              1-69       -----------------------------------------------ATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATGGGAGTAACGATTAACAGGGGCAGTCGGCGGCA--
>85_17_1s             1-68       ----------------------------ATTAGCATGGGATAACATCATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATT----------------------
>II-85-13_E10_1s      1-62       ----------------------------------ATGGGATAACATCATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATT----------------------
>II-85-13_II_4s       1-62       ----------------------------------ATGGGATAACATCATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATT----------------------
>42_3s                1-77       ------------------------------------------------------------------------------------------AATGATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>I-85-62_H9_1S        1-74       ---------------------------------------------------------------------------------------------GATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>II-85-48_G8_2S       1-96       (ATCAATATCGTAAAAAAAAATGCAA) --------------------------------------------------------------------TAACAGGGACAGTCGGGGGCATTTGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>85_15_2s             1-77       ------------------------------------------------------------------------------------------AAAGATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>II-85-48_II_1S       1-67       ----------------------------------------------------------------------------------------------------AGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>85_34_3s             1-67       ----------------------------------------------------------------------------------------------------AGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>II-85-6_E6_1s        1-71       --------------------------------------------------------------------------------------------TGATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGAC----
>85_9_2s              1-75       --------------------------------------------------------------------------------------------TGATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>I-85-70_H11_1s       1-74       ---------------------------------------------------------------------------------------------GATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCGGAGGTGAAATTCTTGGATTTATGAAAGACGAAC
>85_33_2s             1-70       ---------------------------------------------------------------------------------------------GATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTCGGATTTATGAAAGAC----
>42_G4_1s reverse     1-71       --------------------------------------------------------------------------------------------TGATTAACAGGGACAGTCGGGGGCATTCGTATT-TCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGAC---

Matching from 1084 to 1126:
>II_42_83_D3__2s      1-43       ATGAGAAATCAAAGTCTTTGGGTTCCGGGGGGAGTATGGTCGC

Matching from 1141 to 1185:
>85_31_2s             1-47       (AG)--T-AAGG-ATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTT

Matching from 1211 to 1354:
>85_9_1s              1-79       ------ACCAGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_13_1s             1-79       ------ACCAGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTCCTT-----------
>I-85-72_H12__2s      1-76       --------AGGTACCAGACCTAGTAAGGATTGACAGTCTGAGAGCTCTTTTCTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTC-------------
>II-85-35_F11__1s     1-76       ---------AGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_26_3s             1-75       ---------AGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCT------------
>85_45_2s             1-76       ---------AGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTCT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-37_F12_1s      1-76       ---------AGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_15_4s             1-76       ---------AGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>I-85-60_II_2S        1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-27_II_5S       1-70       ---------------AGACATAGTAAGGATTGACAGACTCAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_27_4s             1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_8_2s              1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_10_2as            1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-50_G10_1s      1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-49_G9__1S      1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-27_F6__1s      1-70       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_13_3s             1-70       ---------------ATACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-8_E7__1s       1-69       ----------------GACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II_85_41_G3__1s      1-69       ----------------GACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II_85_40_G2__1s      1-69       ----------------GACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_29_1s             1-66       -------------------ATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>85_27_1s             1-66       -------------------ATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-27_II_2S       1-64       ---------------------AGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-48_G8__1S      1-60       ------------------------AAGGATTGACAGACTGAGAGTTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCT------------
>II-85-50_II_2S       1-66       -------------------AAGTAAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTT-----------
>II-85-48_II_3S       1-61       ------------------------AAGGCTTGACAGACTGAGAGTTCTTT-CTTGATTCTATGGG-CGCCGG-CGCTTGCCCGTTCTT-----------
>II_42-19_II_2S       1-62       -----------------------AAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TACATGGCCGTTCTT-----------
>I-85-60_II_5S        1-61       ------------------------AAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TACATGGCCGTTCTT-----------
>85_27_3s             1-61       ------------------------AAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TACATGGCCGTTCTT-----------
>I-85-60_H8_1         1-61       ------------------------AAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TACATGGCCGTTCTT-----------
>II-85-49_2S          1-54       ---------------------AGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCAT---------------------
>I-85-62_II_1s        1-40       ------------------------AAGGATTGACAGCCTCAGAGATCTTT-CTTGTTTGTATGGG----------------------------------
>42up7_1s             1-45       ---------------------------------------GAGAGCTTTTTTCTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTT-------------
>85_13_4s             1-78       -------------------ATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTGG-TGCATGGCCGTTCTTAGTTGGTGGAGC
>I-85-62_H9__4S       1-83       ------------------------AAGGTTTGCCAGACGGAAAGCTATTT-CTGGATTCTAGGGG-GGGGGG--GCATGGCCGTTCTTATTTGGTGGAGC-------------(TGTTGGCACC)
>85_19_3s             1-88       ---------------AGACATAGTAAGGATTGACAGACTGAGAGCTCTTT-CTTGATTCTATGGG-TGGTG------------------------------------------(TAAAACGACGGCCAGTGAATTGTAATACGACTCA)
>85_3_1s              1-88      ---------------------AGTAAGGATTGACAGACTAAAGATCTTT-CTTGATT--------------------------------------------------------(AAGTTTGTTTATTTATGGGGTGTGCAGGGGTCCC-GTAGCAC-AACTAAAGGGA)
>85_2_2s              1-79       ---------------------------------------------------CTTGATTCTATGGG-TGGTGGG-GCATGGCCGTTCTTAGTTGGCGGAGCGCTTTGTCTGGTTAATTCCGTT--------------------(CTGCTGCACC)
>II_85_1_E2__3s       1-70       ----------------------------------------------------TTGATTCTATGGGGTGGTGGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTT--------------------------------
>II-85-44_G6__1s      1-77       ----------------------------------------------------------CTATGGG-TGGTGG-TGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCTC-----------------
>II-85-44_II_5S       1-76       ----------------------------------------------------------CTATGGG-TGGTGG-TGCATGGCCGT-CTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCTC-----------------
>85_7_2s              1-77       ----------------------------------------------------------CTATGGG-TGGTGG-TGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCTC-----------------
>II-85-44_II_1S       1-76       ----------------------------------------------------------CTATGGG-TGGTGG-TGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCT------------------
>85_4_1s              1-77       ----------------------------------------------------------------------------ATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCTCAGCCTGCTAACTAGCT-
>85_20_2s             1-77       ----------------------------------------------------------------------------ATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGCTAATTCCGTTAACGAACGAGACCTCAGCCTGCTAACTAGCT-
>85_5_2s              1-77       ----------------------------------------------------------CTATGGC-TGGTGGC-GCATGGGCGTTCTTAGTTGGTGGATCAATTTGCCTGTTTAATTCCGATCACTTACGAGACCTC-----------------
>42_27_2S             1-41       -------------------------------------------------------------TGGG-TGGTGG-TGCATGGCCGCTCTTAGTTGGTGGAGCGATT--------------------------------------------------
```

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>II_42-73_C12_1s      1-42       -----------------------------------------------------------TATGGG-TGGTGG-TGCATGGCCGTTCTTAGTTGGTGGAGCGAT---------------------------------------------------
```

Matching from 1426 to 1538:

```
>85_2_4s              1-63       --------------------------------------------------ACTGATGTATTCAACGAGTCTATAGCCTTGGCCGACAGGCCCGGGTAATCTTTGAAAATTCAT
>85_33_1s             1-71       AATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGATGTATTCAACGAGTCT------------------------------------------
```

Matching from 1589 to 1663:

```
>85_43_3s             1-75       ----AGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATT
>II-85-31_F9_2S       1-70       ----AGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCCTTGGTCCACACCGCCCGTCGTTCCTAC-----
>I-85-67_H10_3s       1-74       ----AGTAAGCGCGAGTCATCAGCTCGCGTTGACTACGTCCCTGCCTTTTGACCACACCGCC-GTCGCTCCTACTGATT
>42_8_3s              1-41       ---------------------------CGTTGACTACGTCCCTGCCCTTTGTACACACCGCCCGT--------------(TTT)
```

Matching from 1664 to 1707:

```
>42up2_2s             1-44       GAATGGTCCGGTGAAGTATTGGGATCGTGGCGACGTGGGCGGTT
```

Reference sequence (1757 bases): *Cucurbita pepo* 18S ribosomal RNA gene (GenBank acc # AF206895) plus the missing 26 bases (5′ end; brown underlined) from 5′ *A. thaliana* 18S rRNA (TAIR acc # AT3G41768):

TACCTGGTTGATCCTGCCAGTAGTCATATGCTTGTCTCAAAGATTAAGCCATGCATGTGTAAGTATGAACTAATTCAGACTGTGAAACTGCGAATGGCTCATTAAATCAGTTATAGTTTGTTTGATGGTATTTGCTACTCGGATAACCGTAGTAATTCTAGAGCTAATACGTGCAACAAACCCCGACTTCTGGAAGGGATG
CATTTATTAGATAAAAGGTCGACGCGGGCTCTGCCCGTTGCTCTGATGATTCATGATAACTCGACGGATCGCACGGCCATCGTGCCGGCGACGCATCATTCAAATTTCTGCCCTATCAACTTTCGATGGTAGGATAGTGGCCTACTATGGTGGTGACGGGTGACGGAGAATTAGGGTTCGATTCCGGAGAGGGAGCCTGAG
AAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAATTACCCAATCCTGACACGGGGAGGTAGTGACAATAAATAACAATACCGGGCTCTTCGAGTCTGGTAATTGGAATGAGTACAATCTAAATCCCTTAACGAGGATCAATTGGAGGGCAAGTCTGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTAT
ATTTAAGTTGTTGCAGTTAAAAAGCTCGTAGTTGGACCTTGGGTTGGGTCGATCGGTCCGCCTATGGTGAGCACCGATTGGCTCGTCCCTTCTGTCGGCGATGCGCTCCTGGCCTTAACTGGCCGGGTCGTGCCTCCGGCGCTGTTACTTTGAAGAAATTAGAGTGCTCAAAGCAAGCCTACGCTCTGTATACATTAGCAT
GGGATAACATCATAGGATTTCGATCCTATTCTGTTGGCCTTCGGGATCGGAGTAATGATTAACAGGGACAGTCGGGGGCATTCGTATTTCATAGTCAGAGGTGAAATTCTTGGATTTATGAAAGACGAACAACTGCGAAAGCATTTGCCAAGGATGTTTTCATTAATCAAGAACGAAAGTTGGGGGCTCGAAGACGATCAG
ATACCGTCCTAGTCTCAACCATAAACGATGCCGACCAGGGATTGGCGGATGTTGCTTTAAGGACTCCGCCAGCACCTTATGAGAAATCAAAGTCTTTGGGTTCCGGGGGGAGTATGGTCGCAAGGCTGAAACTTAAAGGAATTGACGGAAGGGCACCACCAGGAGTGGAGCCTGCGGCTTAATTTGACTCAACACGGGGAA
ACTTACCAGGTCCAGACATAGTAAGGATTGACAGACTGAGAGCTCTTTCTTGATTCTATGGGTGGTGGTGCATGGCCGTTCTTAGTTGGTGGAGCGATTTGTCTGGTTAATTCCGTTAACGAACGAGACCTCAGCCTGCTAACTAGCTATGCGGAGGAATCCCTCCGCGGCCAGCTTCTTAGAGGGACTATGGCCGCTTAG
GCCAAGGAAGTTTGAGGCAATAACAGGTCTGTGATGCCCTTAGATGTTCTGGGCCGCACGCGCGCTACACTGATGTATTCAACGAGTCTATAGCCTTGGCCGACAGGCCCGGGTAATCTTTGAAATTTCATCGTGATGGGGATAGATCATTGCAATTGTTGGTCTTCAACGAGGAATTCCTAGTAAGCGCGAGTCATCAGC
TCGCGTTGACTACGTCCCTGCCCTTTGTACACACCGCCCGTCGCTCCTACCGATTGAATGGTCCGGTGAAGTGTTCGGATCGTGGCGACGTGGGCGGTTCGCTGCCTGCGACGTCGCGAGAAGTCCACTGAACCTTATCATTGAGAGGA

Sequence of fragments (n= 105) corresponding to *Cucurbita sp.* 26S ribosomal RNA*:*

Colored sequences: identical; **red**: mismatch/not found

```
Matching from 219 to 277:
>II-85-3-II_1S           1-59    GCGCTCGGACCCTGTCGCACCACGAGGCGCTGTCAACGAGTCGGGTTGTTTGGGAATGC

Matching from 562 to 632:
>II_85_24_F5_-2s         1-68    -AAAGGG-TGTTGGTCGATTAAGACAGCAGGACGGTGGTCATGGAAGTCGAAATCCGCTAAGGAGTGTGT---
>85_34_2s                1-68    -AAAGGG-TGTTGGTCGATTAATACAGCAGGACGGTGGTCATGGAAGTCGAAATCCGCTAAGGAGTGTGT---
>85_5_4s                 1-73    CAAAGGGGTGTTGGTCGATTAAGACAGCAGGACGGTGGTCATGGAAGTCGAAATCCGCTAAGGAGTGTGTAAC

Matching from 675 to 749:
>85_95_5_3s              1-73    ATGTGTGCGAGTTAACGGGCGAGTAAACCCGTAAGGCGCAAGGAAGCTGACTGGTGGGATCCCTTTGTGGG-TT--
>II_85_16_F1_3s          1-62    ------------T-ACGGGCGAGTAAACCCGTAAGGCGCAAGGAAGCTGACTGGTCGGGTCCCTTTGTGGG-TTGC-
>II-85-33_F10_3s         1-64    -------------AACGGGCGAGTTAAACCGTAAGGCGCAAGGAAAGTGACCGGTGGGATCCCTTTGTGGGGTTGCC

Matching from 805 to 885:
>II-42-13_A6_2s          1-41    ACCCGAAAGATGGTGAACTATGCCTGAGCGGGGCGAAGCCA-------------------------------
>85_5_3s                 1-70    -----------GGTGAACTATGCCTGAGCGGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCCCGCAGCGATACTGACGTGC
>85_27_2s                1-61    --------------------TGCCTGAGCGGGGCGAAGCCAGAGGAAACTCTGGTGGAGGCCCGCAGCGATACTGACGTGC
>85_30_2s reverse        1-57    -------------------ATGCCTGAGCGGGGCGAAACCCTAGGAAACTCTGGTGGAGGCCCGCAGCGATACTGT-----
>85_19_4s                1-58    --------------------TGCCTGAGCGGG-CGAAGCCAGAGGAAACTCTGGTGGAGGCCCGCAGCGATACTGACGT--
>42_1_2s                 1-43    -------------------------GAGCGGGGCGAAGCCAGGGGAAACTCTGGTGGAGGCCCGCAGC-------------

Matching from 968 to 1029:
>II_85_44_II_2S reverse  1-63    GATAGCTGGAGCCCGCGTGCGAGTTTTATCGGGTAAAGCCAATGATTAGAGGCATCGGGGGCA

Matching from 1150 to 1206:
>II_42_97_D11_2s         1-54    ACGGCATGAACCGGAAGCCGGGTTACGGAGCCTAACTACGC-CT-----(GTCGGCTCAAT)

Matching from 1383 to 1451:
>85_36_4s                1-68    GCGGTGGTCGCTGCAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGCAGATCTTGGTGGT-
>85_45_1s                1-68    GCGGTGGTCGCTGCAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGCAGATCTTGGTGGT-
>85_50_3s                1-68    GCGGTGGTCGCTGCAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGCAGATCTTGGTGGT-
>85_13_2s                1-67    -CGGTGGTCGCTGCAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGCAGATCTTGGTGGT-
>85_7_1s                 1-68    GCGGTGGTCACTGCAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGCAGATCTTGGTGGT-
>II_42_11_A4_2s          1-40    --------------AAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTG---------------
>85_5_1s                 1-69    GCGGTGGTCACTGAAAAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGTAGCAGATCTTGGTGGTT
>42up2_1S                1-41    ---------------AAACCTTGGGCGCGAGCCCGGGCGGAGCGGCCATCGGTGC--------------

Matching from 1688 to 1736:
>II_42_84_D5_1s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-83_II_4S          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-85_D6_1s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-84_II_4S          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-18_II_4s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-42_II_4S          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II_85_5_E5_1s           1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-18_A8_1s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-42_B8_1s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II_42_83_D4_1s          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)
>II-42-85_II_4S          1-45    CTGTTTAACAGCCTGCCCACCC--------------------------------------(GTTTGGGCGGTTACAAATAGGGT)

Matching from 1739 to 1887:
>II_42_99_D12_1s         1-44    AGCGGCTGGAAGAGCATCGCACGTCGCGCGGTGTCCGGTGCGCC---------------------------------------------------
>II_42_76_D2_1s          1-44    AGCGGCTGGAAGAGCATCGCACGTCGCGCGGTGTCCGGTGCGCC---------------------------------------------------
>II_42_19_II_1S          1-24    ---------------ATCGCACGTCGCGTGGTGTCCGGG--------------------------------------------------------
>85_12_1s                1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>85_36_3s                1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>85_16_3s                1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>85_14_1s                1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCTTTGAAAAT------------------------------
>I_85_60_H8_2S           1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>I_85_60_II_1S           1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>85_36_1s                1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>I_85_60_II_4S           1-48    ---------------ATCGCACGTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>II_42_100_E1_2s         1-30    ---------------------------------TCCGGTGGGCCCCCGG-CGG-CCCTTGAAAAT------------------------------
>85_18_2s                1-59    -------------------------GCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAATCTGGAGGACCGAGTGCCTCCC---------
>85_18_1s                1-55    ----------------------GTCGCGTGGTGTCCGGTGCGCCCCCGG-CGG-CCCTTGAAAATCTGGAGGACCGAGT----------------
>II_42_63_C7_2s          1-48    ---------------------------------GCCTGTGTGCACCCAG-CGG-CCCTTGAAAAGCCGTAGGCGCCATCAAG-------------
>85_2_3s                 1-75    -----------------------------------------------------------------CGAGCGCCTCCAACGCCCGGTCGTCCTCATAACCGCTTCAAGTCTCCAAGGCGGACAGCCTCTGGTCGATGGAAC
>42_38_1s                1-45    -----------------------------------------------------------------------------------------------AACCGCATCAGGTCTCCAAGGTGAACAGCCTCTGGTCGATGGAAC
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Matching from 1990 to 2075:
>42_4_1s                 1-43    TGGTGGACTGCTCGAGCTGCTCCCGCGGCGAGAGCGGGTCGCT------------------------------------------
>II_42_93_D8_-2S         1-39    -------------------------------GAGCGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGA---------------
>II-42-91_D7_2s          1-39    -------------------------------GAGCGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGA---------------
>42_21_1s                1-42    ------------------------------AGAGCGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGAAC-------------
>II-42-91_D7_1s          1-43    ----------------------------------CGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGAACGGCTC--------
>42_31_3s                1-42    -------------------------------------------TGCGTGCCGGCCGGGGGACGGACTGGGAACGGCTCCTTCGGG
>II_42_93_D8_-IS         1-43    ----------------------------------CGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGAACGGCTC--------
>42up4_4s                1-43    ----------------------------CGAGAGCGGGTCGCTGCGTGCCGGCCGGGGGACGGACTGGGAA--------------

Matching from 2269 to 2309:
>II_42UP_41_H3_1s        1-41    AAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCAT
>42up4_1s                1-41    AAGGTAGCCAAATGCCTCGTCATCTAATTAGTGACGCGCAT

Matching from 2460 to 2500:
>85_18_3s                1-69    TTGTGAAATGACTTGAGAGGTGTAGGATAAGTGGGAGCCGAAAAGGCGAAAGTGAAAATACCACTACTT
>42_18_1s                1-39    ---------------------------TAAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_23_1s                1-39    ---------------------------TAAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_24_1s                1-39    ---------------------------TAAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_28_3s                1-39    ---------------------------TAAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_8_1s                 1-38    ----------------------------AAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_27_1S                1-38    ----------------------------AAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_31_1s                1-38    ----------------------------AAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_3_1s                 1-38    ----------------------------AAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>42_20_3s                1-38    ----------------------------AAGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>II_42_64_C8_2s          1-37    -----------------------------AGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>II_42_32_A12_2s         1-37    -----------------------------AGTGGGAGCCGAAA-GGCGAAAGTGAAA-TACCACTACT-
>II_42_37_B4_3s          1-38    ----------------------------AAGTGGGAGC-GAAAAGGCGAAAGTGAAA-TACCACTACT-

Matching from 2573 to 2686:
>42up2_3s                1-43    GCGGGCCGATCCGGGCGGAAGACATTGTCAGGTGGGGAGTTTT
>II_85_11_E8_2S          1-72    -----------------------ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGATGAGCTC---------
>II_85_12_E9_2S          1-71    ------------------------TTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGATGAGCTC---------
>II_85_11_II_1S          1-72    -----------------------ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGATGAGCTC---------
>II_85_12_1S             1-72    -----------------------ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGATGAGCTC---------
>II_85_12_3S             1-72    -----------------------ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCCGGTGTACTAAGATGAGCTC---------
>II_85_11_II_3S          1-91    -----------------------ATTGTCAGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCCGGTGTACTAAGATGAGCTC----------(CGTAGGCCCCATCAATAT)
>85_16_1s                1-75    -----------------------------AGGTGGGGAGTTTGGCTGGGGCGGCACATCTGTTAAAAGATAACGCAGGTGTCCTAAGATGAGCTCAACGAGAAC

Matching from 2695 to 2769:
>85_95_4_1s              1-75    AAAAGGGTAAAAGCTCGTTTGATTCTGATTTCCAGTACGAATACGAACCGTGAAAGCGTGGCCTATCGATCCTTT

Matching from 3221 to 3295:
>II_85_45_G7_1S          1-75    ATCCCCTGCGACGGATGAGTCTCAGGGGCTGCCTTGTAACGTAATTCCCACCGAGCGACGGGTAGAATCCTTTGC

Matching from 3344 to 3389:
>II_427_A2_2s            1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_10_2s                1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42up_1_4                1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42up_3_4s               1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42UP_8_2S               1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_37_2s                1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42up_8_4s               1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>II_42_51_B12_2s         1-45    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGTA
>II_4237_B4_2s           1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_6_1s                 1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>4231_4s                 1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42up2_5s                1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_26_1S                1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_33_2s                1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>42_21_3s                1-45    -CTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>II_427_A2_3s            1-44    --TGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCGT-
>II_426_a1_1s            1-31    ------------CACTGAGATTCAGCCCTTCGTCGCTCCGATT----
>42_24_3S                1-47    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCTTA
>42_38_2s                1-46    GCTGCCACGATCCACTGAGATTCAGCCCTTCGTCGCTCCGATTCAT-
>42_9_3s                 1-43    --TGCCACGATCCACTGAGATTAAACCCTTCGTCG-TCCGATCCTC-
>42_23_3s                1-52    GCTGCCTCGTTCCACTGAGATT-AGCCCTTCGTTGCTCCGATTCTTACTTGTA
```

26S rRNA reference sequence (3389 bases): ***Cucurbita pepo*** **26S rRNA (GB accession number: AF479108) plus 3' end from** ***Cucurbita maxima*** **25s-18s rDNA intergenic spacer (underlined 46 bases at the 3' end; GB accession number: X13059)**

aggtcaggcgggactacccgctgagtttaagcatatcaataagcggaggaaaagaaacttacaaggattcccttagtaacggcgagcgaaccgggaagagcccagcttgagaatcgggcgccctcggcgttcgaattgtagtctggagaagcgtcctcagcgacggaccgggcacaagtcccctggaaggggcgccagag
agggtgagagccccgtt**gcgctcggaccctgtcgcaccacgaggcgctgtcaacgagtcgggttgtttgggaatgc**agccccaatcgggcggtaaattctgtccaaggctaaatatgggcgagagaccgatagcaaacaagtaccgcgagggaaagatgaaaaggactttgaaaagagagtcaaatagtgcttgaaattgt
cgggagggaagcggatgggggccggcgatgtgctccagtcggatgtggaaaggtgataagccagtccgccaatcgacttggggcatggaccgatgcggattgagacggcggccaaagcccaggcctttgttacgcttgtggagacgtcgtcgtcccgatcgtggctggcagcacgcgccttttggcgtgcttcggcatctg
cgtgctcctggcatcggcctgtgggctccccattcgacccgtcttgaaacacggaccaaggagtctgac**atgtgtgcgagttaacgggcgagtaaacccgtaaggcgcaaggaagctgactggtgggatccctttgtgggttgc**accaccgaccgaccttgatcttttgagaagggttcgagtgtgagcatgcctgtcggg
acccgaaagatggtgaactatgcctgagcggggcgaagccagaggaaactctggtggaggcccgcagcgatactgacgtgcaaatcgttcgtctgacttgggtataggggcgaaagactaatcgaaccgtctagtagctggttccctccgaagtttccctcagg**atagctggagcccgcgtgcgagttctatcgggtaaag**
ccaatgattagaggcatcgggggcgcaacgccctcgacctattctcaaactttaaataggtaggacggcatggctgctttgttgagccatgccacggaatcgagagctccaagtgggccatttttggtaagcagaactggcgat**gcgggatgaaccggaagccgggttacggtgcctaactacgcgct**aacctagatccca
caaagggtgttggtcgattaagacagcaggacggtggtcatggaagtcgaaatccgctaaggagtgtgtaacaactcacctgccgaatcaactagccccgaaaatggatggcgctgaagcgcgtgacctatacccggccgtcggggcaagtgctaggccccgatgagtaggagggc**gcggtggtcgctgcaaaaccttggg**
cgtgagcccgggcggagcggccatcggtgcagatcttggtggtagtagcaaatattcaaatgagaactttgaaggccgaagaggggaaaggttccatgtgaacggcacttgcacatgggttagtcgatcctaagagacggggaagcccgtctgatagcgcaataagcgcgagcttcgaaagggaatcgggttaaaattcc
tgaaccgggacgtggcggctgacggcaacgttagggagtccggagacgtcggcgggggcctcgggaagagttatctttt**ctgtttaacagcctgcccaccc**tggaaacggctcagccggaggtagggtcc**agcggctggaagagcatcgcacgtcgcgtggtgtccggtgcgcccccggacgggcccttgaaatctggag**
gaccgagtgcctcccacgcccggtcgtactcataaccgcatcaggtctccaaggtgaacagcctctggtcaatggaccaatgtaggcaagggaagtcggcaaaatggatccgtaacctcgggaaaaggattggctctgagggctgggcacgggggtcccagtcccgaacccgtcggctgt**tggtggactgctcgagctgct**
cccgcggcgagagcgggtcgctgcgtgccggccgggggacggactgggaacggctccttcgggggccttccccgggcgtcgaacagtcaactcagaactggtacggacaaggggaatccgactgtttaattaaaacaaagcattgcgatggtccctgcggatgctaacgcaatgtgatttctgcccagtgctctgaatgtc
aaagtgaagaaattcaaccaagcgcgggtaaacggcgggagtaactatgactctctt**aaggtagccaaatgcctcgtcatctaattagtgacgcgcat**gaatggattaacgagattcccactgtccctgtctactatccagcgaaaccacagccaagggaacgggcttggcagaatcagcggggaaagaagaccctgttga
gcttgactctagtccgact**ttgtgaaatgacttgagaggtgtaggataagtgggagccgaaaggcgaaagtgaaataccactactt**ttaacgttattttacttattccgtgaatcggaagcggggcactgcccctcttttggacccaaggcctacttcg**gtgggccgatccgggcggaagacattgtcaggtggggagtt**
tggctggggcggcacatctgttaaaagataacgcaggtgtcctaagatgagctcaacgagaacagaaatctcgtgtggaac**aaaagggtaaaagctcgtttgattctgatttccagtacgaatacgaaccgtgaaagcgtggcctatcgatcctttt**agaccttcggaatttgaagctagaggtgtcagaaaagttaccaca
gggataactggcttgtggcagccaagcgttcatagcgacgttgctttttgatccttcgatgtcggctcttcctatcattgtgaagcagaattcaccaagtgttggattgttcacccaccaatagggaacgtgagctgggtttagaccgtcgtgagacaggttagttttaccctactgatgacagtgtcgcaatagtaattc
aacctagtacgagaggaaccgttgattcgcacaattggtcatcgcgcttggttgaaaagccagtggcgcgaagctaccgtgcgctggattatgactgaacgcctctaagtcagaatccgggctagaagcgacgcatgcgcccatcgcttgattgccgaccagcagtagggggccttttggcccccaaaggcacgtgtcgttg
gcta**agcccttgtgacggatgagtctcaagggccgccttgtaacgtaattcccactgagcgatgggtagaatcctttgc**agacgacttaaatatgcgacagggtattgtaagtggcagagtggcctt**GCTGCCACgatccactgagattcagcccttcgtcgctccgattcgt**

Sequence of fragments related to splicosomal small nuclear RNA (n=34) and 7SRP RNA (n=1):

Colored sequences: identical; **red**: mismatch.

7SRP RNA

Corresponding to L.esculentum gene for 7S signal recognition particle RNA (Z46748)

```
>42_31_2s             1-43       GAGCTTGTAACTCAATTGGGGGCATTAAAGTGGTTGGAGGTTC
```

U1 snRNA

```
>85_8_1s              1-66       ACCTGGACGGGGTCAATGGGTGATCATGAAGACTCATTACCTAGGTTGGTGACCTCCTTTGCACTT
>85_10_1s             1-66       ACCTGGACGGGGTCAATGGGTGATCATGAAGACTCATGGCCTAGGTTGGTGACCTCCATTGCACT-

>II_42_57_C5_2s       1-38       --------------------------------------TTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCA
>II_42-94_D9_2S       1-38       --------------------------------------TTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCA
>II_42_53_C2_2s       1-38       --------------------------------------TTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCA
>II_42_56_C4_2s       1-38       --------------------------------------TTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCA
>II_42-95_D10_2s      1-38        -------------------------------------TTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCA
>II_42_48_B10_3S      1-38       --------------------------------------TTGTGGTAGTGGGGGCCTGCGTGCGCGCGCCCCCTCCT
>42_35_2s             1-41       -----------------------------------AATTTGTGGTAGCGGGGGCCTGCGTTCGCGCGGCCCCCTCT
>II_85-48_II_2S       1-51       --AAGGTCTGTCCAACGTGGCAGAGCCTACGTCATAATTTGTGGTAGTGGGGC-----------------------
>II_42UP_41_H3_3s     1-42       ----------------GTGGCAGAGCCTACATCATAATTTGTGGTAGTGGGGGCCT------------------CA
>42up4_3s             1-42       ----------------GTGGCAGAGCCTACATCATAATTTGTGGTAGTGGGGGCCT------------------CA
```

Reference sequence: Glycine max non-coding U1 small nuclear RNA (GB accession number: X06809)

```
ATACTTACCTGGACGGGGTCAATGGATGATCAAGAAGGTCCATGGCCTAGGGAAGTAACCTCCATTGCACTGAGGAGGGGTGCCTTTCTAAGGTCTGTCCAAGTGACAGAGCCTACGTCATAATTTGTGGTAGTGGGGGCCTGCGTTCGCGCGGCCCCCTT
```

U2 snRNA

```
>85_42_4s             1-70       ----TTAGCTTGCTACCTGGGCCTTCGAGCGTCGCCCTCGCGTTGCACTACAGTATGGGCTTGGCGCACCCCTC
>II_85_28_F7_2s       1-69       -----TAGCTTGCTATCTGGGCCTTCGAGCGTCGCCCTTGCGTTGCACTACTGCATGGGCCTGGCGCATCCCTT
>85_95_6_1s           1-68       -----TGCTAAATGGGCCTTGGCCCTCCAGCGTCG-CCCTGCGTTGCACTACTGCATGGGCCTGGCGCATCCCT
>85up_2_1s            1-66       -----------TGCTATCTGGGCCTTCGAGCGTCGCCCTTGCGTTGCACTACTGCAAGGGCCAGGCGCATCCCACCA
>85_95_6_2s           1-60       ---------------ATCTGGGCCTTCGAGCGTCGCCCTTGCGTTGCACTACGGCATGGGCCTGGCGCATCCCTC
>85_3_2s              1-60       ---------------ATCTGGGCCTTCGAGCGTCGCCCTTGCGTTGCAATACGGCATGGGCCTGGCGCATCCCTC
>II_42_48_B10_2S      1-45       -AAGGTAGCTTGCTACCTGGGC-CTTCGAGCGTCGCCCTTGCGTTGC
```

Reference sequence: Solanum tuberosum U2 small nuclear RNA (GB accession number: M72889)

```
atacctttctcggccttttggctaagatcaagtgtagtatctgttcttatcagtttaatatctgatatgtgggccattggtccacacgatattaactcaatttttttaaggggaagagtccattaaggtagcttgctacctgggctcttgcgcgtcgcccatgcgttgcactactgcatgggcctggcgcaccccac
```

U3 snRNA

```
>II_42_30_A10_2S      1-42       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCTTT
>II_42_83_II_2S       1-40       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCT--
>II_42_84_II_2S       1-40       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCT--
>II_42_85_II_2S       1-40       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCT--
>II_42_18_II_2s       1-40       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCT--
>II_42_42_II_2S       1-40       GCTGCTGTGCGACTAGAGCGTGACTAACGGCTAATGGGCT--
```

Reference sequence: A. thaliana U3 small nucleolar RNA (TAIR accession number AT5G54075) (361 bases)
CATAAGCTTATGATTTCTTTTTTCTTACGAATTTTGCGTCCCACATCGGTAAGCGAGTGAAGAAATAACTGCTTTATATATGGCTACAAAGCACCATTGGTCACGACCTTACTTGAACAGGATCTGTTCTATAGGCTCGTACCTCTGTTTCCTTGATTTCTCAAGAGACAGGCCCTTAACCCTGGTTGATGAACCATGACC
GTGCGGCTAGAGCGTGATTGACGGCTACGATCGTCCTCGGACGCATCCGGTGCTGTAGAGGATCGTTACTCGGCTCGGTTCTACCTTGCCGGGGTGGTCGCACGGCGGTCTGACAGGTTCTTTTATTTTTTCACCCTCAAAACTTTGAATGAATTTCTTC

U4 snRNA

```
>II_42-30_A10_3S      1-45       ------GGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGG-TAAAGCCCTA
>42_32_2s             1-46       ------GGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>42up3_2s             1-52       GGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>42_1_3s              1-52       GGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>42up1_2s             1-52       GGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>II_42-61_C6_2s       1-52       GGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>42up1_3s             1-52       TGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
>42up3_3s             1-52       TGCCCAGGCCTTCGAGAATTTCTGGAAGGGCTCCCTTCGGGGTAAAGCCCTA
```

Reference sequence: Arabidopsis thaliana U4.2 small nuclear RNA (TAIR accession number AT3G06900)

TTTCCCTGCAAGTGATCGAAAGACCCTTGGATCTTCAGTAACTACAAAGCTACAGAGTTATATATGTGAACGAATCTTGTCGCTTTCAGATTTAAAGTTGTATTGAGAAAGAAGAGGTTGCCGTCTTCTGGTAGAGACTTGGAGAAGAAGAGAGTCTGTTCAATTCATCTAGCGAATAGGTTTCTTTCTAGAATAATATAA
CTAGAGGGAGTCCCACATCGAAAAGAAATTGTAAGATGGTTGGTTTTGTTCGGGTATAAATAAAGAGGGTTTAGTTCGGTTGAAAGTCATCTTTGCGCTTGGGGCAATGACGCAGCTAATGAGGTACTAACCGAGGCGCGTCTATTGCTGGTTGAAAACTATTTCCAAACCCCCTCCTGGGCCTAAGCTTGTCTTGGGCCT
TCGAGAATTTCTGGAAGGGCTCCCTTTGGGGTAAAGCCCTACAATAACTAGTCTAAATGTTTTTCGAGTTTTGAAATTTAGAAAATCAAATATCATGGAAAGTATATATCACACAATCTAGGCCCAAGAAAACATCACTTGCTGATGATGAGGCCTGATAGTGAAAATTGAA

snR8b

```
>II_42UP_20_H2_1s     1-44       GCCATGGCATGACAGACA-CCCTACACCCATAGAATATGAGCAAC
```

Arabidopsis thaliana partial small nucleolar RNA snoR8b (snoR8b gene), clone Ath-55, 5' end incomplete; AJ505629
CGGACGCGGTGGGAAAAGTAATTCCTCGTACTGAATGCTCATAAGGCATGATAGACTTACATTACTACCCATAGAATATGAGCAT

Sequence of fragments corresponding to transfer RNAs (n=151):

Blue: anticodon; **orange**: post-transcriptional 3' added -CCA bases; other **colored** sequences: identical; **red**: mismatch.

```
>tRNA-Asp (anticodon:GTC)(TAIR accession number: AT5G40545); n=57:
reference             1-72       GTCGTTGTAGTATAGTGGTAAGTATTCCCGCCTGTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CG
>II_42_7_A2_1s        1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42_13_1s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42up6_4s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>II_42_36_B3_1s       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42_34_1s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42up2_4s             1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>II_42-72_C11_2s      1-41       ---------------------------------GTCACGCGGTTGACCCGGGTT-CGATCCCCGGCAACGG--CCCA-
>42_11_3s             1-38       -------------------------------------CGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42_9_2s              1-38       -------------------------------------CGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42_29_3s             1-38       -------------------------------------CGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>42_2_3s              1-38       ------------------------------------ACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCC--
>II_42-95_D10_3s      1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>II_42_8_A3_1s        1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGATCCCCGGCAACGG-CGCCA-
>II_42-38_II_1S       1-45       ------------------------------CCTGTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42-12_II_1S       1-45       ------------------------------CCTGTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42-68_C10_1s      1-42       ---------------------------------GTCACGCGGCTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42up8_1s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_19_1s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_20_1s             1-42       ---------------------------------GTCACGCGGGTGACCCAAGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42_54_C3_2s       1-40       -----------------------------------CACGCGGGTGACCCGAGTT-CGTTCCCCGCCAACGG-CGCCA-
>II_42_56_C4_3s       1-39       -----------------------------------CACGCGGGTGACCCG-GTT-CGTTCCCTGGCAACGG-CGCCA-
>I_42-UP-12_G12_1s    1-39       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCC--
>II_42_53_C2_3s       1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>I_42-UP-10_G11_3s    1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_30_1s             1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42_57_C5_3s       1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGA-CGCCA-
>II_42-61_C6_1s       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_17_2s             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_2_1s              1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42_11_A4_1s       1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42_35_B2_1s       1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_34_2s             1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>42_26_3S             1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCA-
>II_42-94_D9_3S       1-41       -----------------------------------CACGCGGGTGACCCGGGTT-CGTTCCCCGGCAACGG-CGCCCA
>42_34_4s             1-39       ------------------------------------ACGCGGGTGACCCGGGTT-CGTTCCCCGGCAGCGG-CGCCA-
>II_42-12_II_2S       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAGCGG-CGCCA-
>II_42-38_II_2S       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAGCGG-CGCCA-
>II_42_12_A5_2s       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAGCGG-CGCCA-
>II_42_38_B5_2s       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAGCGG-CGCCA-
>II_42-67_C9_2S       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAGCGG-CGCCA-
>II_42_83_D3_1s       1-38       -------------------------------------CGCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCCA-
>II_42_54_C3_1s       1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>II_42_56_C4_1s       1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>II_42_57_C5_1s       1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>II_42-94_D9_1S       1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>II_42-95_D10_1s      1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>II_42_53_C2_1s       1-36       --------------------------------------GCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCC--
>42_25_2s             1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCCA-
>42_25_3s             1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCCA-
>II_42-13_A6_3s       1-42       ---------------------------------GTCACGCGGGTGACCCGGGTT-CGGTCCCCGGCAACGG-CGCCA-
>II_42-51_B12_1s      1-41       ----------------------------------TCACGCGGGTGACCCGGGTT-CGCTCCCCGGCAACGG-CGCCA-
>42up8_3s             1-40       -----------------------------------CACGCGGGTGACCCGGGTT-CGCTCCCCGGCAACGG-CGCCA-
>42_17_1s             1-39          ---------------------------------ACGCGGGAGACCGGGGTT-CGATTCCCCGCCGGGG-AGCCA-
>II_42_57_C5_4s       1-39       -----------------------------------CACGCG-TTGACCCGG-TT-CGATCCCCCGCAACGGGCGCAC-
>II_42_53_C2_4s       1-30       -----------------------------------CACGCGGGAGACCCGG-TT-CGATCCCCGACA-----------
>II_42-94_D9_4S       1-40       -----------------------------------CACGCGGCGGCCCCGGTTT-CGACCCCCGGCAACGG-CGCCA-
>II_42_38_B5__3s      1-47       ------------------------------CCTGTCAGCGGGGTGACCCGGGTTTCGTTCCCCGGCAACGGGCGCCA-

>tRNA-Lys(anticodon: CTT)(TAIR accession number: AT5G14035); n=45:
reference             1-73       GCCCGTCTAGCTCAGTTGGTAGAGCGCAAGGCTCTTAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCG
>II_42_35_B2_2s       1-41       -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_38_II_3S       1-41       -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_36_B3_2s       1-41       -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_12_A5_1s       1-41       -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_38_B5_1s       1-41       -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
```

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>II_42_67_C9_1S      1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>42_1_4s             1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>42_2_2s             1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>42_32_1s            1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_12_II_3S      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGAGCCCCACGGTGGGCGCCA
>II_42_52_C1_1s      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_41_B7_1s      1-43      ----------------------------------TTAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_33_B1_3s      1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>42_33_1s            1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>42UP3_1s            1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>42UP_1_1s           1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_30_A10_1S     1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_17_A7_1s      1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_72_C11_1s     1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_83_II_1S      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_84_II_1S      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_18_II_1s      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_42_II_1S      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_85_II_1S      1-39      -------------------------------------ACCTTGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>42_27_3S            1-41      -----------------------------------CAACCTCGTGGTCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_39_B6_1s      1-41      -----------------------------------TAACCTTGTGATCGTGGGTTCGTGCCCCACGGTGGGCGCCA
>II_42_84_D5_2s      1-38      --------------------------------------CCTTGTGATCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_85_D6_2s      1-42      --------------------------------- TTAACCTTGTGGTCGTGGTTTCGGGCCCCACGGTGGGCGCCA
>II_42_83_D4_2s      1-41      --------------------------------- TTAACCTTGTGTTCGTGGGT-CGGGCCCCACGGTGGGCGCCA
>II_42_83_II_3S      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_84_II_3S      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_85_II_3S      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_18_II_3s      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_42_II_3S      1-42      --------------------------------- TTAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_100_E1_1s     1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_45_B9_1S      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>42_18_2s            1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGGGCCCCACGGTGGGCGCCA
>II_42_42_B8_2s      1-42      ----------------------------------TTAACCTTGTTGTCGTGGGTTCGGGCCCCACGGTGGGCGCCC
>42_32_3s            1-40      -----------------------------------TAACCTTGTGGTCGTGGGTTCGG-CCCCACGGTGGGCGCCG
>42_37_1s            1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGCGCCCCACGGTGGGCGCCA
>II_42_19_II_2S-AS   1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAACCCCACGGTGGGCGCCA
>II_42_19_A9_1S      1-41      -----------------------------------TAACCTTGTGGTCGTGGGTTCGAACCCCACGGTGGGCGCCA
>II_42_63_C7_1s      1-40      ------------------------------------AACCTTGTGGTCGTGGGTTCCGGGGTCACGGTCGGCGCCA
>II_42UP_20_H2_2s    1-46      -----------------------------------TAACCTTGTGGACGGGGGGTCGTGCCCCACTGGGGGCGCCACTGCT
>II_42_45_B9_2S      1-41      -----------------------------------TAT-CTTGTGGTCGTGGGTTCGAGCACCCACGGTGGGCGCCA


>tRNA-Lys(anticodon: TTT)(TAIR accession number: AT5G48465); n=1:
reference            1-72      -GCCTTCTTAGCTCAGTGGTAGAGCGCGTGGCTTTTAACCACGTGGTCGTGGGTTCGATCCCCACAGACGGCG
>42UP6_1s            1-41      -----------------------------------TAACCACGTGGTCGTGGGTTCGTTCCCCACAGACGGCGCCA


>tRNA-Gly(anticodon: TCC)(TAIR accession number: AT5G59385); n=16:
reference            1-73      GCGTCTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAGCAATAGACCCGGGTTCGACTCCCGGCAGACGCA
>II_42_52_C1_2s      1-40      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAGC--------------------------------
>42_34_3s            1-40      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAGC--------------------------------
>II_42-41_B7_2s      1-40      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAGC--------------------------------
>42up4_2s            1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42-39_B6_2s      1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42-13_A6_1s      1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42UP_41_H3_2s    1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42-68_C10_2s     1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42_33_B1_2s      1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>II_42-41_B7_3s      1-38      GCGTTTGTA-TCCAACGGTTAGGATAATTGCCTTCCAAG---------------------------------
>42_28_1s            1-39      GCGTTTGTAGTCCAACGGTTAAGATAATTGCCTTCCAAG---------------------------------
>II_42_52_C1_3s      1-39      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCATG---------------------------------
>42_20_2s            1-38      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCCCA----------------------------------
>42_26_2S            1-36      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCC------------------------------------
>42_6_2s             1-36      GCGTTTGTAGTCCAACGGTTAGGATAATTGCCTTCC------------------------------------
>42up5_1s            1-31      GCGTTTGTAGTCCAACGGTTAGGATAATTGC-----------------------------------------


>tRNA-Gly (anticodon: CCC)(TAIR accession number: AT5G53487); n=1:
reference            1-71      GCGCATCTGGTGTAGTGGTATCATAGTACCCTCCCACGGTACTGACCAGGGTTCGATTCCCTGGATGCGCA
>85_23_3s            1-60      -------------AGTGGTATCATAGTACCCTCCCACGGTACTGACCGGGGTTCGATTCCCCGGATGCGCACC
```

```
>tRNA-Gly (anticodon: GCC)(TAIR accession number: AT5G07135); n=1:
reference             1-71       GCACCAGTGGTCTAGTGGTAGAATAGTACCCTGCCACGGTACAGACCCGGG-TTCGATTCCCGGC-TGGTGCA
>II_42-17_A7_2s       1-41       -----------------------------------ACGGTACAGACCCGGGTTTCGTTTCCCGGCCTGGTGCACCA


>tRNA-Met (anticodon: CAT)(TAIR accession number: AT5G67455); n=12:
reference             1-72       -------ATCAGAGTGGCGCAGCGGAAGCGTGGTGGGCCCATAACCCACAGGTCCCAGGATCGAAACCTGGCTCTGATA
>42_22_1s             1-41       GAAAAAAATCAGAGTTGCGCAGCGGAAGCGTGGTGGGCCC---------------------------------------
>II_42_33_B1_1s       1-39       -CTGAAAATCAGAGTGGCGCAGCGGAAGCGTGGTGGGCCC---------------------------------------
>42_15_1s             1-45       -CTGAAAATCAGAGTCGCGCAGCGGAAGCGTGGTGGGCCCATAACC---------------------------------
>42_3_2s              1-38       -CTGAAAATCAGAGT-GCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_25_1s             1-32       -------ATCAGAGT-GCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_35_1s             1-33       -------ATCAGAGTCGCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>II_42_97_D11_1s      1-34       ------AATCAGAGTAGCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_16_2s             1-32       -------ATCAGAGT-GCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_7_3s              1-32       -------ATCAGAGT-GCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_22_3s             1-33       -------ATCAGAGTGGCGCAGCGGAAGCGTGGTGGGCCT---------------------------------------
>42_1_s               1-34       -------ATCAGAGTTGCGCAGCGGAAGCGTGGTGGGCCTT--------------------------------------
>42_15_2s             1-33       -------ATCAGAGT-GCGCAGCGGAAGCGTGGTGGGCCTT--------------------------------------


>tRNA-Glu (anticodon: CTC)(TAIR accession number: AT5G09755); n=6:
reference             1-73       TCCGTTGTAGTCTAGCTGGTCAGGATACTCGGCTCTCACCCGAGAGACCCGGGTTCGAGTCCCGGCAACGGAG
>II-85-15_E12_1s      1-60       ----------------TGGTCAGGATATTCGGCTCTCACCCGAAAGACCCGGGTTCAAGTCCCGGCAACGGAACCA
>II_85_18_F2_1as      1-59       ----------------TGGTCAGGATATTCGGCTCTCACCCGAAAGACCCGGGTTCATGTCCCGGCAACGGAACC-
>II_85_19_F3_1s       1-59       ----------------TGGTCAGGATATTCGGCTCTCACCCGAAAGACCCGGGTTCATGTCCCGGCAACGGAACC-
>85_50_1s             1-60       ----------------TGGTCAGGATATTCGGCTCTCACCCGAAAGACCCGGGTTCAAATCCCGGCAACGGAACCA
>II-85-38_II_1S       1-58       ----------------TGGTCAGGATATTCGGCTCTCACCCGAAAGACCCGGGTTCAAATCCCGGCAACGGAAC--
>II_85_38_G1_1s       1-60       ----------------TGGTTAGGATACTCGGCTCTCACCCGAGAGACCCGGATTCAAATCCCGGCAACGGAACCA


>tRNA-Ser (anticodon: GCT) (TAIR accession number: AT5G06685); n=2:
reference             1-82       GTCGCTTTGGCCGAGTGGTTAAGGCGTTTGCCTGCTAAGTAAATGGGGTTTCCCCGCGAGAGTTCGAATCTCTCAGGCGACG
>I-42-UP-10_G11_1s    1-42       -------------------------------------------TGGGGTTTCCCCGCGAGAGTTCGAATCTCTCAGGCGACGCCA
>II_42UP_17           1-47       -------------------------------------------TGATGTTTCCCAGCGAGACTTCGAATCTCTCAGGCGAAGCCCCTGTC


>tRNA-Ser (anticodon: AGA) (TAIR accession number: AT3G46875); n=2:
reference             1-82       GTGGGCGTGCCGGAGTGGTTATCGGGCATGACTAGAAATCATGTGGGCTTTGCCCGCGCAGGTTCGAATCCTGCCGCTCACG
>II-42-48_B10_1S      1-37       GTGGGCGTGCCGGAGTGGTTATCGGACATGATCGGAA---------------------------------------------
>II-42-61_C6_3s       1-39       GTGGCCGTGCCGGAGCGGTTATCGGAAATGATTGGAAAT-------------------------------------------


>tRNA-Ser (anticodon: TGA) (TAIR accession number: AT5G52355); n=1:
reference             1-82       GTCGATATGTCCGAGTGGTTAAGGAGACAGACTTGAAATCTGTTGGGCTTCGCCCGCGCAGGTTCGAACCCTGCTGTCGACG
>I-42-UP-10_G11_2s    1-42       -------------------------------------------TGGGCTTCGCCCGCGCAGGTTCGAACCCTGCTGTCGACGCCA


>tRNA-Pro (anticodon: AGG)(TAIR accession number: AT5G39535); n=4:
reference             1-73       GGGCATTTGGTCTAGTGGTATGATTCTCGCTTAGGGTGCGAGAGGTCCCGAGTTCAATTCTCGGAATGCCCC
II_42_76_D2__2s       38         -------------------------------------GCGAGAGGTCCCGAGTTCGCTTCTCGGAACGCCCCCCA
42_22_2s              41         ----------------------------------GCTGCGAGAGGTCGCGAGTTCGATTCTCGCAACGCCCCCCA
II-42-68_C10__3s      41         ----------------------------------GCTGCGAGAGGCCCCGAGTTCGATTCTGGGAATGCCCCCAA
II_42_8_A3__2s        41         ----------------------------------GCTGCGAGAGTTCCCGAGTTCATTTCTCGGAATGCCCCCCA


>tRNA-Arg (anticodon: TCG) (TAIR accession number: AT5G02615); n=2:
reference             1-75       GACCGCATAGCGCAGTGGATTAGCGCGTTTGACTTCGGATCAAAAGGTCGTGGGTTCGACTCCCACTGTGGTCG
>II-42-19_II_1S       1-41       ------------------------------------GGATCAAAAGGTCGTGGGTTCGACTCCCACTGTGGTCGCCA
>II-42-19_A9_2S       1-41       ------------------------------------GGATCAAAAGGTCGTGGGTTCGACTCCCACTGTGGTCGCCA


>tRNA-Arg (anticodon: ACG) (TAIR accession number: AT5G65015); n=1:
reference             1-74       GACTCCGTGGCCCAATGGATAAGGCGCTGGTCTACGAAACCAGAGATTCTGGGTTCGATCCCCAGCGGAGTCG
>II_42_37_B4_1s       1-48       ----------------------------CCTGAAGGAAACCAGAGATTCTGGGTTCGATCCCCAGCGGAGTCGCCA
```

Sequence of fragments corresponding to chloroplastic, mitochondrial & bacterial RNA (n=19):

Colored: identical; **red**: mismatch.

chloroplastic RNA (n=6):

chloroplastic tRNA: Reference sequence: Chlamydomonas reinhardtii tRNA-Glu (trnE1; anticodon TTC); GB accession number: BK000554 (REGION: 14463-14535)

```
Reference            1-73       GCCCCCATCGTCTAGAGGCCTAGGACACCTCCCTTTCACGGAGAAAACGCGGATTCGAATTCCGCTGGGGGTA
>85_34_1s            1-62       -------------AGAGGCCCAGGACACCGCCCTTTCACGGCGGTAACAGGGGTTCGAATCCCCTAGGGGACG-CC
```

chloroplastic tRNA: Reference sequence: Chlamydomonas reinhardtii tRNA-Asp (trnD; anticodon GTC); GB accession number: L26265

```
Reference            1-74       GGGATTGTAGTTCAATTGGTTAGAGCACCGCCCTGTCACGGCGGAAGTTGCGGGTTCGAGTCCCGTCAATCCCG
>85_41_1s            1-56       -------------------------------------ACGCCGGGGGTCGCGGGTTCGAGTCCCGTCCACTCCGCCA-AAATTTGCCGCTTGGT
```

chloroplastic protein coding RNA:

```
>II_85_11_E8_1s       REVERSE    1-60       TAGATATTGATGGTATTCGTGAACCTGTTTCTGGATCTCTTCTTTACGGAAACAATATTA
>II_85_11_II_4s       REVERSE    1-60       TAGATATTGATGGTATTCGTGAACCTGTTTCTGGATCTCTTCTTTACGGAAACAATATTA
>II_85_12_4s          REVERSE    1-60       TAGATATTGATGGTATTCGTGAACCTGTTTCTGGATCTCTTCTTTACGGAAACAATATTA
>II_85_12_E9_1s       REVERSE    1-49       -----------GGTATTCGTGAACCTGTTTCTGGATCTCTTCTTTACGGAAACAATATTA
```

Arabidopsis thaliana chloroplast psbA ORF (X79898; TAIR accession number ATCG00020); 1062 bases
Matching from 173 to 232

```
ATGACTGCAATTTTAGAGAGACGCGAAAGCGAAAGCCTATGGGGTCGCTTCTGTAACTGGATAACTAGCACTGAAAACCGTCTTTACATTGGATGGTTTGGTGTTTTGATGATCCCTACCTTATTGACCGCAACTTCTGTTTTTATTATCGCATTCATTGCTGCTCCTCCAGTAGATATTGATGGTATTCGTGAACCTGTT
TCTGGATCTCTTCTTTACGGAAACAATATTATTTCCGGTGCCATTATTCCTACTTCTGCAGCTATTGGATTGCATTTTTACCCAATCTGGGAAGCTGCATCCGTTGATGAATGGCTATACAACGGCGGTCCTTATGAACTAATTGTTCTACACTTTTTACTTGGTGTAGCTTGTTATATGGGTCGTGAGTGGGAACTTAGT
TTCCGTCTGGGTATGCGTCCTTGGATTGCTGTTGCATATTCAGCTCCTGTTGCAGCTGCGACTGCTGTTTTCTTGATCTATCCAATTGGTCAGGGAAGTTTTTCTGATGGTATGCCTCTAGGAATCTCTGGTACTTTCAACTTTATGATTGTATTCCAGGCTGAGCACAACATTCTTATGCACCCATTTCACATGTTAGGT
GTAGCTGGTGTATTCGGCGGCTCCCTTTTTAGTGCTATGCATGGTTCCTTGGTAACTTCTAGTTTGATCAGGGAAACCACAGAAAATGAATCTGCTAATGAAGGTTACAGATTCGGGCAAGAAGAAGAAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTAGTTTCAACAATTCT
CGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTGGTTTACTGCTTTAGGTATTAGTACTATGGCTTTCAACCTAAATGGTTTCAATTTCAACCAATCCGTAGTTGATAGTCAAGGACGTGTTATTAATACTTGGGCTGATATTATTAACCGTGCTAACCTTGGTATGGAAGTTATGCATGAACGTAAT
GCTCACAACTTCCCTCTAGACCTAGCTGCTGTTGAGGCTCCATCTACAAATGGATAA
```

mitochondrial 26S rRNA (rrn26; n=4):

Matching from 1971 to 2029

```
>II_85_40_G2_2s       1-66       CTCTCGGTCGTAGTTTGGCGACCTATCTTCAGTAGGGGCCTTTATTCTTTTGATTAGAG---(AAAAAAA)
>II_85_41_G3_2s       1-66       CTCTCGGTCGTAGTTTGGCGACCTATCTTCAGTAGGGGCCTTTATTCTTTTGATTAGAG---(AAAAAAA)
>II_85_8_E7_2s        1-66       CTCTCGGTCGTAGTTTGGCGACCTATCTTCAGTAGGGGCCTTTATTCTTTTGATTAGAG---(AAAAAAA)
```

Matching from 2108 to 2149

```
>42_16_1s             1-42       AACAAGG-TGGAAACTTCCAGGAAAAAACTTCGAATTGGGAGG
```

Nicotiana tabacum mitochondrial 26SrRNA (BA000042); 3406 bases

```
GGGTACAAGATCGAAAAGAATGCATTGGATGGATGCCCGGGCATTGAGAAGGAAGGACGCTTTCAGAGGCGAAAGGCCATGGGGAGATACCGTCTGTGATCCATGGATCTCCGATCGGGAAACCGTATCCAAGCTCCGTGGCTAGTCTGCGCTCTTTGGACTTTTCAAACTTAGCGAACTGAAACATCTTAGTAGCTAAAG
GAAGGGAAATCAACCGAGACCCCGTTAGTAGCGGCGAGCGAGAGCGGATTGGGGGTTTGAAGAAAAACAAACACGAAGCTTCGTTCCTCAGCAAAGTGTTCACTTCTTTTTCGCCAGGTTTCATTCGATTTGTTGTGGATTGGATGATGGAAAAACCAGCAAGCTACGGCTTCAAAGCTTACCTTATTTAGAAAAGGAGAA
AGGGCTTTTTTATAGATGTTGAGGTTGAGTAAGGGGGGCGGAGCTTGAAGAGCGAAGCGAGCCGCGCTAGCCTAGCAACGTTTTTCAGCAGCAAGCTACGGTCTAACGACCCCCTAACCTAGGTTGGGGCGAAAACTCCAAAATCCAAAACGTTGGTTAGGGTTCCAAACCTTTCTCTAATAATAAGGTAAGCTTTCAAGC
CGCCGCCCTTTAAAGGAGCGGGCGCAGTGAACTGTAATTGTGAAAAGATTGGAAGATCTGGCCAAAGAAGGTGATAGCCCTGTAGATTCGTTCCCATGGTTCGATCCTTCCCAGTAAAACGCGGCGTGTTCGAATTCTGATCGCTTTTACGCGAGAAAGGGGGACCACCCTCTAAGCCTAAGTATTCCTCAATGACCGATA
GCGTACAAGTACCGTGAGGGAAAGGTGAAAAGAACCCTATTTAGGGAGTGCAATAGAGAACCTGAGATCCGATGCGAACAATCAGTCGAAGGAGCGGAGCTTAGAGCCTTTACTTTATGTAAAGCGCACTCACTCTAACGGCGTACCTTTTGCATGATGGGTCAGCGAGGAAATGGGAACAGCGGCTTAAGCCATTAGGTG
TAGGCGCTTTCCAGAGGTGGAATCTTCTAGTTCTTCCTATTTGACCCGAAACCGATCGATCTAGCCATGAGCAGGTTGAAGAGAGCTCTAACAGGCCTTGGAGGACCGAACCCACGTATGTGGCAAAATACGGGGATGACTTGTGGCTAGGGGTGAAAGGCCAACCAAGATCGGATATAGCTGGTTTTCCGCGAAATCTAT
TTCAGTAGAGCGTATGATGTCGATGGCCCGAGGTAGAGCACTCAATGGGCTAGGGTGGCCTCATTTCGCCTTACCAACCCCAGGGAAACTCCGAATACAGGCCTAGATCGTTTGTACAGACAGACTTTTTGGGTGCTAAGATCCAAAGTCGAGAGGGAAACAGCCCAGATCGTACGCTAAGGTCCCTAAGCAATCACTTAG
TGGAAAAGGAAGTGATCGAGCGATGACAACCAGGAGGTGGGCTTGGAAGCAGCCATCCTTTGAAGAAAGCGTAATAGCTCACTGGTCTAGCTCCATGGCACCGAAAATGTATCAGGGCTCAAGTGATTCACCGAAGCGACGAGACCTTGAAAGCTGCTTTTTCAAGTGTCAGTAGCGGAACGTTCTGTCAATCGGGGAAGG
TTTTTGGTGACAAGACCTGGAGATATCAGAAGTGAGAATGCTGACATGAGTAACGAAAAATCCTGTGAAAAACACGATCGCCTGCCAGTGGAAGGTTTTCTGCGTTCAGTCAATCTACGCAGAGTGAATCGGTCCCTAAGGAACCCCCGAAAGGGCTGCCGTCCGATGGGTACACGAAAGTGACGAAGTTGCTTTGACTAC
AGAACCATGCCTGTCTGTTGGAGCGAATTGGATGATCGGGCCGAGGGCTGCCCCCTCTTCCCCTCACTCTCCTTTCCCTAATATGAACCTTGAGTCATCAAAGCCTTTCTGACTCGGCCTGGCCCGGTCGCCCTACGCGACTGGCGCTTCAAAAGGCGAAACTCTCGGTCGTAGTTTGGCGACCTATCTTCAGTAGGGGCC
TTTAGTCTTTTGATTAGAGTAGGGGTCGCGAGAGAGCAGAGCGTACCGCCCTGCCATAGTCACGAGTCTGTTTATAGTCGCGACTGTTGTCATAGTCAACAAGGTTGAAACTTCCAGGAAAAAACTTCGAATTGGGAGGGCGATCCTCCCGGTGAACTGACCGTACCCCAAACCGACACAGGTGAACAAGTAGAGTATACT
AGGGCGCTTGAGAGAACCATGTCGAAGGAACTCGGCAAAATGACCCCGTAACTTCGGGAGAAGGGGTGCTCTCCTATCTTTTGATTAGGAAAGCGGCACATACCAGGGGGTAGCGACTGTTTATTAAAAACACAGGACTCTGCTAAGTGGTAACACGATGTATAGAGTCTGACACCTGCCCGGTGCTGGAAGGTCGGAAGG
AGAAGTGTTATAAGCTTTGAATGGAAGCCCCGGTAAACGGCGGCAGTAACTCTAACTGTCCTAAGGTAGCGAAATTCCTTGTCGCATAAGTAGCGACCTGCACGAATGGTGTAACGACTGCCCCGCTGTCTCCGACATGGACCCGGTGAAATTGAATTCTCCGTGAAGATGCGGAGTACCAACGGCTAGACGGTAAGACCC
CGTGCACCTTAACTATAGCTTCGCAGTGACAACCTTAATCGAATGTGTAGGATAGGTGGGAGGTGGTGACACACAACGACCAATCCTGAAAGACCACTCTTTCGTCTAAGGATGCCTAACCGCCGCACCGATCATTCGGGGGGAGGCGGGACACTGCGAGGTGGGTAGTTTATCTGGGGCGGATGCCTCCTAAAGAGTAAC
GGAGGTGTGCGAAGGTAGGCTCAAGCTAAGATTCTGCTCGTGAGCGTAATGGTATAAGCCTGCCTGACTGTGAGACCGACTGGTCGAACAGAGACGAAAGTCGGCCATAGTGATCCGGGAGTCCCGTGTGGAAGGGCTCTCGCTCAACGGATCAAAGGTACGCCGGGGATAACAGGCTGATGACTCCCAAGAGCTCTTATC
GACGGAGTCGTTTGGCACCTCGATGTCGACTCATCACATCCTGGGGTTGAAGAAGGTCCCAAGGGTTCGGTTGTTCGCCGATTCAAGTGGTACGTGAGTTGGGTTTAGAACGTCGTGAGACAGTTCGGTTCCTATCTACCGTTGGTGTTAAAGGGAGAACTGCGAGGAGCCAACCCTAGTACGAGAGGACTGGGTTGGGCT
AACCTATGGTGTACCGGTTGTTATGCCAATAGCAGCGCCGGGCAGCTAAGTTGGTATGGAAGAACTGCTGCGCCGCGGGAAATCCTTCTCTATACAAGTTCTCGGACGAGGTTTTTGAACAGAACTTCGATAGGCGAGAGGTGTAAGCACCGCGAGGTGTGAAGCGATCTCGTACTAAACGAAACGACTT
```

Bacteria-related (non-chloroplastic; n=9):

Corresponding to Janthinobacterium sp. Marseille 5S ribosomal RNA (CP000269)

```
>85_18_4s           1-73      ATCGAACAGGACCGTGAAACGACTTTGCGCC-ATGATAGTGCTGCA-CCCGTGCGAAAGT-TGTTATCGTCAGGCT
```

Corresponding to Pectobacterium sp. 16S ribosomal RNA (EU490611)

```
>II_42_32_A12_1s    1-42      CCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAG
>II_42_64_C8_1s     1-42      CCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCCCTTGAG
```

Corresponding to Uncultured bacterium clone B31_52 16S ribosomal RNA (EU790472)

```
>85_23_1s           1-61      CATCCACGGAAGTTTTCAGAGATGAGAATGTGCCTTCGGGAACCGTGAGACAGGTGCTGCC
```

Corresponding to Comamonas testosteroni strain LMG1800 (Wheat associated bacterium) 23S ribosomal RNA gene (DQ150550)

```
>II_85_44_II_3S     1-75      GTAACAGGTACTGGAGGTCCGAACCCACTACTGTTGCAAAAGTAGGGGATGAGCTGTGGATAGGGGTGAAAGGCT

>42up5_2s           1-40      GGTTAAGCGACTAAGCGTACACGGTGGATGCCCTGGCAGT

>II_85_4_E4_1s      1-61      AAGTTGCAGGGTATAGACCCGAAACCCGGTGATCTAGCCATGGGCAGGTTGAAGGTTGGGT
```

Corresponding to uncultured gamma proteobacterium clone 692 23S ribosomal RNA gene (EF188328)

```
>85_37_1s           1-71      CCTGTACTTGGTGTTACTGCGAAGGGGG-GACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTT
>85_40_1s           1-65      ------CTTGGTGTTACTGCGAAGGGGG-GACGGAGAAGGCTATGTTGGCCGGGCGACGGTTGTCCCGGTTT
```

Sequence of fragments corresponding to mRNA and fragments ambiguous/not matching to know sequences:

Colored sequences: identical; **red**: mismatch

Protein coding mRNAs:

```
>42_11_1s           1-23      -GGGGAATAACGAGAAGGCTGGCA
>42_29_1s           1-23      -GGGGAATAACGAGAAGGCTGGCA
```

Some similarity to an Arabidopsis thaliana protein phosphatase 2C family protein (TAIR accession number AT5G06750) (orange ORF)

```
CGATATGCACGAGACTCCACTGGGATCTCATAGTATCCAAGCTGATATTGATGATCCAACAACTTTGAAGTCAAGACCACAAACTCATGATGTAGAACCTAATCAGTTTCCCATTACTTCCTCATCAAGGGATCACCCGCAAGGAGCGTGATATTATCAAGCTCAAAGCCCAGTTTGTGGCTGATTTTGGAATGCCTTTTG
GGCAGGATTTGGTGATGAAGAGTGTGTTTATGAAACCTGAGCTTGAGCGGTTGATCCTCTGTTTAGGAGTTTCGAGAGAAAGGAGTTGTATTTCAGAGGAGGCTTTAAGAGCTGCATTTTCTGCTACTGAGGAAGGGTTTCTCACGCTTGTGCGAAGGACTTGCGGGTTGAAACCGTTGATTGCAGCTGTTGGATCTTGTT
GTTTGGTTGGAGTTATTTGGAAAGGGACTTTGCTTATCGCTAATGTTGGTGATTCTCGTGCTGTGCTTGGTTCCATGGGTAGTAATAATAATAGGTCAAACAAGATTGTAGCTGAGCAACTGACTAGTGATCACAATGCTGCTTTGGAAGAAGTTAGACAAGAGCTTAGGTCGTTGCATCCTGATGATTCACATATCGTTG
TCCTTAAACATGGTGTGTGGCGCATCAAAGGCATCATTCAGGTATCTAGATCAATAGGGGATGCATATTTAAAGCGCCCAGAGTTCTCACTTGACCCTTCATTTCCGCGGTTCCATCTCGCTGAAGAACTACAAAGACCTGTTTTATCAGCAGAGCCTTGTGTCTACACAAGAGTCTTACAAACAAGTGACAAGTTTGTGA
TATTCGCATCAGATGGACTCTGGGAACAAATGACCAACCAGCAAGCTGTAGAGATAGTGAATAAACACCCCCGTCCTGGAATAGCGAGAAGGCTGGTGAGAAGAGCGATAACCATAGCTGCGAAAAAGAGAGAGATGAATTACGATGATTTGAAGAAAGTGGAGAGAGGAGTGAGGAGATTCTTTCATGATGATATAACAG
TGGTTGTGATATTCATAGACAATGAGCTTCTTATGGTGGAGAAAGCTACTGTTCCTGAATTGTCCATTAAAGGTTTTTCTCATACCGTTGGACCTTCCAAGTTCAGTATCTTCCTCTCTTAGACATTTTTGTTACATTTCTTTACTTTACTATCACAGTCTTCACAAATATGATAAAAATGAACACGGATCGATTTTGTAC
CAACACGTTTGAGTTTAGATACAAAATTGTAGGTTAAT
```

```
>42_3_3as           1-57      GGGAAGCTTGGGGGTGGAGCAGGTAGCTTGAGAGAAGTGGAGGTGCTCTGTAGGCCC
```

Similar to Arabidopsis thaliana cDNA with unknown function (TAIR accession number AT2G26570):

```
ATGGAGGACTTAAAAACTGTTGAAGCATCTGATAATGTTGTTAGTGATAATGTTGAGAAAGTCAATCCTGAGTTGATTGATTCCACCATTCGAGAATCTAACATACAATCTGCAACAAAGGTTGATAATATTCCACAATCTCAAACTGACACTGAAGAGACTCAACAATCTCAAACTGATACTGAAGAGACTCAACAATCT
CAAACTGATGACACTACCGGCAATGCGAAGATTTATGTCGATGACACGTTTTCGCCTTCTGATGCTGCAACCGCTGCGGTGTTAACCGGAAAAGATAGTACGAGTACAACAATTGTAGAAGAAGTGATGGAGCCAGATGAGATTGGTTTACCTAGTGTCAAGATTACCGAGGCTGCGACGGGTACAGCAAGAAATGGTGGG
GGGTCACCTAGAACTGTATCATCTCCTAGATTTTCAGGATCACCGGTGAGCACTGGAACACCGAAAAATGTGGACTCACATCGAGGTTTAATCGATACCGCAGCGCCATTTGAATCTGTTAAAGAAGCTGTATCAAAATTTGGAGGAATTACTGACTGGAAGTCTCACCGAATGCAAGCGGTAGAGAGACGAAAGCTTATT
GAAGAAGAGCTTAAAAAGATTCATGAGGAGATTCCTGAGTACAAAACACATTCAGAAACTGCAGAGGCTGCAAAACTGCAAGTGCTTAAGGAGCTGGAAAGCACAAAGAGACTTATAGAACAGTTGAAGCTTAATTTGGACAAGGCACAAACAGAAGAACAACAGGCGAAGCAAGACTCGGAGCTTGCTAAGCTGAGGGTT
GAAGAGATGGAACAAGGAATAGCTGAAGATGTCAGTGTTGCAGCTAAAGCGCAACTTGAGGTGGCTAAGGCGAGGCATACAACAGCGATTACAGAGTTGTCTTCTGTCAAGGAGGAACTAGAAACTCTGCATAAGGAATATGATGCTCTGGTGCAAGATAAAGATGTGGCTGTAAAGAAAGTAGAAGAAGCAATGTTGGCG
TCAAAAGAAGTTGAGAAGACAGTGGAAGAACTCACCATAGAGTTGATAGCTACAAAGGAGTCATTGGAATCAGCACATGCTTCTCATTTAGAGGCGGAAGAACAGAGGATTGGAGCAGCTATGGCTAGAGACCAGGATACTCACCGTTGGGAGAAGGAACTGAAGCAAGCGGAAGAGGAACTCCAAAGACTTAACCAACAG
ATACATTCTTCGAAAGATCTAAAATCGAAGCTCGACACTGCCTCAGCGCTGCTTCTTGATTTGAAGGCGGAATTGGTAGCTTATATGGAATCCAAGCTAAAACAAGAAGCGTGTGACTCAACCACAAACACCGATCCTTCGACAGAAAACATGAGCCATCCAGATTTACATGCAGCTGTTGCCTCTGCAAAGAAGGAACTT
GAAGAGGTCAATGTCAATATTGAGAAAGCAGCTGCTGAAGTGAGTTGCTTGAAATTGGCCTCCTCTTCCTTGCAACTGGAACTCGAGAAAGAAAAGTCTACTCTTGCCTCTATCAAACAGAGAGAAGGAATGGCCTCTATAGCAGTAGCTTCTATAGAGGCTGAAATTGACAGAACGAGGTCGGAAATAGCTTCGGTTCAG
TCAAAGGAGAAAGACGCGAGAGAGAAAATGGTGGAGCTACCGAAGCAACTTCAGCAAGCAGCAGAAGAGGCTGATGAAGCAAAGTCACTTGCTGAAGTTGCTCGCGAAGAGCTACGAAAGGCGAAAGAAGAAGCAGAGCAAGCAAAAGCTGGAGCAAGTACAATGGAGAGCAGGCTATTTGCTGCGCAGAAGGAAATCGAA
GCAGCTAAAGCTTCAGAGAGGCTGGCCTTAGCTGCCATCAAGGCTTTGGAGGAGAGTGAATCAACATTGAAAGCTAATGACACCGATTCTCCACGAAGCGTTACACTTTCGCTAGAAGAGTACTATGAGCTCAGCAAACGTGCTCACGAGGCAGAAGAACTCGCGAACGCAAGAGTAGCAGCAGCGGTTTCAAGAATCGAG
GAAGCTAAAGAAACAGAAATGAGAAGCTTGGAGAAGTTGGAAGAAGTAAACAGAGACATGGATGCGAGAAAGAAGGCATTAAAAGAAGCAACTGAAAAGGCTGAGAAGGCCAAAGAAGGGAAGTTGGGGGTGGAGCAGGAGCTGAGGAAATGGAGGGCAGAACATGAACAAAAGAGAAAGGCTGGTGATGGAGTCAACACT
GAGAAAAACCTAAAAGAAAGCTTTGAAGGAGGAAAGATGGAGCAATCACCTGAAGCTGTTGTTTATGCCTCCAGCCCAAGTGAGTCATATGGAACAGAAGAAAACTCTGAAACCAATCTATCCCCACAGACCAAGTCTCGAAAGAAAAAGAAGAAGCTTTCTTTCCCCCGGTTTTTTATGTTCTTGTCAAAGAAGAAGTCA
CATAATAATTGA
```

Sequences with ambiguous or non-significant matches in the databases:

```
>42_23_4s            1-59       TCGTAAGGTACCTGAAACTGAAGGCACCATCAATGTCGTAGGCACCATCCCCCTCATAA
>42_23_2s            1-54       -CGTAAGGTACCTGAAACTGAAGGCACCATCAATGTCGTAGGCACCATCCCCCTC----

>II_85_31_F9_1s      1-77       CCTGTTTAACAAAAATCACTTTCATGATTTATCAGCCATAGCCTGATATTTTGCTTTTAAACGGCTAAATACATCCT

>42up6_2s            1-67       TTACCCTTGTAACGTGGTGCGCGCCCAATTCGAGCCCCCACGTGGCCCTCTTGTGGGCACTTCAATA

>II_85_3_II_3s       1-65       TGGGGGCATTAATGTGACGGAATGGGAAGGCCCAACCCGGTTGCCTTCACCGAACCATCATTTTT

>II_42_67_C9_3s      1-51       GATTGTAAGGAACTGTAGGCACCATCAATATCGTAAGGGCCCCTAAACGTA

>42_9_1s             1-47       AGCACCTGAAGGCACCTGAAAAGCACCTGAAGGCACCTGAAAAGCAC

>85_11_1s            1-47       GTGAATTGCTATGATTGGTTTAATTTGCTTGTGGTTATGTTGCTATC

>42_13_2s            1-46       AAGCAATGATGATGTTAAGCACTTGGACGTCGTCCAAGTGCTTAAC

>42_21_2s            1-45       CCTGAAACTGAAACCTGAAAGGCACCTGAAACCTGAAACTGAAAC

>42up6_3s            1-43       ATGAAAATTGTGGGCCCCATTAATTTTCGTAGGGACCTGAAAT

>42_36_2s            1-41       TACAGTGTGATGTTAATGTGAATCCCGACAGGTTCCGATCG

>42_24_2s            1-40       CTGTATGCACCATTTTTGTCGTGGCACCATCAATATTTAA

>42_36_1s            1-39       TATCCCTGCCTGGGATGGCCGCACAGCGGTCTGACAGAC

>42_10_1s            1-39       TTGGGCCGGTGTGCTGGGCGTGTCGCTGCCGCTGTTCGA

>II_42_49_B11_1s     1-38       CCGTTGGGCCCCACAAAAACTGTGGGGCCCATCAAAAC

>42_12_1s            1-37       TGTTCCAGCAATGACGACTGCCTGCTGTCGGAGCCTC

>I_42_UP_32_H7_1s    1-36       TCACCTTGTGGCCAAGGGTTCGTATAATTGCGTTCC

>II_42_75_D1_1s      1-33       TCAGAGTTGCGCAGTTTCAGCGTGGTGGCCCTC

>42_19_2s            1-25       ATCAATTGAAGGAAGGAAAGAGTGC

>42_5_1s             1-25       GAAGTTGTTCCATCGAATCTTTTTG

>II_42_52_C1_4s      1-24       ATACCCCCGCTAAAAAAAAAAACA

42_7_2s              1-21       GGCACCTCAAACGTAAGGCAC
```

Transcript corresponding to Homo sapiens genomic DNA (AC027319)

```
>II_85_3_II_2s       1-79       TTCATTTCAGCCATGCAGGGCCTTGCAGGCAAAGCCAGGCCTTTTGGATTTTACTTCAAATGCTGTAGGCACATCAATA
```