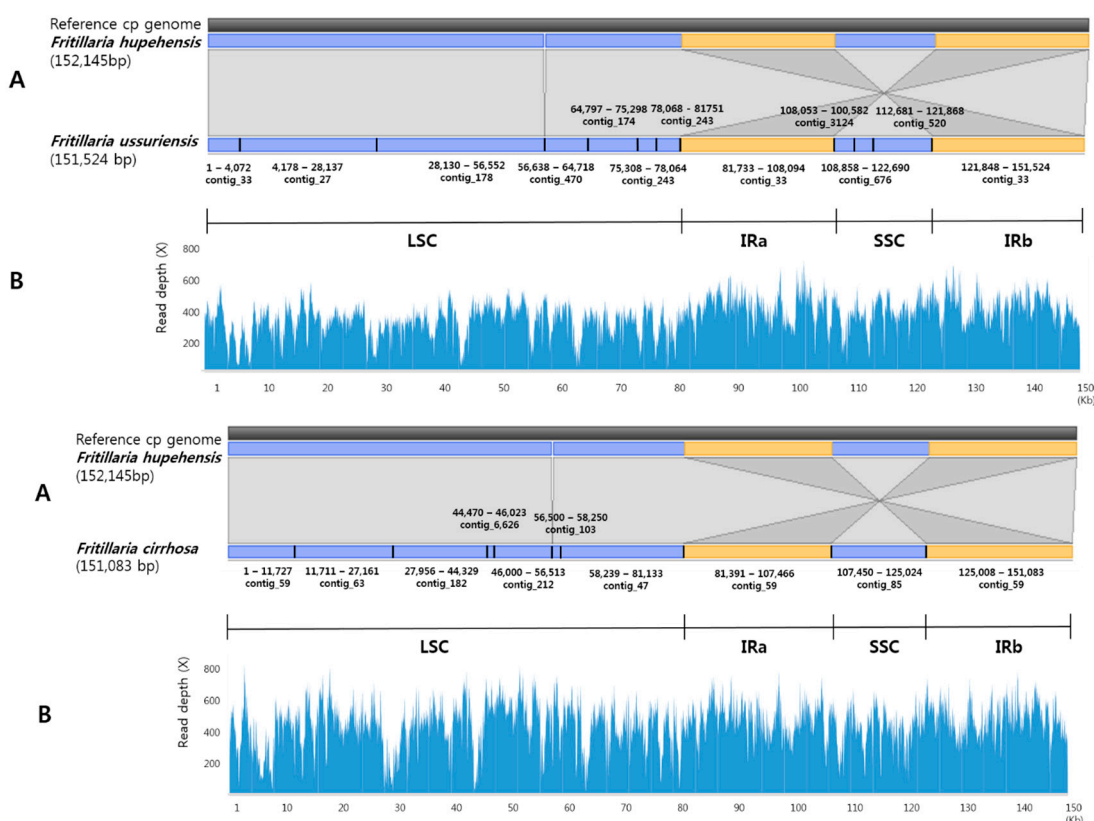


# Supplementary Materials: The Complete Chloroplast Genome Sequences of *Fritillaria ussuriensis* Maxim. and *Fritillaria cirrhosa* D.Don, and Comparative Analysis with Other *Fritillaria* Species

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**Figure S1** Assembly of the complete chloroplast genome sequences of *Fritillaria* species a. Our assembly result validated to reference of *Fritillaria hupehensis* (GenBank accession NC\_024736) using BLASTZ analysis. Alignment of initial contigs was represented on the complete cp genome. The matching contigs position are denoted at the complete genome sequence. Reference genome and assembly are compared to corresponding regions. b. Mapping of Paired - end reads on the completed cp genome of *Fritillaria* species are represented.

**Table S1** Raw read and trimmed read data

| Scientific name                | Total reads | Total raw bases | Trimmed reads | (%)   | Trimmed bases | (%)   |
|--------------------------------|-------------|-----------------|---------------|-------|---------------|-------|
| <i>Fritillaria ussuriensis</i> | 72,445,104  | 10,893,057,091  | 40,109,727    | 55.37 | 5,045,153,661 | 46.32 |
| <i>Fritillaria cirrhosa</i>    | 66,247,268  | 9,961,547,618   | 36,032,152    | 54.39 | 4,511,872,088 | 45.29 |

**Table S2** *Fritillaria cp* genome assembly information

| Scientific name                | Aligned reads # | Coverage (x) | Genome length (bp) | # of contig |
|--------------------------------|-----------------|--------------|--------------------|-------------|
| <i>Fritillaria ussuriensis</i> | 316,479         | 256.63       | 151,524            | 10          |
| <i>Fritillaria cirrhosa</i>    | 553,582         | 452.84       | 151,083            | 8           |

**Table S3** Base composition of two *Fritillaria* chloroplast genomes

| <i>Fritillaria ussuriensis</i> | A (%) | T (%) | G (%) | C (%) | length (bp) |
|--------------------------------|-------|-------|-------|-------|-------------|
| LSC                            | 32.0  | 33.3  | 16.9  | 17.8  | 81,732      |
| SSC                            | 34.4  | 35.0  | 14.4  | 16.3  | 17,114      |
| IR                             | 28.8  | 28.8  | 21.2  | 21.2  | 52,678      |
| total                          | 31.1  | 31.9  | 18.1  | 18.8  | 151,524     |
| CDS                            | 31.1  | 31.5  | 20.0  | 17.5  | 78,951      |
| First position                 | 31.2  | 24    | 26.5  | 18.4  | 26,317      |
| Second position                | 29.6  | 32    | 17.7  | 20.2  | 26,317      |
| Third position                 | 32.3  | 38    | 15.8  | 13.8  | 26,317      |
| <i>Fritillaria cirrhosa</i>    | A (%) | T (%) | G (%) | C (%) | length (bp) |
| LSC                            | 31.9  | 33.3  | 16.9  | 17.9  | 81,390      |
| SSC                            | 34.5  | 35.1  | 14.4  | 16.1  | 17,537      |
| IR                             | 28.7  | 28.7  | 21.3  | 21.3  | 52,156      |
| total                          | 31.1  | 31.9  | 18.1  | 18.8  | 151,083     |
| CDS                            | 31.1  | 31.5  | 19.9  | 17.4  | 79,835      |
| First position                 | 30.2  | 29    | 22.7  | 18.1  | 26,612      |
| Second position                | 31.1  | 32    | 18.9  | 18.1  | 26,612      |
| Third position                 | 32.1  | 34    | 18.2  | 16.2  | 26,611      |

**Table S4** Genes with introns in *Fritillaria* chloroplast genomes and the lengths of the exons and introns

| <i>Fritillaria ussuriensis</i> |        |          |         |           |          | <i>Fritillaria cirrhosa</i> |        |          |         |           |          |
|--------------------------------|--------|----------|---------|-----------|----------|-----------------------------|--------|----------|---------|-----------|----------|
| Gene                           | exon I | intron I | exon II | intron II | exon III | Gene                        | exon I | intron I | exon II | intron II | exon III |
| trnk-UUU                       | 37     | 2613     | 35      |           |          | trnk-UUU                    | 37     | 2562     | 35      |           |          |
| rps16                          | 39     | 882      | 210     |           |          | rps16                       | 39     | 883      | 210     |           |          |
| trnG-UCC                       | 23     | 701      | 37      |           |          | trnG-UCC                    | 37     | 697      | 23      |           |          |
| atpF                           | 144    | 791      | 411     |           |          | atpF                        | 144    | 786      | 411     |           |          |

|              |     |      |      |     |     |              |     |      |      |     |     |
|--------------|-----|------|------|-----|-----|--------------|-----|------|------|-----|-----|
| rpoC1        | 432 | 770  | 1623 |     |     | rpoC1        | 432 | 779  | 1623 |     |     |
| ycf3         | 126 | 733  | 228  | 711 | 159 | ycf3         | 126 | 742  | 228  | 711 | 159 |
| trnL-<br>UAA | 35  | 533  | 50   |     |     | trnL-<br>UAA | 35  | 535  | 50   |     |     |
| trnV-<br>UAC | 39  | 604  | 37   |     |     | trnV-<br>UAC | 39  | 605  | 37   |     |     |
| rps12*       | 114 | -    | 232  | -   | 26  | rps12        | 114 | -    | 232  | -   | 26  |
| clpP         | 71  | 759  | 292  | 593 | 252 | clpP         | 71  | 773  | 292  | 591 | 252 |
| petB         | 6   | 829  | 642  |     |     | petB         | 6   | 826  | 642  |     |     |
| petD         | 6   | 772  | 642  |     |     | petD         | 6   | 761  | 498  |     |     |
| rpl16        | 9   | 996  | 411  |     |     | rpl16        | 9   | 991  | 411  |     |     |
| rpl2         | 393 | 674  | 432  |     |     | rpl2         | 393 | 674  | 432  |     |     |
| ndhB         | 810 | 616  | 756  |     |     | ndhB         | 810 | 617  | 756  |     |     |
| trnI-<br>GAU | 42  | 933  | 35   |     |     | trnI-<br>GAU | 42  | 934  | 35   |     |     |
| trnA-<br>UGC | 38  | 812  | 35   |     |     | trnA-<br>UGC | 38  | 812  | 35   |     |     |
| ndhA         | 552 | 1036 | 540  |     |     | ndhA         | 552 | 1039 | 540  |     |     |

\*rps12 gene is trans-splicing gene.

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**Table S5** Codon-anticodon recognition pattern and codon usage in *Fritillaria* genomes

| Amino acid | Codon  | <i>Fritillaria ussuriensis</i> |       | <i>Fritillaria cirrhosa</i> |      | tRNA                    |
|------------|--------|--------------------------------|-------|-----------------------------|------|-------------------------|
|            |        | Count                          | RSCU* | Count                       | RSCU |                         |
| Phe        | UUU(F) | 965                            | 1.29  | 988                         | 1.23 |                         |
| Phe        | UUC(F) | 530                            | 0.71  | 622                         | 0.77 | trnF-GAA                |
| Leu        | UUA(L) | 904                            | 2     | 763                         | 1.7  | trnL-UAA                |
| Leu        | UUG(L) | 520                            | 1.15  | 580                         | 1.29 | trnL-CAA                |
| Leu        | CUU(L) | 573                            | 1.27  | 513                         | 1.14 |                         |
| Leu        | CUC(L) | 183                            | 0.41  | 249                         | 0.55 |                         |
| Leu        | CUA(L) | 364                            | 0.81  | 390                         | 0.87 | trnL-UAG                |
| Leu        | CUG(L) | 165                            | 0.37  | 205                         | 0.46 |                         |
| Ile        | AUU(I) | 1094                           | 1.42  | 1039                        | 1.36 |                         |
| Ile        | AUC(I) | 450                            | 0.59  | 553                         | 0.73 | trnI-GAU<br>trnI-CAU    |
| Ile        | AUA(I) | 763                            | 0.99  | 695                         | 0.91 | trn(f)M-CAU<br>trnM-CAU |
| Met        | AUG(M) | 638                            | 1     | 560                         | 1    | trnM-CAU                |
| Val        | GUU(V) | 510                            | 1.45  | 485                         | 1.43 |                         |
| Val        | GUC(V) | 186                            | 0.53  | 208                         | 0.61 | trnV-GAC                |
| Val        | GUA(V) | 512                            | 1.46  | 447                         | 1.32 | trnV-UAC                |
| Val        | GUG(V) | 195                            | 0.56  | 217                         | 0.64 |                         |
| Ser        | UCU(S) | 576                            | 1.68  | 522                         | 1.49 |                         |
| Ser        | UCC(S) | 325                            | 0.95  | 331                         | 0.94 | trnS-GGA                |
| Ser        | UCA(S) | 441                            | 1.29  | 467                         | 1.33 | trnS-UGA                |
| Ser        | UCG(S) | 179                            | 0.52  | 254                         | 0.73 |                         |
| Pro        | CCU(P) | 406                            | 1.52  | 334                         | 1.34 |                         |
| Pro        | CCC(P) | 224                            | 0.84  | 208                         | 0.83 | trnS-GCU                |
| Pro        | CCA(P) | 317                            | 1.19  | 312                         | 1.25 |                         |
| Pro        | CCG(P) | 123                            | 0.46  | 144                         | 0.58 |                         |
| Thr        | ACU(T) | 531                            | 1.58  | 390                         | 1.31 | trnP-UGG                |
| Thr        | ACC(T) | 246                            | 0.73  | 238                         | 0.8  |                         |
| Thr        | ACA(T) | 416                            | 1.24  | 394                         | 1.32 |                         |
| Thr        | ACG(T) | 153                            | 0.45  | 173                         | 0.58 | trnT-GGU                |
| Ala        | GCU(A) | 603                            | 1.75  | 433                         | 1.65 | trnT-UGU                |
| Ala        | GCC(A) | 220                            | 0.64  | 183                         | 0.7  |                         |
| Ala        | GCA(A) | 403                            | 1.17  | 305                         | 1.17 |                         |
| Ala        | GCG(A) | 155                            | 0.45  | 126                         | 0.48 | trnG-UCC                |
| Tyr        | UAU(Y) | 826                            | 1.64  | 827                         | 1.45 | trnA-UGC                |
| Tyr        | UAC(Y) | 181                            | 0.36  | 317                         | 0.55 |                         |
| Stop       | UAA(*) | 45                             | 1.61  | 438                         | 1.17 |                         |
| Stop       | UAG(*) | 20                             | 0.71  | 318                         | 0.85 | trnY-GUA                |
| His        | CAU(H) | 501                            | 1.58  | 483                         | 1.44 |                         |
| His        | CAC(H) | 132                            | 0.42  | 189                         | 0.56 |                         |
| Gln        | CAA(Q) | 692                            | 1.5   | 682                         | 1.43 |                         |
| Gln        | CAG(Q) | 228                            | 0.5   | 271                         | 0.57 |                         |
| Asn        | AAU(N) | 1020                           | 1.57  | 892                         | 1.46 | trnH-GUG                |
| Asn        | AAC(N) | 280                            | 0.43  | 332                         | 0.54 | trnQ-UUG                |
| Lys        | AAA(K) | 1048                           | 1.46  | 1026                        | 1.4  |                         |
| Lys        | AAG(K) | 389                            | 0.54  | 441                         | 0.6  |                         |

|      |        |      |      |     |      |          |
|------|--------|------|------|-----|------|----------|
| Asp  | GAU(D) | 861  | 1.61 | 646 | 1.51 | trnN-GUU |
| Asp  | GAC(D) | 211  | 0.39 | 211 | 0.49 | trnK-UUU |
| Glu  | GAA(E) | 1021 | 1.49 | 851 | 1.43 |          |
| Glu  | GAG(E) | 346  | 0.51 | 341 | 0.57 |          |
| Cys  | UGU(C) | 231  | 1.5  | 290 | 1.25 | trnD-GUC |
| Cys  | UGC(C) | 77   | 0.5  | 173 | 0.75 | trnE-UUC |
| Stop | UGA(*) | 19   | 0.68 | 367 | 0.98 |          |
| Trp  | UGG(W) | 452  | 1    | 469 | 1    |          |
| Arg  | CGU(R) | 351  | 1.33 | 248 | 0.92 | trnC-GCA |
| Arg  | CGC(R) | 96   | 0.36 | 106 | 0.39 | trnW-CCA |
| Arg  | CGA(R) | 352  | 1.34 | 309 | 1.15 | trnR-ACG |
| Arg  | CGG(R) | 131  | 0.5  | 165 | 0.61 |          |
| Ser  | AGU(S) | 435  | 1.27 | 355 | 1.01 |          |
| Ser  | AGC(S) | 99   | 0.29 | 173 | 0.49 |          |
| Arg  | AGA(R) | 503  | 1.91 | 534 | 1.99 | trnR-UCU |
| Arg  | AGG(R) | 147  | 0.56 | 249 | 0.93 |          |
| Gly  | GGU(G) | 546  | 1.25 | 471 | 1.19 |          |
| Gly  | GGC(G) | 186  | 0.42 | 211 | 0.53 | trnG-GCC |
| Gly  | GGA(G) | 706  | 1.61 | 558 | 1.41 | trnG-UCC |
| Gly  | GGG(G) | 315  | 0.72 | 340 | 0.86 |          |

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\*RSCU – Relative synonymous codon usage

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30  
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**Table S6** Distribution of tandem repeats in two *Fritillaria* species cp genomes

| <i>F. ussuriensis</i> | position                 | Repeat unit length (bp) | Repeat unit sequence                                        | Repeat numbers | Region |
|-----------------------|--------------------------|-------------------------|-------------------------------------------------------------|----------------|--------|
| 1                     | Intron (rps16, rps16)    | 13                      | TTATAAATTTATA                                               | 2              | LSC    |
| 2                     | IGS (rps16, trnQ-UUG)    | 14                      | TATAATATTAAATA                                              | 3              | LSC    |
| 3                     | IGS (trnR-UCU, atpA)     | 13                      | AATTATTATTCTT                                               | 2              | LSC    |
| 4                     | IGS (trnT-UGU, trnL-UAA) | 54                      | TAATTATTAATTATCTCTAAAATAAAATTATAT<br>AATAAATTATATTATATAATAT | 2              | LSC    |
| 5                     | IGS (trnF-GAA, ndhJ)     | 13                      | CATATATATCTAA                                               | 2              | LSC    |
| 6                     | IGS (rbcL, accD)         | 15                      | TTATTTGTATTGTTTA                                            | 2              | LSC    |
| 7                     | IGS (psaJ, rpl33)        | 13                      | TTATTTTTTTTTT                                               | 2              | LSC    |
| 8                     | IGS (petD, rpoA)         | 33                      | TAAATCCATTCTATAATATATATATAAAATTA<br>TA                      | 2              | LSC    |
| 9                     | CDS (rps11)              | 24                      | TACGTCATTCTTACGTGAACCAA                                     | 2              | LSC    |
| 10                    | IGS (rps8, rpl14)        | 24                      | TTTAATAAAAAATAATTAATTTA                                     | 2              | LSC    |
| 11                    | IGS (rpl22, rps19)       | 1                       | AAAAAAAAAAAAAAAAAAAAAAAAAAAA                                | 25             | LSC    |
| 12                    | CDS (ycf2)               | 21                      | CTTTTGTCCAAGTCACTTCC                                        | 2              | IR     |
| 13                    | CDS (ycf2)               | 24                      | TGACGATATCGATTTTGATGATAG                                    | 2              | IR     |
| 14                    | IGS (psaC, ndhE)         | 47                      | TATTATTATATAATTTATATAATGAAAATCA<br>ATGATTATATAATGAA         | 2              | SSC    |
| 15                    | CDS (ycf1)               | 15                      | CATAATTAATATATT                                             | 2              | SSC    |
| <i>F. cirrhosa</i>    |                          |                         |                                                             |                |        |
| 1                     | IGS (matK, trnK-UUU)     | 14                      | AATGATACATAGTG                                              | 2              | LSC    |
| 2                     | IGS (trnS-GCU, trnG-UCC) | 17                      | TATACATATATTAAATA                                           | 2              | LSC    |
| 3                     | IGS (trnG-UCC, trnR-UCU) | 47                      | AAAGAATTGAAAAGTTAGGAATGAAAAGC<br>GTCCATTGTCTAATGGA          | 2              | LSC    |
| 4                     | IGS (psbM, trnD-GUC)     | 1                       | AAAAAAAAAAAAAAAAAAAAAAAAAAAA                                | 27             | LSC    |
| 5                     | IGS (trnT-GGU, psbD)     | 22                      | ATACATATATAACATATATAAC                                      | 3              | LSC    |
| 6                     | IGS (trnT-UGU, trnL-UAA) | 12                      | TATATTATATAA                                                | 2              | LSC    |
| 7                     | IGS (trnT-UGU, trnL-UAA) | 21                      | TAAGATAAGAATAAAGATCAT                                       | 2              | LSC    |
| 8                     | IGS (trnF-GAA, ndhJ)     | 13                      | CATATATATCTAA                                               | 2              | LSC    |
| 9                     | IGS (rbcL, accD)         | 14                      | TAAATATATAAGTA                                              | 2              | LSC    |
| 10                    | CDS (ycf2)               | 24                      | TGACGATATCGATTTTGATGATAG                                    | 3              | IR     |
| 11                    | CDS (ycf2)               | 24                      | ATATCGTCACTATCATCAATATCG                                    | 3              | IR     |
| 12                    | CDS (ycf1)               | 15                      | CATAATTAATATATT                                             | 2              | SSC    |
| 13                    | CDS (ycf1)               | 15                      | ATTATTATTACTAGT                                             | 2              | SSC    |

33

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**Table S7** Palindromic repeats in two *Fritillaria* cp genomes

|                       | Position              | Repeat unit length (bp) | Repeat units sequences                   | Repeat numbers | Loop (bp) | Region |
|-----------------------|-----------------------|-------------------------|------------------------------------------|----------------|-----------|--------|
| <i>F. ussuriensis</i> | IGS (accD, psal)      | 30                      | ATAATATATCATATTTGAATCTTAAAT<br>ATTA      | 2              | 4         | LSC    |
|                       | IGS (petD, poA)       | 29                      | TAAATCCATTCTATAATATATATATA<br>AAT        | 2              | 1         | LSC    |
|                       | IGS (ccsA, dhD)       | 28                      | ATGTATCTCGAGTTTTTGCGAACCATT<br>T         | 2              | 13        | SSC    |
|                       | IGS (rps15, ycf1)     | 28                      | TTTTATTCTATCGAAATCCCATTTTTA<br>T         | 2              | 7         | SSC    |
| <i>F. cirrhosa</i>    | IGS (petN, psbM)      | 36                      | AATCATGAGATAGTGTGTAGAAAAA<br>ACTATAGATAT | 2              | 1         | LSC    |
|                       | IGS (accD, psal)      | 31                      | ATAATATATCATATTTGAATCTTAAAT<br>ATTA      | 2              | 4         | LSC    |
|                       | IGS (petD, rpoA)      | 25                      | TAAATCCATTCTATAATATATAAAT                | 2              | 5         | LSC    |
|                       | IGS (rpl32, trnL-UAG) | 24                      | TTTTTCTTTATCAATTAAATATTC                 | 2              | 6         | SSC    |
|                       | IGS (ccsA, ndhD)      | 28                      | ATGTATCTCGAGTTTTTGCGAACCATT<br>T         | 2              | 13        | SSC    |
|                       | IGS (rps15, ycf1)     | 25                      | TTTTATTCTATCGAAATCCCATTTT                | 2              | 12        | SSC    |

<sup>a</sup> IGS; Intergenic sequence <sup>b</sup> LSC; Large single copy, IR; Inverted repeat region, SSC; Small single copy

**Table S8** Polymorphic SSRs between *F. ussuriensis* and *F. cirrhosa* cp genomes

| No. | Location   | Region | Motif | Repeat number         |                    |
|-----|------------|--------|-------|-----------------------|--------------------|
|     |            |        |       | <i>F. ussuriensis</i> | <i>F. cirrhosa</i> |
| 1   | psbA-trnK  | IGS    | T     | 13                    | 17                 |
| 2   | trnK-rps16 | IGS    | A     | 17                    | 8                  |
| 3   | trnK-rps16 | IGS    | T     | 22                    | 11                 |
| 4   | rps16-trnQ | IGS    | T     | 10                    | 11                 |
| 5   | trnS-trnG  | IGS    | A     | 11                    | 14                 |
| 6   | trnS-trnG  | IGS    | T     | 11                    | 10                 |
| 7   | atpF-atpF  | Inton  | A     | 14                    | 15                 |
| 8   | atpH-atpI  | IGS    | T     | 12                    | 9                  |
| 9   | atpH-atpI  | IGS    | A     | 11                    | 10                 |
| 10  | rps2-rpoC2 | IGS    | T     | 11                    | 16                 |
| 11  | trnD-trnY  | IGS    | T     | 13                    | 14                 |
| 12  | trnE-trnT  | IGS    | T     | 14                    | 18                 |
| 13  | trnT-psbD  | IGS    | A     | 11                    | 14                 |
| 14  | trnT-psbD  | IGS    | AT    | 8                     | 10                 |
| 15  | psbZ-trnG  | IGS    | A     | 24                    | 12                 |
| 16  | ycf3-ycf3  | intron | A     | 17                    | 12                 |
| 17  | ycf3-ycf3  | intron | A     | 9                     | 8                  |
| 18  | trnS-rps4  | IGS    | A     | 10                    | 12                 |
| 19  | rps4-trnT  | IGS    | T     | 9                     | 8                  |

|    |             |        |      |    |    |
|----|-------------|--------|------|----|----|
| 20 | trnT-trnL   | IGS    | A    | 21 | 17 |
| 21 | trnT-trnL   | IGS    | A    | 9  | 17 |
| 22 | trnL-trnL   | IGS    | AT   | 10 | 12 |
| 23 | trnL-trnF   | IGS    | T    | 13 | 18 |
| 24 | trnF-ndhJ   | IGS    | T    | 9  | 8  |
| 25 | accD-psaI   | IGS    | A    | 10 | 15 |
| 26 | accD-psaI   | IGS    | A    | 17 | 8  |
| 27 | accD-psaI   | IGS    | A    | 9  | 12 |
| 28 | ycf4-petA   | IGS    | A    | 17 | 20 |
| 29 | petA-psbJ   | IGS    | AT   | 8  | 10 |
| 30 | psbE-petL   | IGS    | T    | 13 | 14 |
| 31 | trnW-trnP   | IGS    | A    | 13 | 15 |
| 32 | trnP-psaJ   | IGS    | T    | 11 | 8  |
| 33 | psaJ-rpl33  | IGS    | A    | 11 | 16 |
| 34 | clpP-clpP   | intron | T    | 16 | 15 |
| 35 | clpP-clpP   | intron | A    | 11 | 13 |
| 36 | clpP-clpP   | intron | A    | 9  | 8  |
| 37 | clpP-clpP   | intron | T    | 10 | 11 |
| 38 | clpP-psbB   | IGS    | A    | 10 | 13 |
| 39 | petD-rpoA   | IGS    | AT   | 10 | 14 |
| 40 | rpl16-rpl16 | intron | T    | 17 | 14 |
| 41 | rpl16-rps3  | IGS    | T    | 18 | 15 |
| 42 | rps3        | exon   | T    | 11 | 8  |
| 43 | rpl22-rps19 | IGS    | A    | 25 | 23 |
| 44 | ndhF-rpl32  | IGS    | A    | 8  | 10 |
| 45 | rpl32-trnL  | IGS    | T    | 13 | 11 |
| 46 | ndhG-ndhI   | IGS    | AAAT | 12 | 16 |
| 47 | ndhA-ndhA   | intron | A    | 13 | 12 |
| 48 | ndhH-rps15  | IGS    | A    | 8  | 9  |