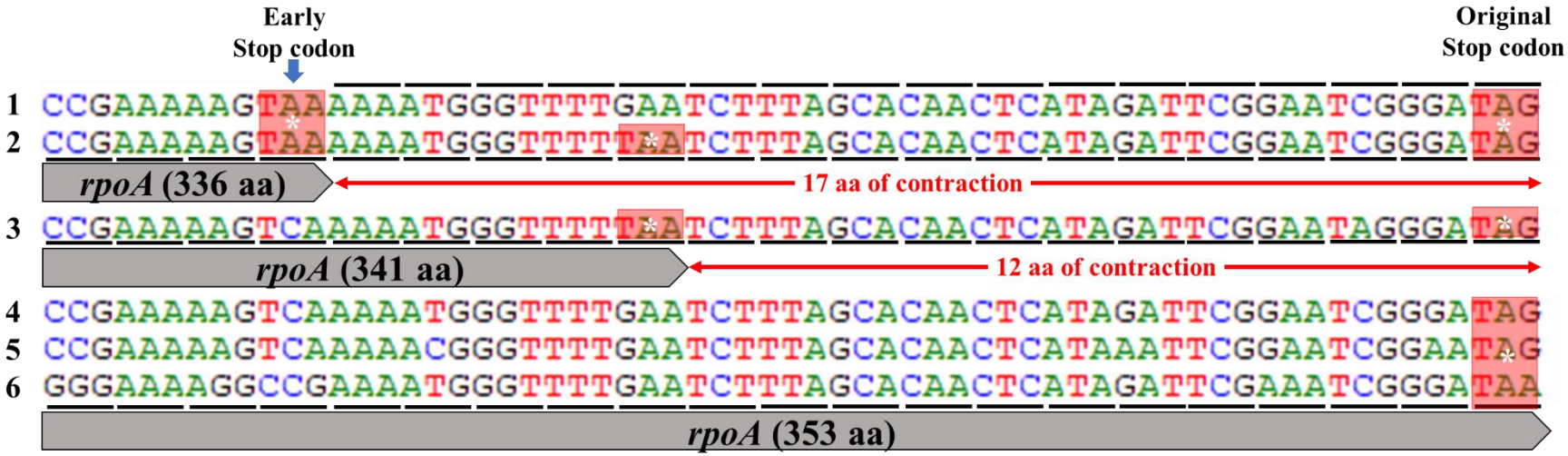
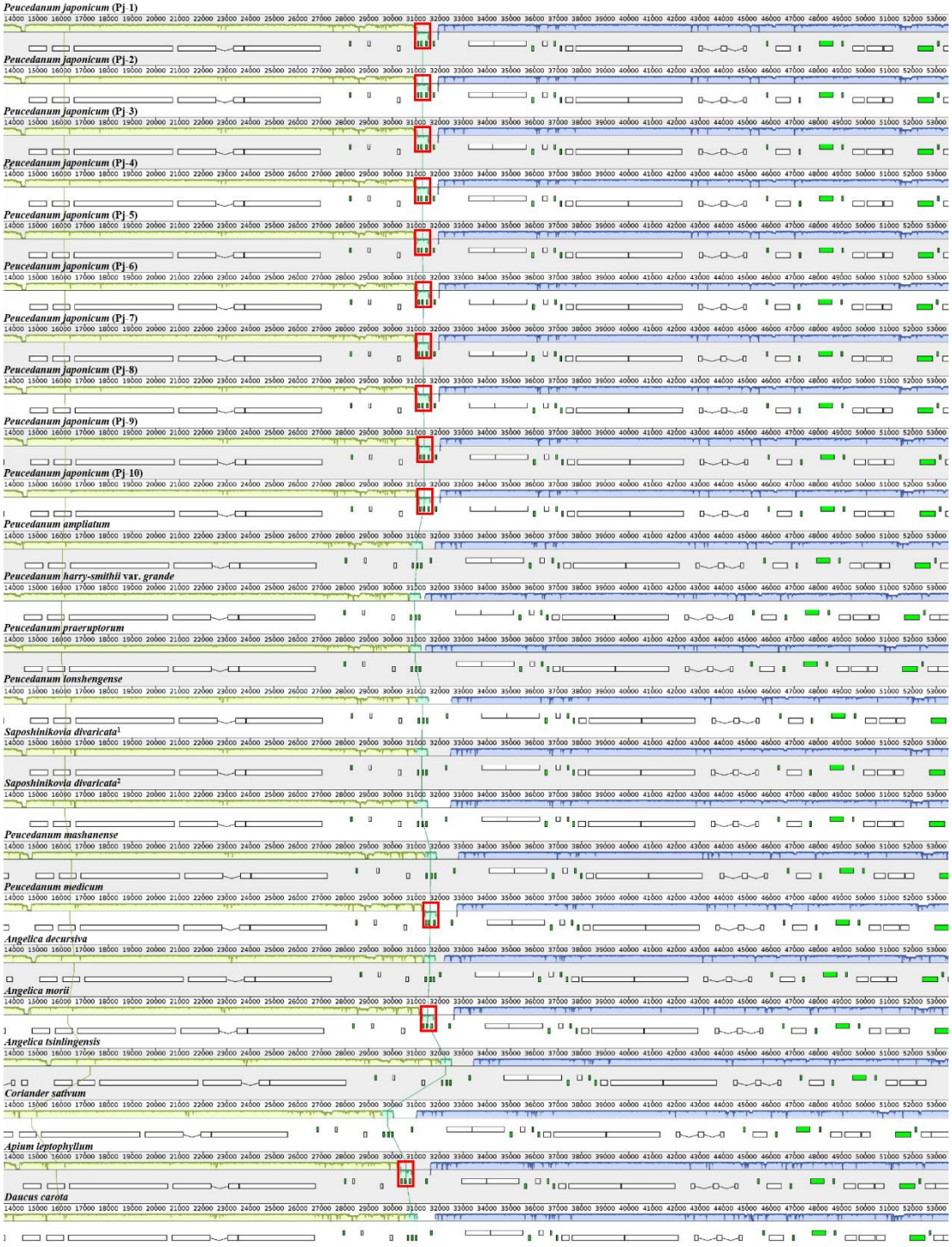
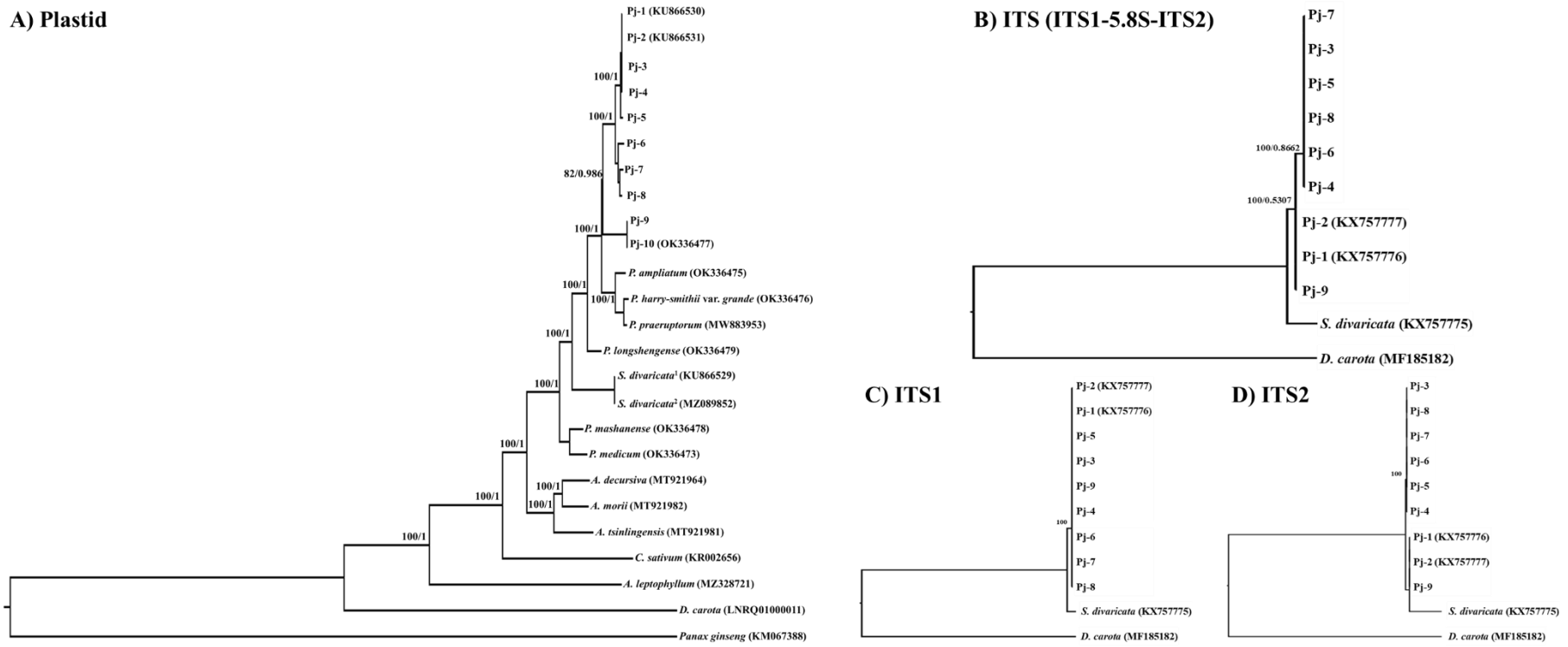


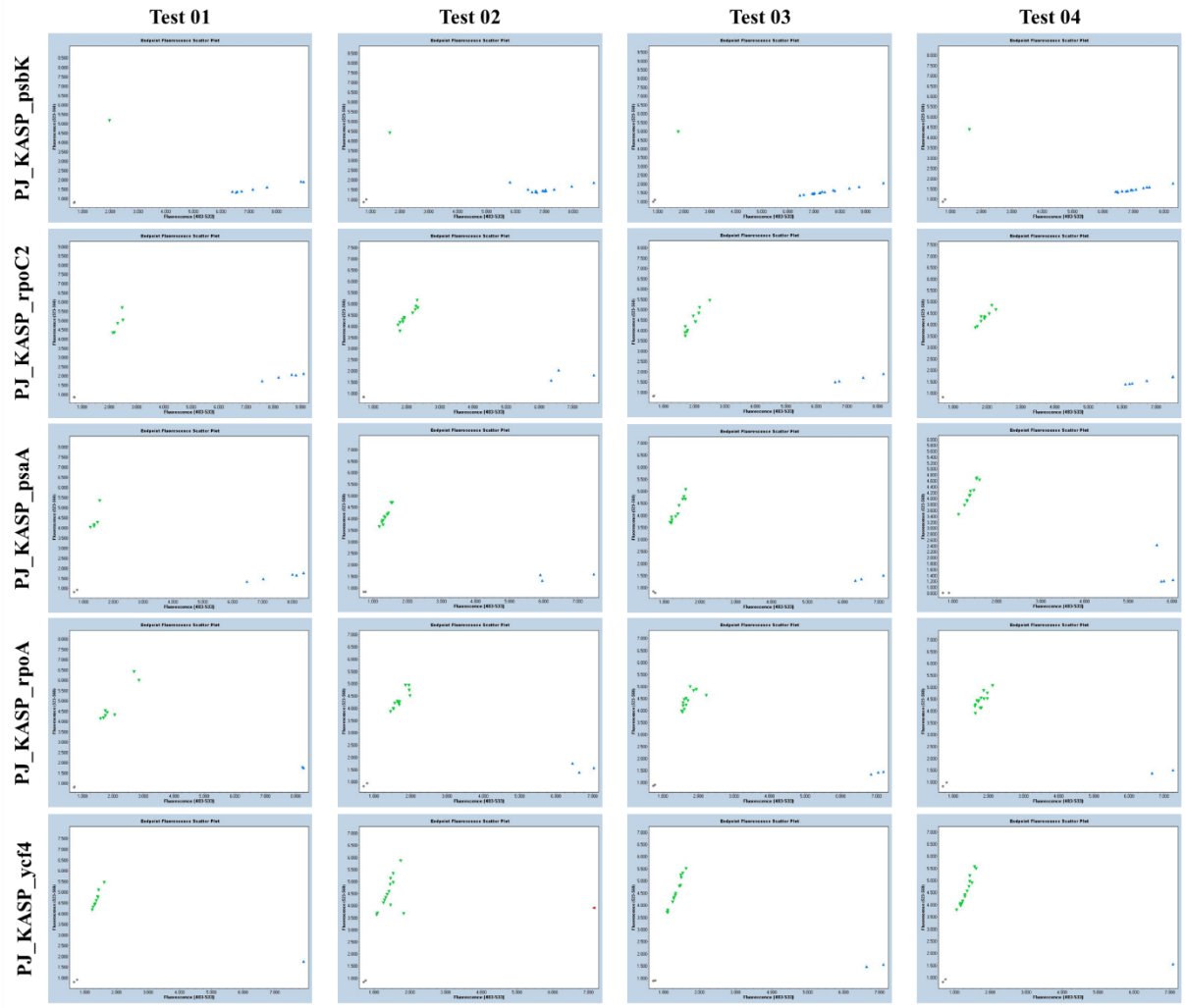
Supplementary Figure S1. Early termination of the *rpoA* gene in the PJ plastomes by an internal stop codon. Blue arrow indicates nucleotide transversion (cytosine to adenine) occurred in Pj-1, Pj-2, Pj-3, Pj-4, Pj-5, Pj-9 and Pj-10 induced early termination point occurrence. 1: Pj-1, Pj-2, Pj-3, Pj-4, and Pj-5, 2: Pj-9 and Pj-10, 3: *A. tsinlingensis*, 4: Pj-4, Pj-5, Pj-6, *P. ampliatum*, *P. harry-smithii* var. *grande*, *P. praeuptorum*, *P. longshengense*, *L. seseloides*, *S. divaricata*, *P. mashanense*, *P. medicum*, and *C. sativum*, 5: *A. leptophyllum*, 6: *D. carota*



Supplementary Figure S2. Inversion of *trnD-trnY-trnE* genes in plastomes of PJ and its related species. The Mauve alignment result was utilized to detect inverted regions. In ten PJ accessions, *P. medicum*, *A. morii*, and *A. leptophyllum*, inverted regions of *trnD-trnY-trnE* genes were observed. Inverted regions of each species were marked with red line box.



Supplementary Figure S3. Phylogenetic relationship from ML and BI methods using plastid CDS sequences and ITS regions. Bootstrap support value and posterior probabilities (BP/PP) are shown above the branches. A) Topology of a plastome-based tree used 76 plastid gene sequences. B) Topology of a ITS-based tree used internal transcribed spacers (ITS1 and ITS2) and 5.8S rDNA. C) Topology of a ITS1 tree. D) Topology of a ITS2 tree. The topology of the ML tree was used for the ITS1 and ITS2 trees, as the polytomy of the BI tree.



Test 01 result

No	*psbK*	*rpoC2*	*psaA*	*rpoA*	*ycf4*
6	Y	Y	Y	Y	Y
35	Y	Y	Y	Y	Y
8	Y	Y	Y	Y	Y
31	Y	Y	Y	Y	Y
14	Y	Y	Y	Y	Y
11	Y	X	X	Y	Y
10	Y	X	X	Y	Y
40	Y	X	X	X	Y
18	X	X	X	X	X
42	Y	X	X	Y	Y

Test 02 result

No	*psbK*	*rpoC2*	*psaA*	*rpoA*	*ycf4*
48	X	X	X	Y	Y
49	X	X	X	Y	Y
50	X	X	X	Y	Y
51	X	X	X	Y	Y
52	X	X	X	Y	Y
53	X	X	X	Y	Y
54	X	X	X	Y	Y
55	X	X	X	Y	Y
43	X	X	X	Y	Y
46	X	X	X	Y	Y
39	X	X	X	Y	Y
9	X	X	X	Y	Y
23	X	X	X	Y	Y
20	X	X	X	X	Y
2	X	X	X	X	Y
C	Y	Y	Y	X	X

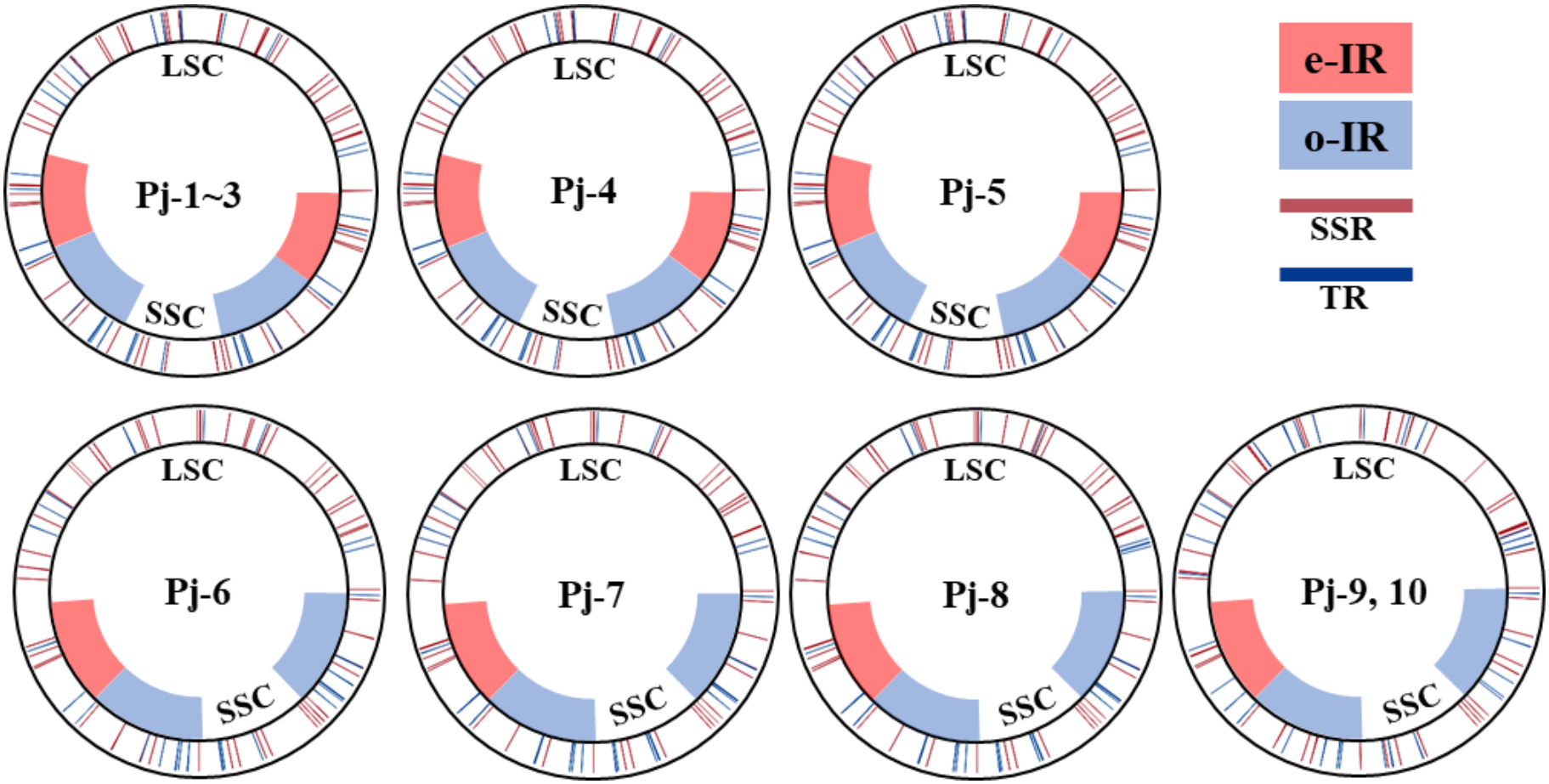
Test 03 result

No	*psbK*	*rpoC2*	*psaA*	*rpoA*	*ycf4*
5	X	Y	Y	Y	Y
4	X	Y	Y	Y	Y
3	X	X	X	X	Y
24	X	X	X	X	X
1	X	Y	Y	Y	Y
41	X	Y	Y	Y	Y
44	X	Y	Y	Y	Y
45	X	X	X	Y	Y
22	X	X	Y	Y	Y
25	X	Y	Y	Y	Y
33	X	Y	Y	Y	Y
34	X	Y	Y	Y	Y
36	X	Y	Y	Y	Y
37	X	Y	Y	Y	Y
38	X	Y	Y	Y	Y
C	Y	-	-	X	X

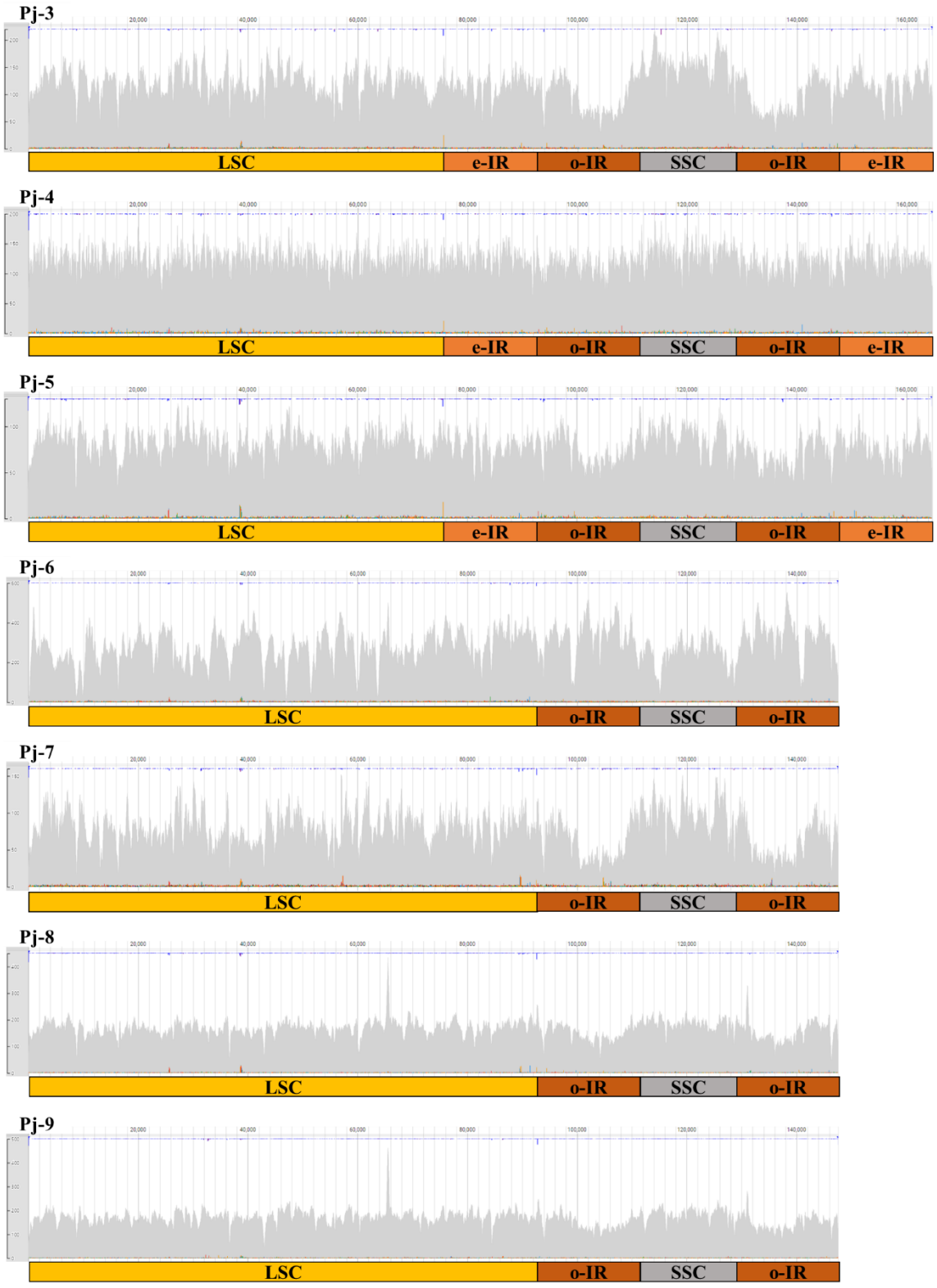
Test 04 result

No	*psbK*	*rpoC2*	*psaA*	*rpoA*	*ycf4*
47	X	X	X	X	Y
21	X	X	X	X	Y
26	X	Y	Y	Y	Y
27	X	Y	Y	Y	Y
28	X	Y	Y	Y	Y
29	X	Y	Y	Y	Y
30	X	Y	Y	Y	Y
32	X	Y	Y	Y	Y
19	X	X	Y	Y	Y
12	X	X	X	X	Y
13	X	Y	Y	Y	Y
15	X	Y	Y	Y	Y
16	X	Y	Y	Y	Y
17	X	Y	Y	Y	Y
7	X	X	X	X	Y
C	Y	X	-	-	X

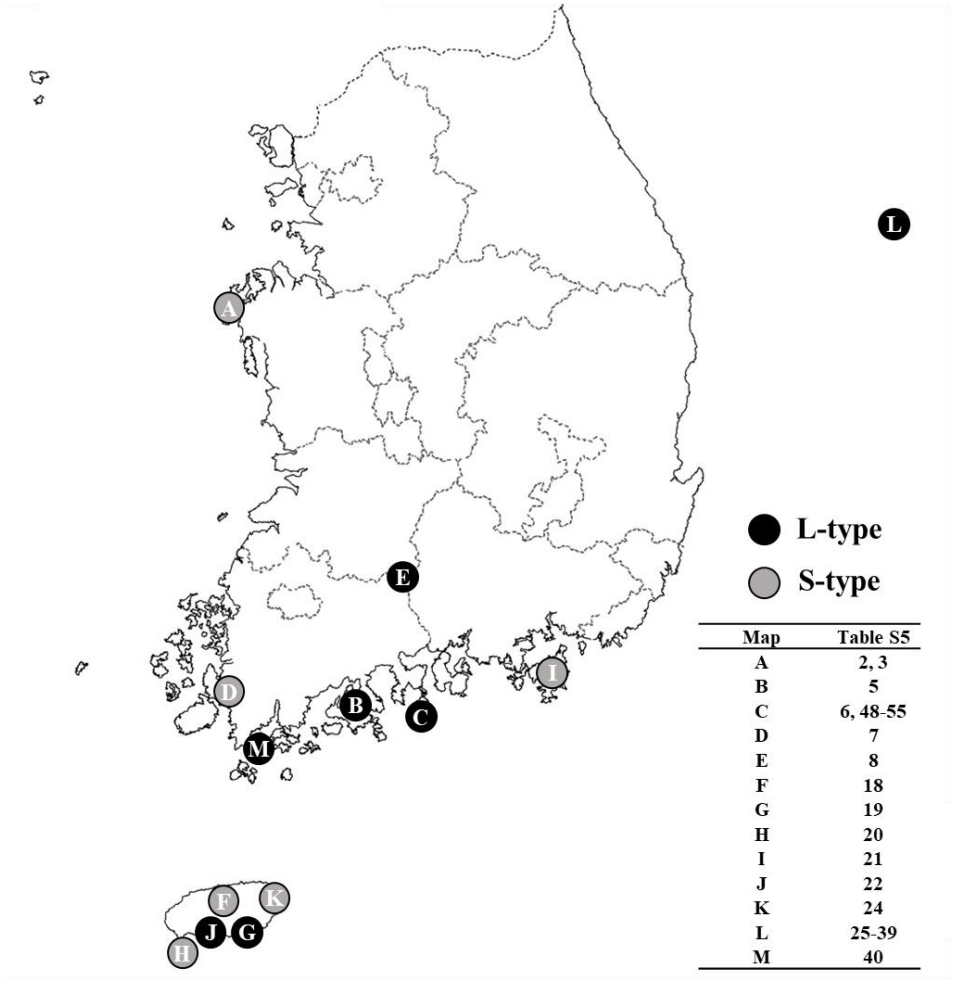
Supplementary Figure S4. Whole KASP marker plots and its genotyping results. X and Y genotypes were marked A and B respectively in Fig 5. C is control.



Supplementary Figure S5. Repeat distribution in the plastomes of *P. japonicum*. Red lines indicate SSR (simple sequence repeat) and blue lines indicate TR (tandem repeat). Red and blue shadows indicate e-IR (expanded IR) and o-IR (original IR), respectively. L-type plastomes (Pj-1~5) have expanded IR regions (eIR and o-IR), while S-type plastomes (Pj-6~10) have original form (o-IR).



Supplementary Figure S6. Validation of the seven newly assembled PJ plastomes. The grey shadow regions displayed the coverage, while the colored lines below the bottom lines indicated the variations in the assembled results.



Map	Table S5
A	2, 3
B	5
C	6, 48-55
D	7
E	8
F	18
G	19
H	20
I	21
J	22
K	24
L	25-39
M	40

Supplementary Figure S7. Collected sample information used in this study. Black-colored circles and gray-colored circles indicate the collected site in South Korea and indicate L-type and S-type, respectively. The table bottom right indicates the collected site and detail ID information marked on Supplementary Table S5.