

**Downstream of *rpl5***

342428 TAGGTTTTCATAGCAAATAGAGACACCGAGGCCCTCTCCACAACCTAGTAGTTGATGGG  
 342368 TATGGGGAGGGGAGAGA-AGAGTGGGTATGAGGGCTTCGTCGCTTGT 342340

**284s** Repeat site A

337381 acaaaagagatgggatagagggcagagagatggagtg-gaggg-ttcgcatcgcaagattcct  
 337441 attggtgcggaaatgggtagaggttaaagcgaagcacagagaccagaccacggatcccc  
 337501 cttttcaattgacatagtttgaccagtgaactccctgctgogtgcaatagttgttccgag  
 337561 gacaatcaatgggtatataaaagaccaacgaaacgacgagtgagaaggataagggggagt  
 337621 agtaggaggagctttcattgaagtagaggtttcatcgagtcacgagagatagaatga  
 gacaaagcataaaggggagagcgctt

Formation of the start codon of *orf367*

**cs4**

3781 TAGGTATCCA TCTATACTAA TAGATATACC GAGGCCCCCC AACCTACTAG TTGTTGGTGG  
 3841 GGGAAAGAAG AGTGGGAATG TGGGCTTCTT TCATTGATT TTTGCTTGGT GACGACTGAG  
 3901 TTAGGGTTCT AGGACTGTTT TATGGGAAGG GGGTTACGG ATTCCAGGCC GTAGTAGACA

AAAAAATA ATTGGAACTA TTGAGCGCTG

Repeat site G

**Upstream flanking sequence of *atp6***

acgcagcaaa ccgagggccct gogtgcgcgcg tacgtatccgc 3840  
 ctacgaataa Taggtagccc caccaccaggc agagtttgtg agccgtgtaa taggcgaaca 3900

**cs7**

3841 CTACTTGTGGTTTGGTGGGGAAAGAAGAGTGGGTATGAGGGCTTCTTTTCACTTTTTGT  
 3901 TTTGTGTTGGTGAAGGAGAGAGGCATTAGTTCGGGGGAAGCACCATAGGAAGGAATGGAG

Repeat site B

Repeat site B'

**Upstream flanking sequence of *rps3***

ggagcataaaa aTGTAGGTGA

3901 -GTCAATTGC GTGTGCCTT CAAGTATTC GTATTGTAAC AATATTGCAT CGCATCCAA  
 3961 ACAAAGGTGC ATGTACGGTT CTAAGGGAT ACAATTTTGT CTAAATCAT CGAGAAAGAT

**S367**

2881 AGGTATCCAT CTTAGCAAAT AGAGATACCG AGCCCCACCA ACGTACTACT TGTTGGTTTG  
 2941 GTGGGAAAAG AAGAGTGGGT ATGAGGGCTT CTTTCACTTT TTGTTTTTGT GTTGGTGA  
 3001 AGAGAGGCAT TAGTTCGGGG GAAGGCACCA TAGGAAGGAA TGGAGAAAAG GGAATGCCTA

site B

**S352a**

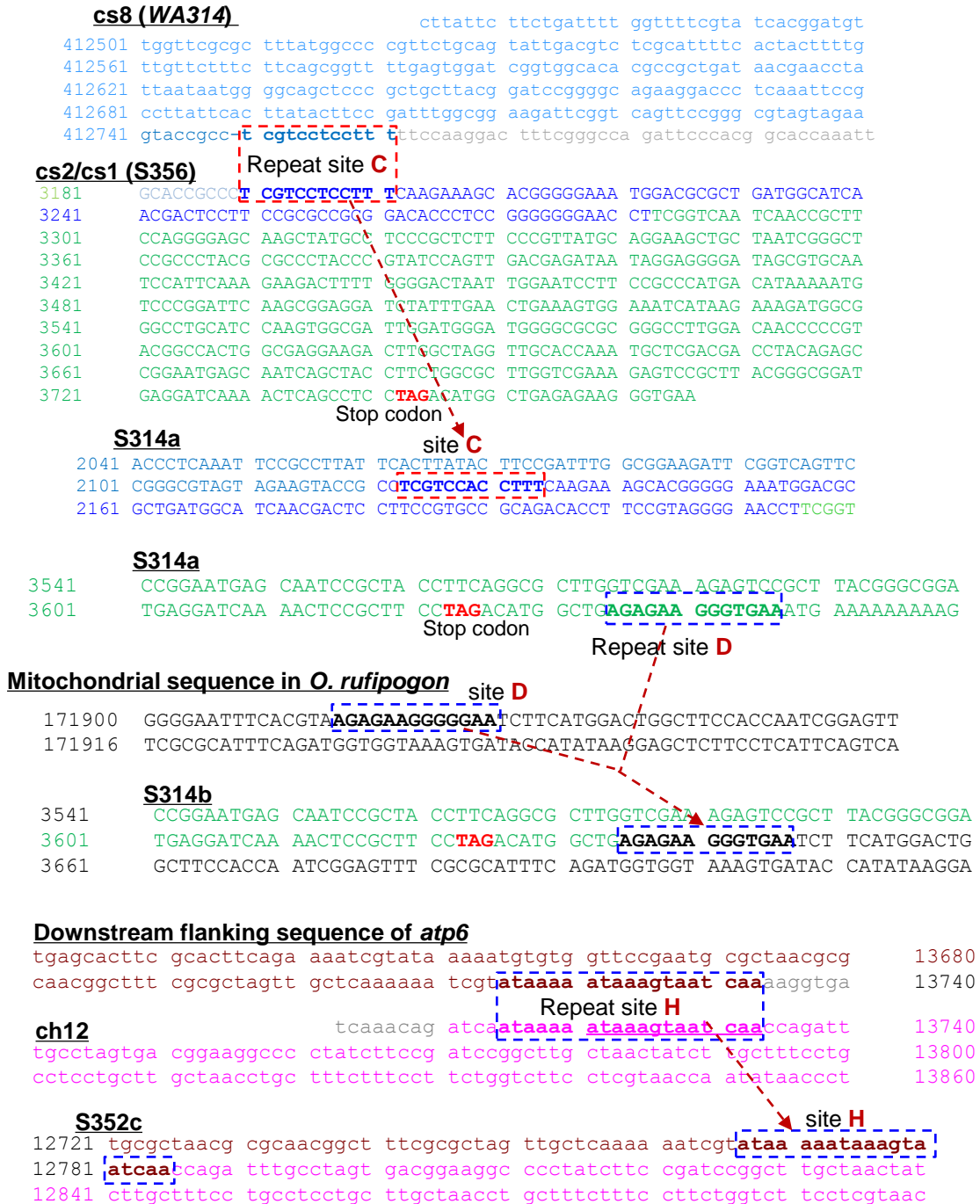
2881 CTACTTGTG GTTTGGTGGG GAAAGAAGAG TGGGTATGAG GGCTCTTTC ACTTTTTGTT  
 2941 TTTGTGTAGG TGAATCAATT GCGTGTGGCC TTCAAGTATT TCGTATTGTA ACAATATTCC  
 3001 ATCGGCATCC AAACAAAGT GCATGTACGG TTCCTAAGGG ATACAATTT GTCTTAAATC

site B'

**S352c**

2821 actattgagc gctgtaggta tccatctata ctaatagata taccgagccc ctgocgtgcgc  
 2881 cgtacgtacc gctacgaat aaTaggtagc cccaccocag gcagagittg tgagccogtgt

site G



**Figure S6.** The repeat sites for recombination events among the donor (source) sequences to generate the new structures. Site A is for recombination between the fragment 284s from *orf284* and the downstream position of *rpl5*; site B is for recombination between cs4 and cs7; site B' (a part of site B) is for recombination between cs4 of S356 and the *rps3*-containing sequence to generate S352a; site C is for recombination between cs2 of S356 and cs8 to produce S314a; site D is for recombination between S314a and a mitochondrial sequence to produce S314b; sites G and H are for integration of the *atp6*-containing sequence into S352b to generate S352c. The sites E and F are shown in Figure S6.