

Supplementary Materials: Detection of Ribosomal DNA Sequence Polymorphisms in the Protist *Plasmidiophora brassicae* for the Identification of Geographical Isolates

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Table S1. Nucleotide sequence variation among 11 *P. brassicae* isolates in “region 2” of large subunit (LSU) as in Figure 4.

Isolate	T	C	A	G	GC (%)	Total
AB526843	23.2	22.4	25.9	28.5	50.9	509
Gangneung 1	22.0	23.5	24.3	30.2	53.7	510
Yeoncheon	22.0	23.5	24.3	30.2	53.7	510
Daejon	22.0	23.5	24.3	30.2	53.7	510
Haenam 2	23.8	21.7	25.8	28.7	50.4	512
Seosan	23.8	21.7	25.8	28.7	50.4	512
Phyongchang	23.5	21.7	26.5	28.3	50	506
Gangneung 2	22.0	23.5	24.3	30.2	53.7	510
Haenam 1	21.8	24.1	24.1	30.0	54.1	510
Hoengseong	21.8	24.1	24.1	30.0	54.1	510
Geumsan	23.6	21.8	26.5	28.1	49.9	509
Goesan	23.6	21.8	26.5	28.1	49.9	509
Average	22.8	22.7	25.3	29.2	51.9	510

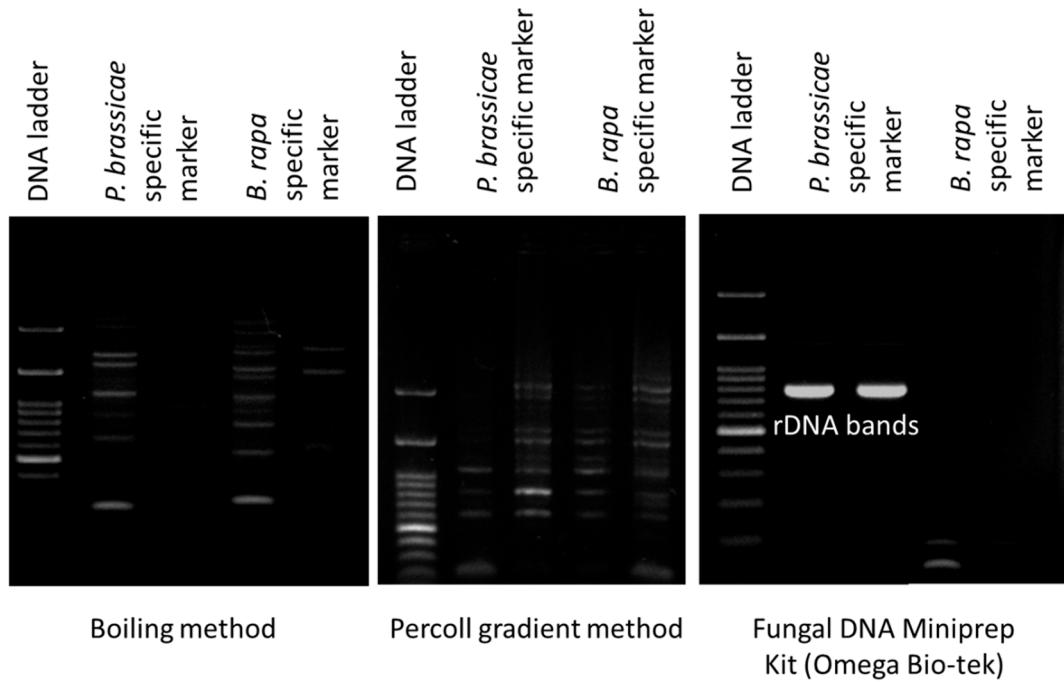


Figure S1. *P. brassicae*-specific markers and *B. rapa*-specific markers show rDNA bands of *P. brassicae* and DNA bands of Chinese cabbage.

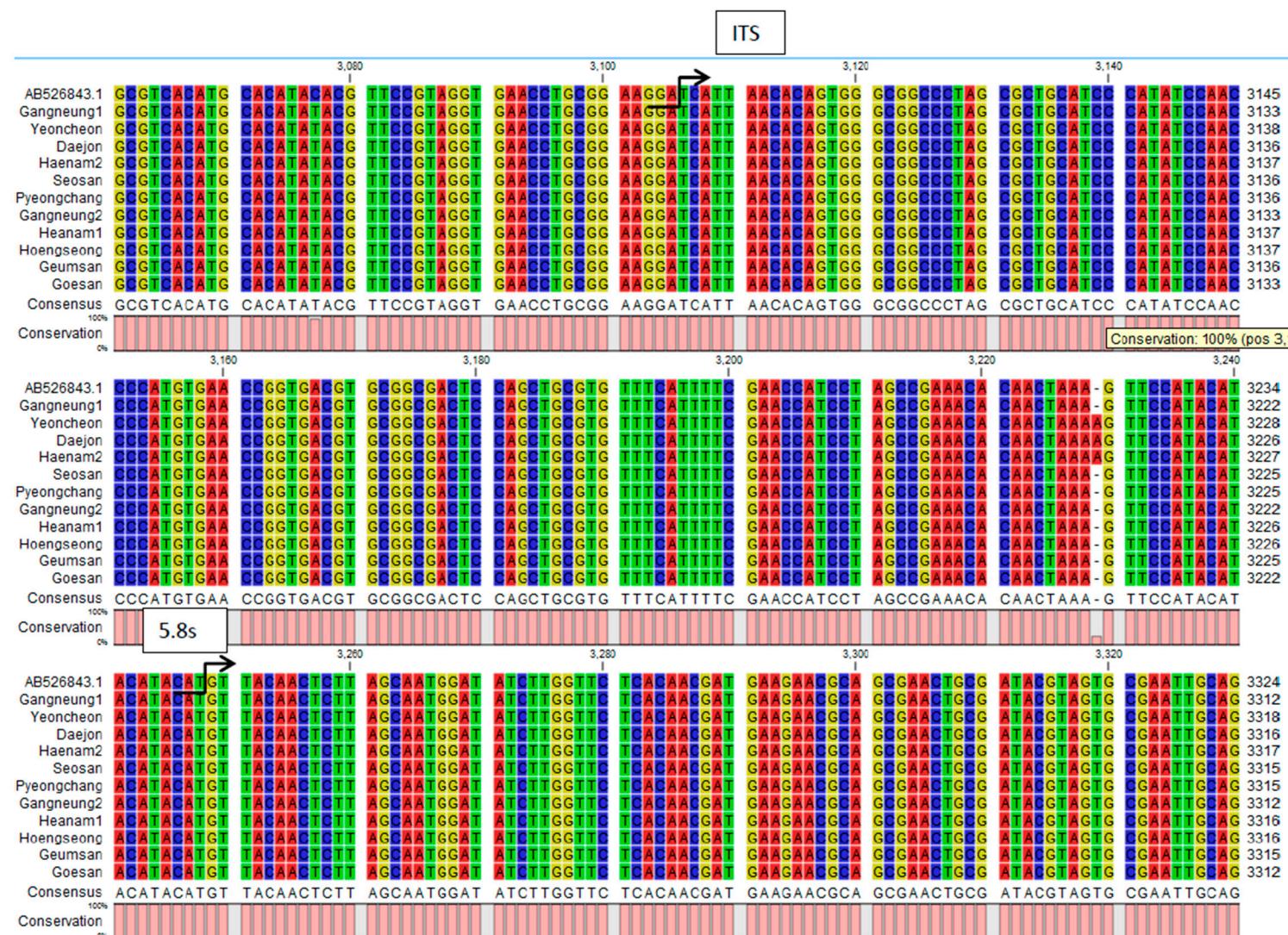


Figure S2. Cont.

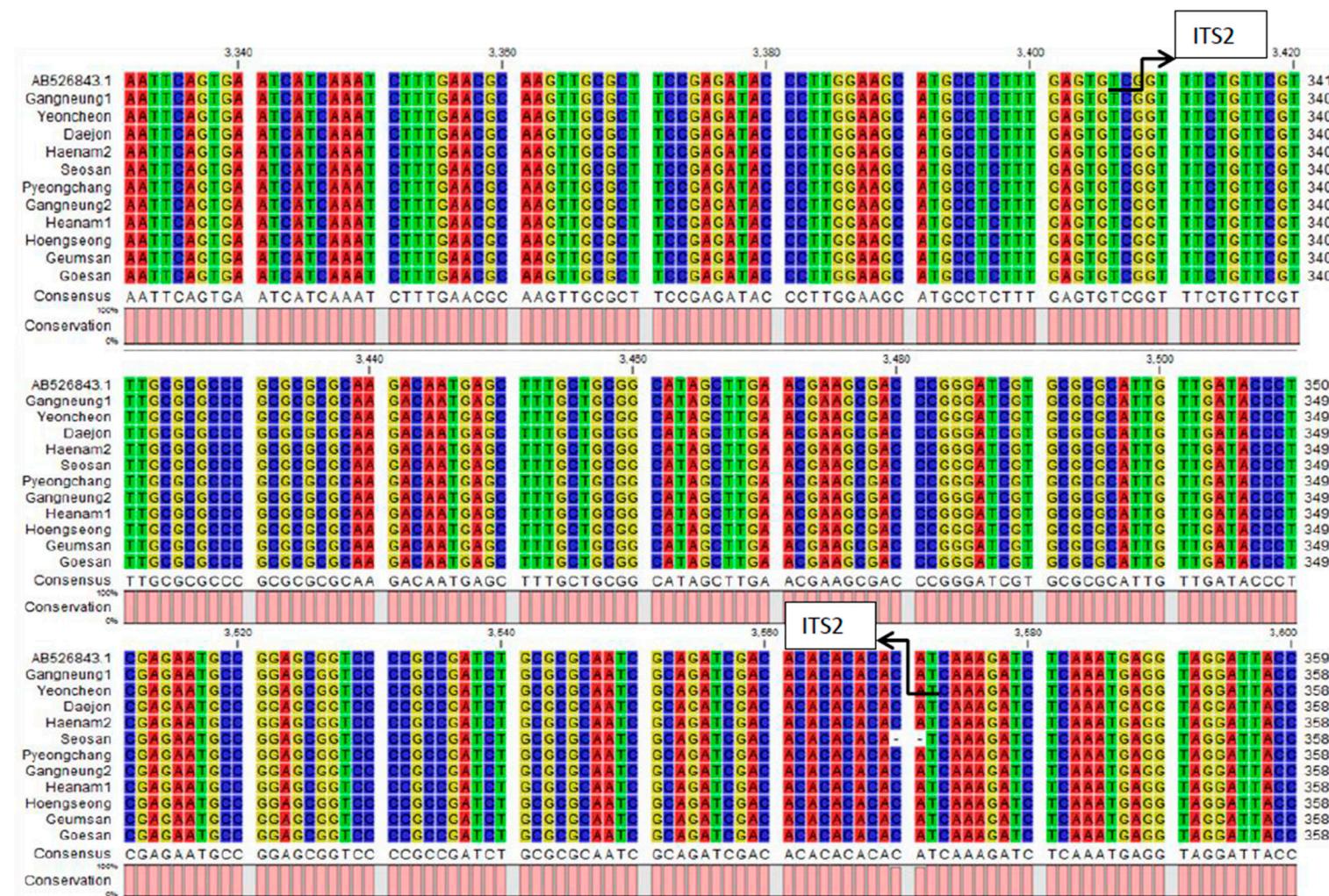


Figure S2. Nucleotide Sequence of ITS1 (3106–3247 bp), 5.8s (3248–3408) and ITS2 (3409–3570) region. Blue, yellow, red and green colors represent C, G, A and T residues.

<pre> SSU-del : GGACTGCTAATTGGAATGAGAACAAAGTTAACCTATTATCGAGGATCCATTGGAGGGCAAAGTCTGGTC----- : 68 U18981.1 : GGACTTAATTGGAATGAGAACAAAGTTAACCTATTATCGAGGATCCATTGGAGGGCAAAGTCTGGTGACGATTCGACAGTGTCTGTTG : 91 GGACT TAATTGGAATGAGAACAAAGTTAACCTATTATCGAGGATCCATTGGAGGGCAAAGTCTGGTG 100 * 120 * 140 * 160 * 180 SSU-del : ----- U18981.1 : CTGTTGGGCCAGAGATAGTACCGGCTCTCTTTAAAGAAGTTATGCGTGTAGTCGAGCAGCCCATCTAGTTGGCTGGCTGCCGGC : 182 * 200 * 220 * 240 * 260 * SSU-del : ----- U18981.1 : GAGGTAACCTGGTACGAGGAAGGCTAACGGATTTTGATAATCCTATGCTAATCTCGTGGCGACCTGTGCCGAAGCGATCGGCATAG : 273 280 * 300 * 320 * 340 * 360 SSU-del : ----- U18981.1 : AGGCCGTCGTAACGCCGGAAAGGTACCGGGCGGCTTCCACAGTCGCTCAAGAACCTGCTAATCCCATTGCAAAGAAAATGCCATG : 364 * 380 * 400 * 420 * 440 * SSU-del : ----- U18981.1 : GACTGGTAGCGCCCACAACGCAAAGGACGATCGTCAGTGTGGCGCGTGTGGAGGAATGCCATCAGACGAGACCCGTATATGTTG : 455 460 * 480 * 500 * 520 * 540 SSU-del : CCAGCAGCCCGGTAATCCAGCTCCAATAGCGTATATTAAAGTTGCGAGTTAAAGCTCGTAGTTGGACTTGTGTGCCCTGCGCGT : 158 U18981.1 : CCCAGCAGCCCGGTAATCCAGCTCCAATAGCGTATATTAAAGTTGCGAGTTAAAGCTCGTAGTTGGACTTGTGTGCCCTGCGCGT : 546 CCCAGCAGCCCGGTAAT CCAGCTCCAATAGCGTATATTAAAGTTGCGAGTTAAAGCTCGTAGTTGGACTTGTGTGCCCTGCGCGT * 560 * 580 * 600 * 620 * SSU-del : TTCAAGCGGTCTCGCGTCAAAAGAGCGTTACGACATGCGGCCCGGGCGTACAATCTCAACTGGATCGCGCTGGCTTGATGACTGG : 249 U18981.1 : TTCAAGCGGTCTCGCGTCAAAAGAGCGTTACGACATGCG---CGCGGGCGTACAATCTCAACTGGATCGCGCTGGCTTGATGACTGG : 634 TTCAAGCGGTCTCGCGTCAAAAGAGCGTTACGACATGCG CGCGGGCGTACAATCTCAACTGGATCGCGCTGGCTTGATGACTGG 640 * 660 SSU-del : GCGCTGCCTATTCGGTTGATCGTTACTGTGA : 281 U18981.1 : GC-TGCTATTCGGTTGATCGTTACTGTGA : 664 GC TGCTATTCGGTTGATCGTTACTGTGA </pre>
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Figure S3. SSU sequence comparison between two groups of Korean *P. brassicae* isolates showing a 388-bp deletion.

Sequences 4425-4594

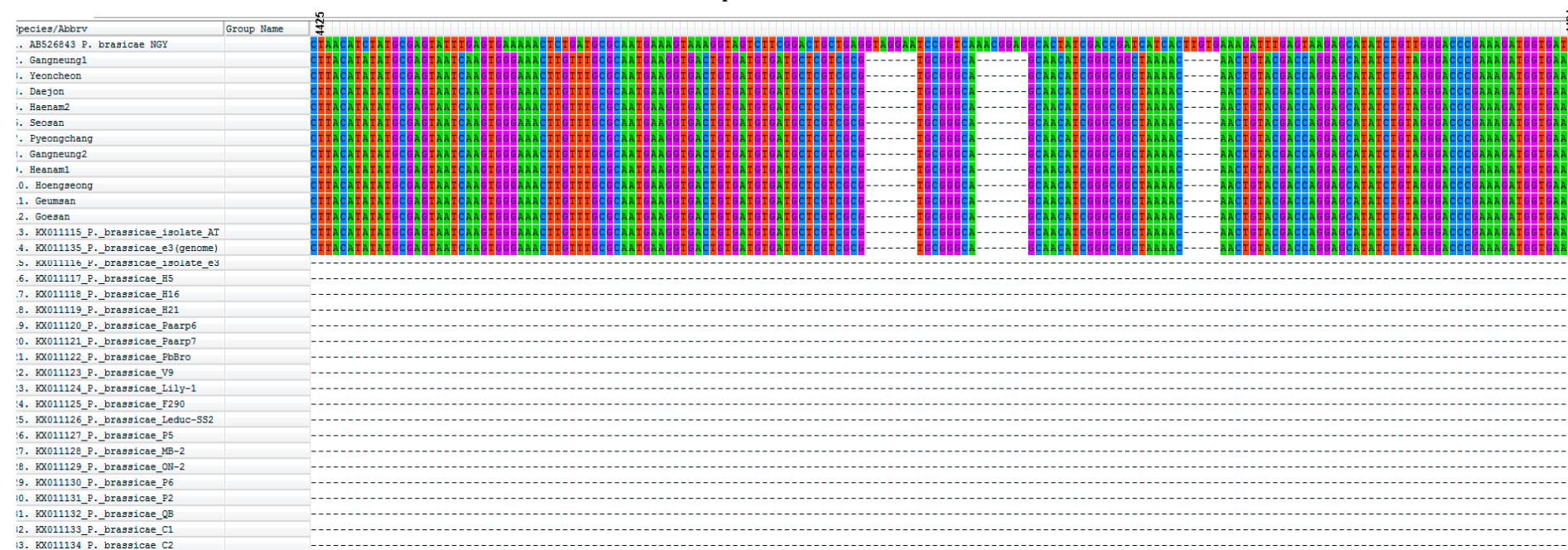


Figure S4. Cont.

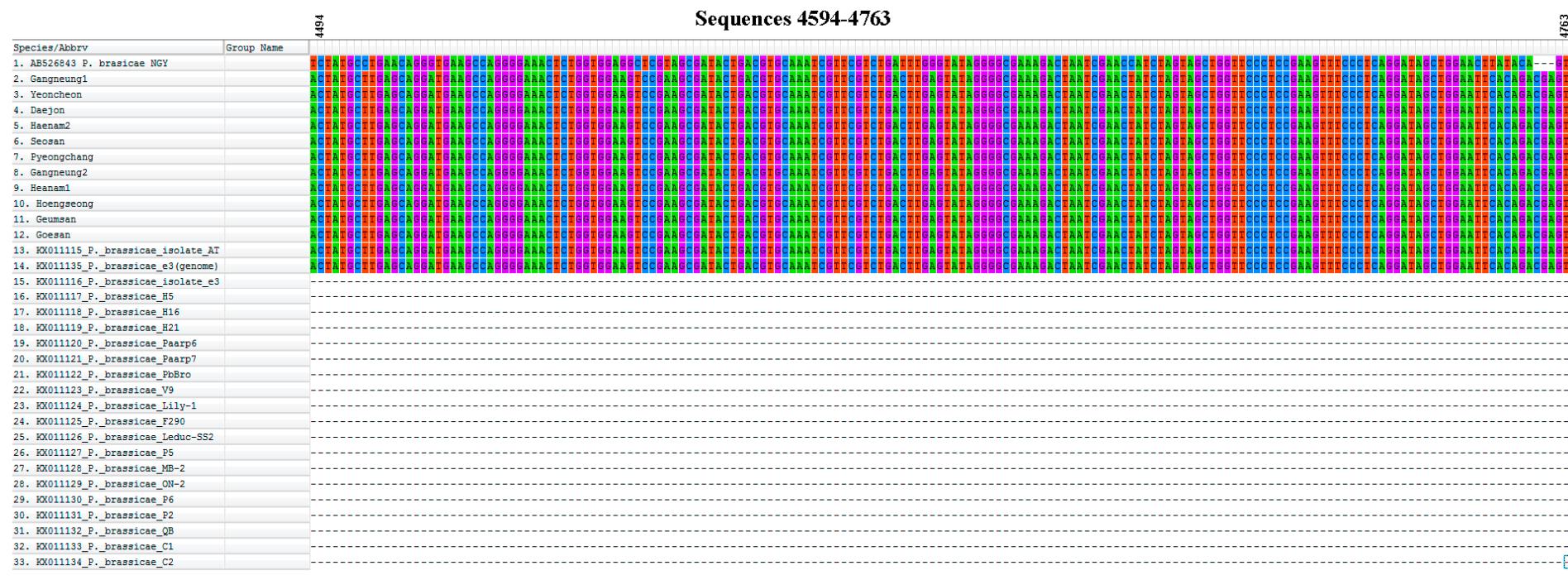
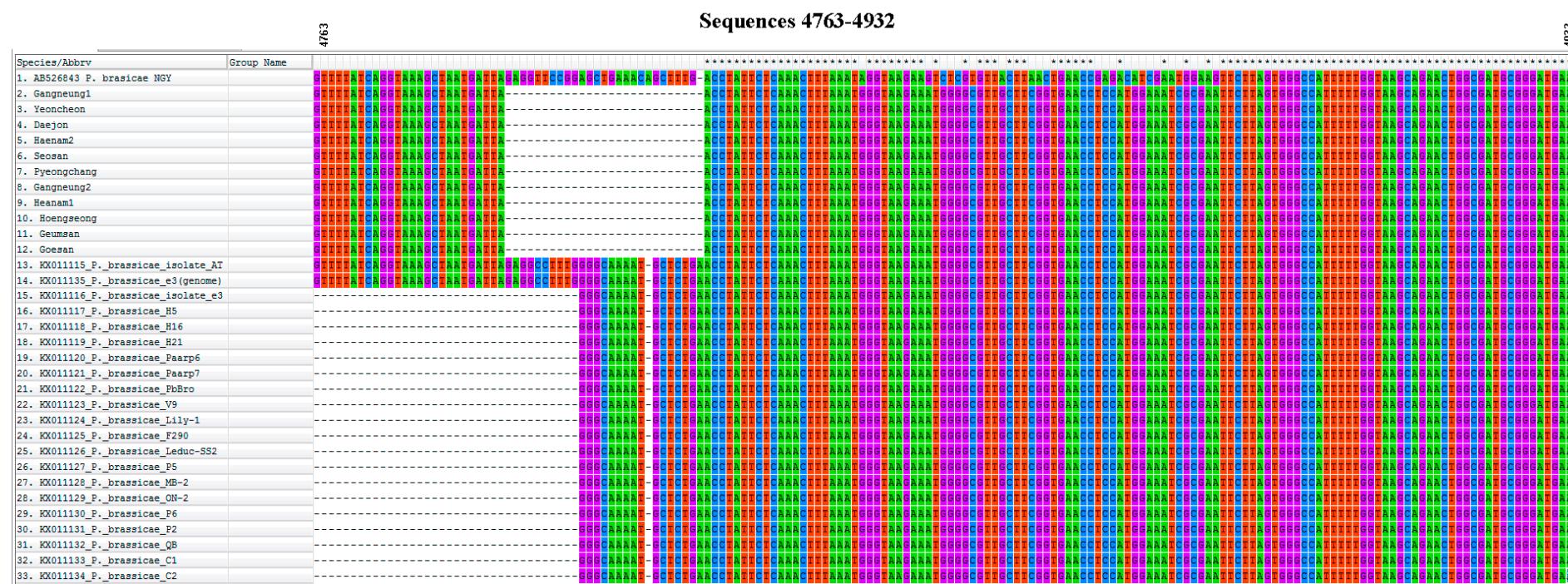


Figure S4. Cont.

**Figure S4. Cont.**

Species/Abbrv	Group Name	Sequences 4932-5101
1. ABS26843	P. <i>brassicaceae</i> NGY
2. Gangneung1
3. Yeoncheon
4. Daejon
5. Haenam2
6. Seosan
7. Pyeongchang
8. Gangneung2
9. Heanam1
10. Hoengseong
11. Geumsan
12. Goesan
13. KK011115	<i>P. brassicaceae</i> _isolate_AT
14. KK0111135	<i>P. brassicaceae</i> _e3(genome)
15. KK011116	<i>P. brassicaceae</i> _isolate_e3
16. KK011117	<i>P. brassicaceae</i> _H5
17. KK011118	<i>P. brassicaceae</i> _H16
18. KK011119	<i>P. brassicaceae</i> _H21
19. KK011120	<i>P. brassicaceae</i> _Paarp6
20. KK011121	<i>P. brassicaceae</i> _Paarp7
21. KK011122	<i>P. brassicaceae</i> _PbBro
22. KK011123	<i>P. brassicaceae</i> _V9
23. KK011124	<i>P. brassicaceae</i> _Lilly-1
24. KK011125	<i>P. brassicaceae</i> _F290
25. KK011126	<i>P. brassicaceae</i> _Leduc-SS2
26. KK011127	<i>P. brassicaceae</i> _P5
27. KK011128	<i>P. brassicaceae</i> _MB-2
28. KK011129	<i>P. brassicaceae</i> _ON-2
29. KK011130	<i>P. brassicaceae</i> _P6
30. KK011131	<i>P. brassicaceae</i> _P2
31. KK011132	<i>P. brassicaceae</i> _QB
32. KK011133	<i>P. brassicaceae</i> _C1
33. KK011134	<i>P. brassicaceae</i> _C2

Figure S4. Cont.

Species/Abbrv	Group Name	5101	Sequences 5101-5270	5270
1. AB526843 <i>P. brassicae</i> NGY		*	*	*
2. Gangneung1		*	*	*
3. Yeoncheon		*	*	*
4. Daejon		*	*	*
5. Haenam2		*	*	*
6. Seosan		*	*	*
7. Pyeongchang		*	*	*
8. Gangneung2		*	*	*
9. Heanam1		*	*	*
10. Hoengseong		*	*	*
11. Geumsan		*	*	*
12. Goesan		*	*	*
13. KK011115_ <i>P. brassicae</i> _isolate_AT		*	*	*
14. KK011135_ <i>P. brassicae</i> _e3(genome)		*	*	*
15. KK011116_ <i>P. brassicae</i> _isolate_e3		*	*	*
16. KK011117_ <i>P. brassicae</i> _H5		*	*	*
17. KK011118_ <i>P. brassicae</i> _H16		*	*	*
18. KK011119_ <i>P. brassicae</i> _H21		*	*	*
19. KK011120_ <i>P. brassicae</i> _Paarp6		*	*	*
20. KK011121_ <i>P. brassicae</i> _Paarp7		*	*	*
21. KK011122_ <i>P. brassicae</i> _PbBro		*	*	*
22. KK011123_ <i>P. brassicae</i> _V9		*	*	*
23. KK011124_ <i>P. brassicae</i> _Lily-1		*	*	*
24. KK011125_ <i>P. brassicae</i> _F290		*	*	*
25. KK011126_ <i>P. brassicae</i> _Leduc-SS2		*	*	*
26. KK011127_ <i>P. brassicae</i> _P5		*	*	*
27. KK011128_ <i>P. brassicae</i> _MB-2		*	*	*
28. KK011129_ <i>P. brassicae</i> _ON-2		*	*	*
29. KK011130_ <i>P. brassicae</i> _P6		*	*	*
30. KK011131_ <i>P. brassicae</i> _P2		*	*	*
31. KK011132_ <i>P. brassicae</i> _QB		*	*	*
32. KK011133_ <i>P. brassicae</i> _C1		*	*	*
33. KK011134_ <i>P. brassicae</i> _C2		*	*	*

Figure S4. Cont.

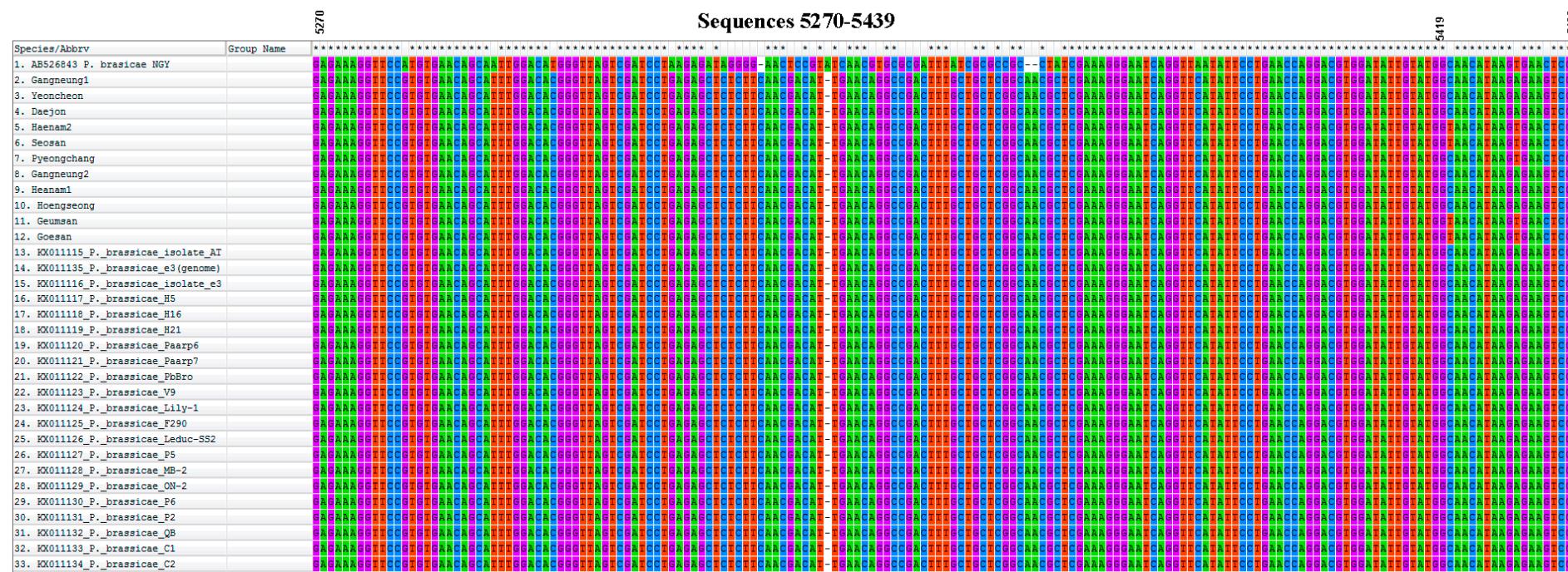
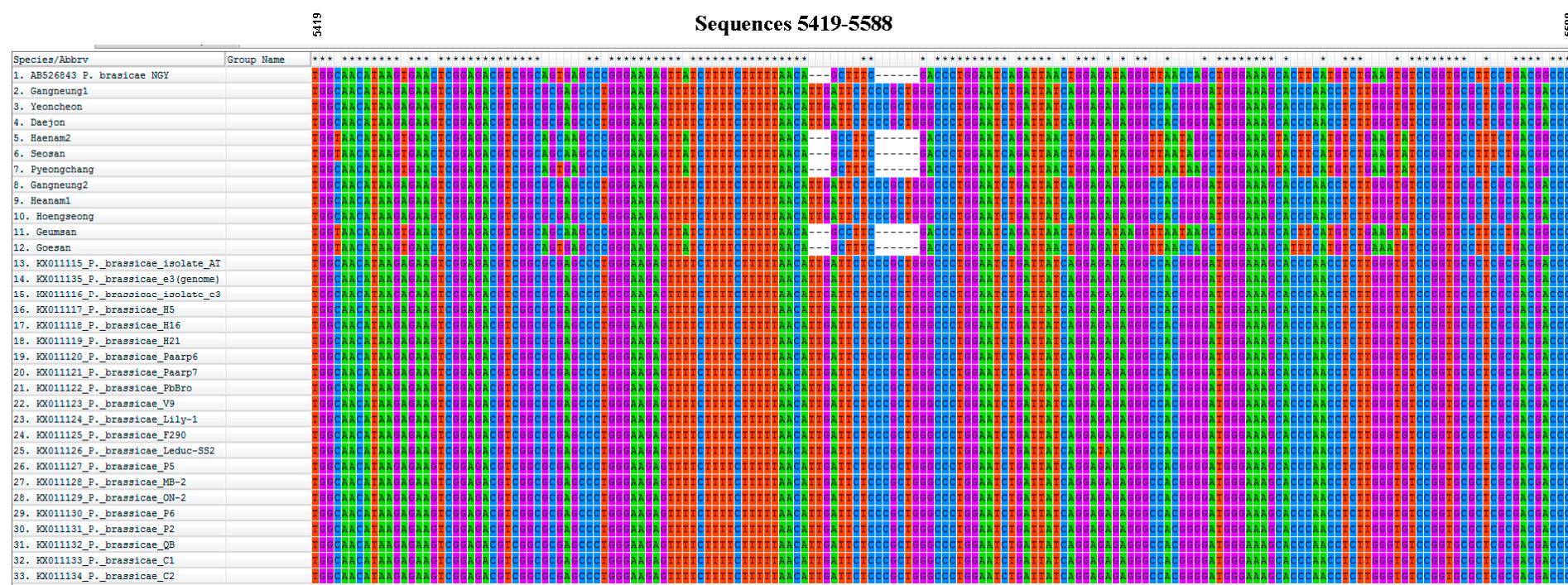
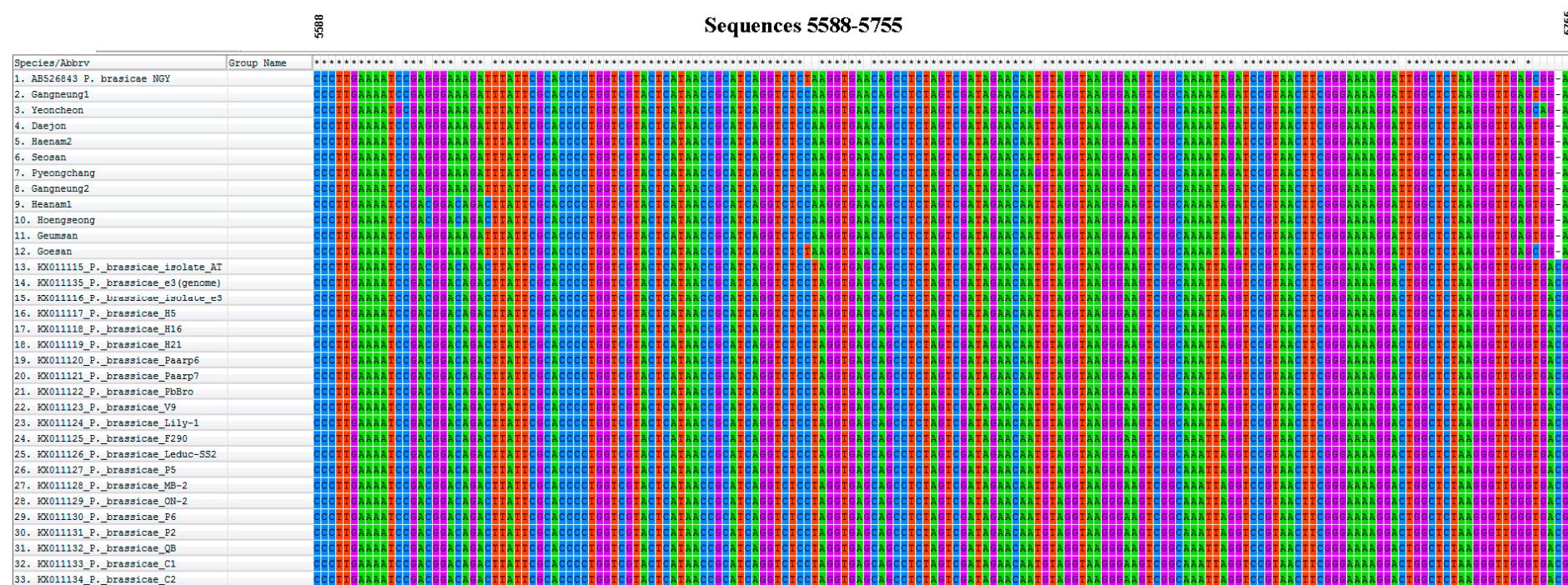


Figure S4. *Cont.*

**Figure S4. Cont.**

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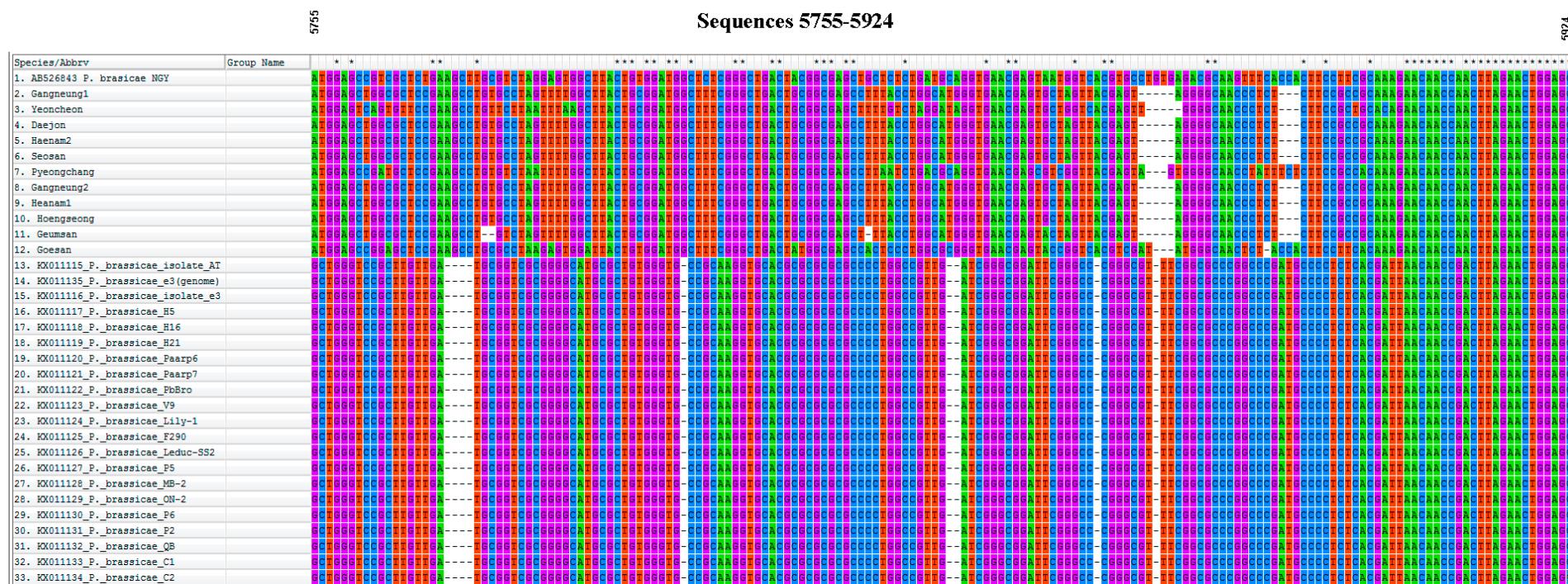


Figure S4. *Cont.*

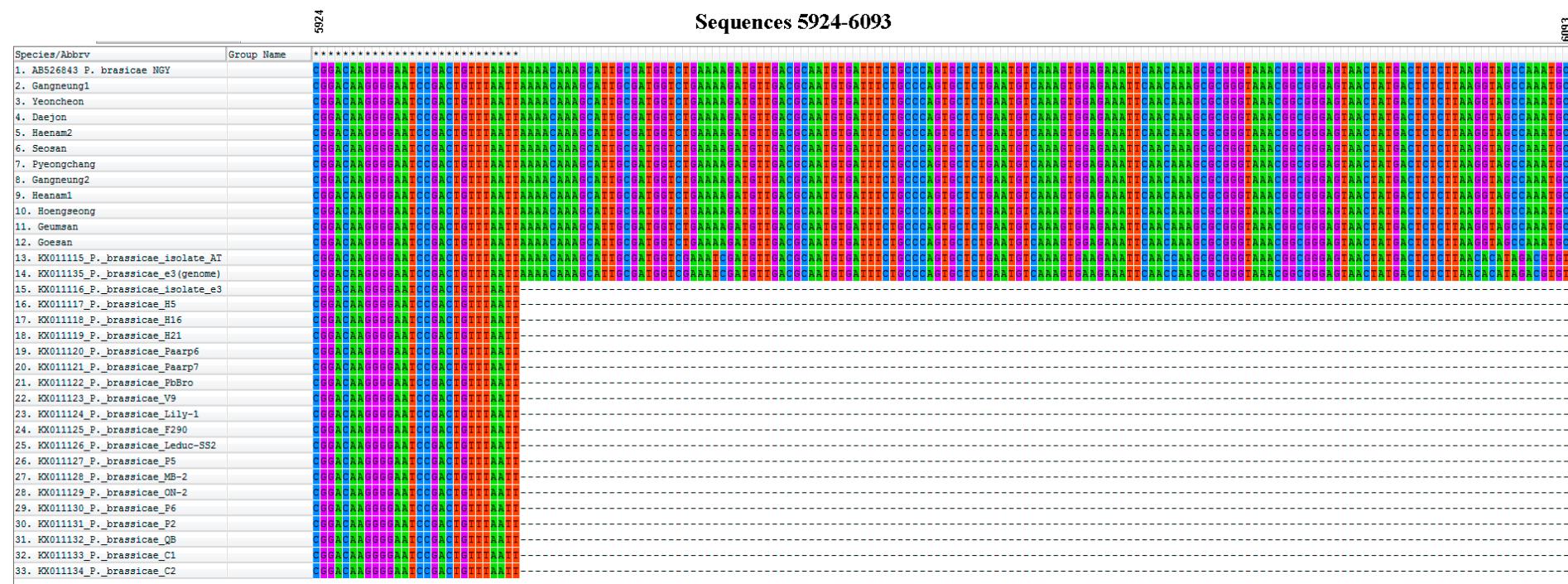


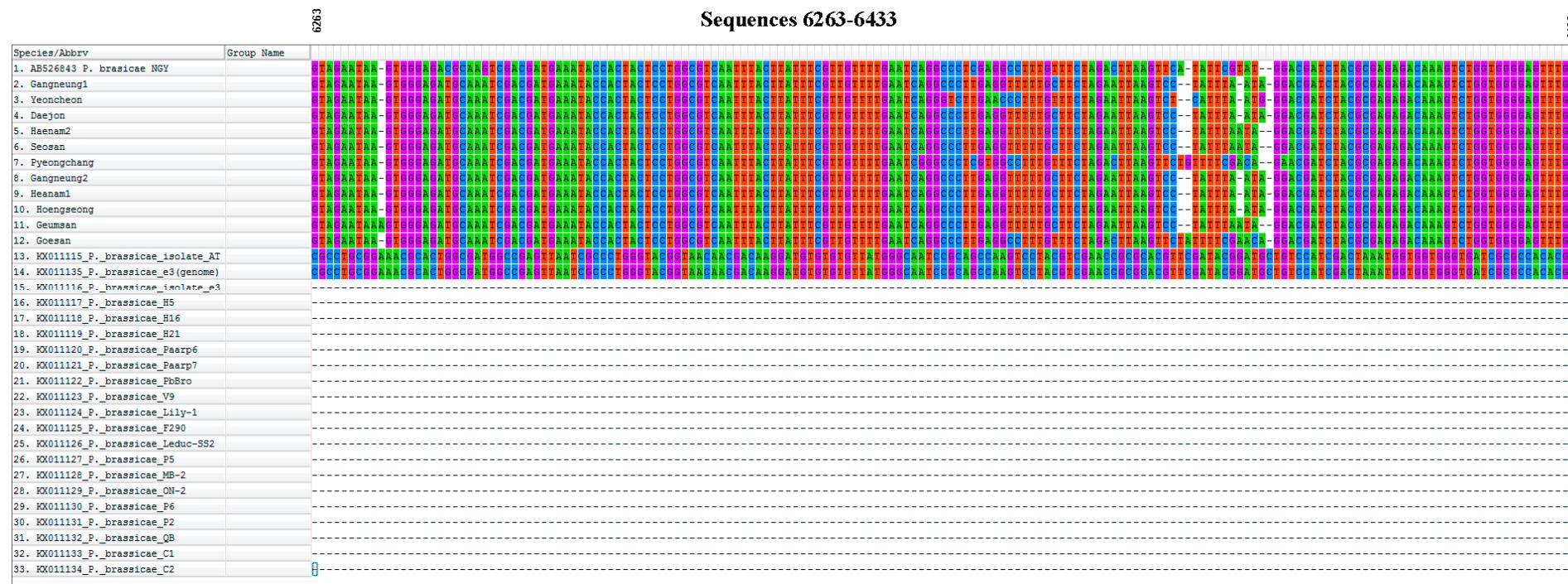
Figure S4. *Cont.*

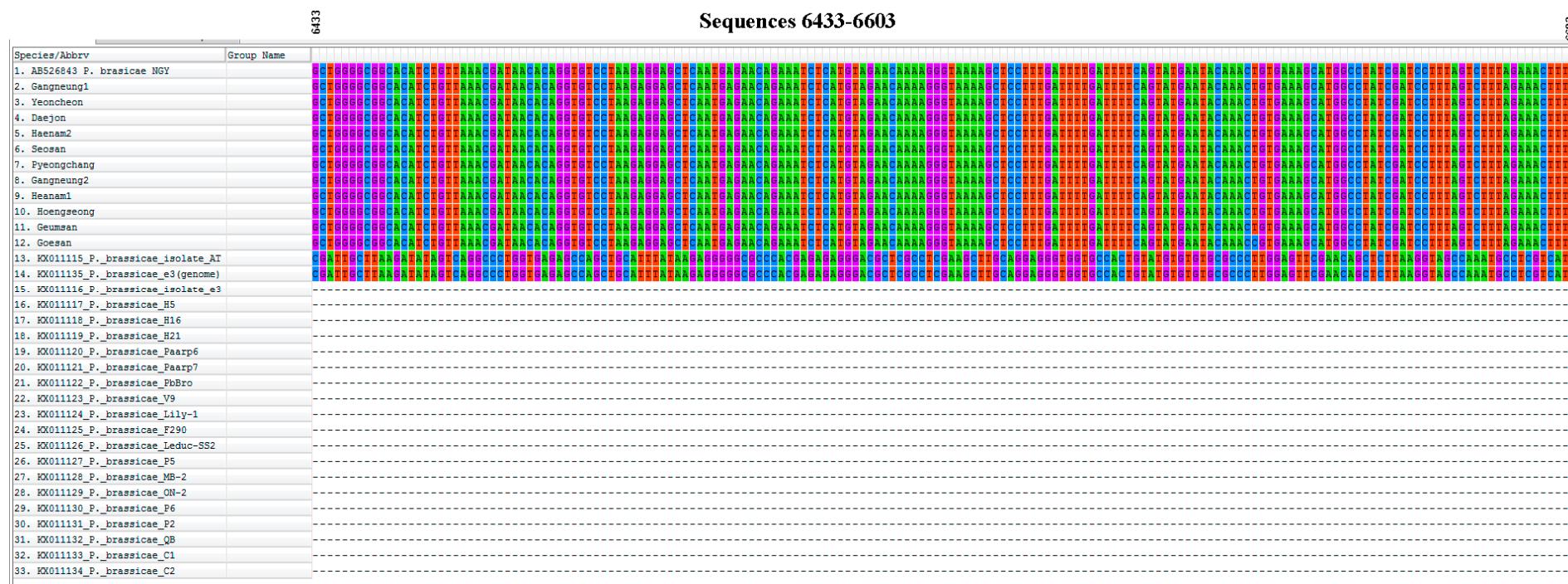
Sequences 6093-6263

6093 6263

Species/Abbrv	Group Name
1. ABS26843 <i>P. brassicae</i> NGY	
2. Gangneung1	
3. Yeoncheon	
4. Daejon	
5. Haenam2	
6. Seosan	
7. Pyeongchang	
8. Gangneung2	
9. Heanam1	
10. Hoengseong	
11. Geumsan	
12. Goesan	
13. KK011115_ <i>P. brassicae</i> isolate_AT	
14. KK011135_ <i>P. brassicae</i> e3(genome)	
15. KK011116_ <i>P. brassicae</i> isolate_e3	
16. KK011117_ <i>P. brassicae</i> H5	
17. KK011118_ <i>P. brassicae</i> H16	
18. KK011119_ <i>P. brassicae</i> H21	
19. KK011120_ <i>P. brassicae</i> Paarp6	
20. KK011121_ <i>P. brassicae</i> Paarp7	
21. KK011122_ <i>P. brassicae</i> PbBro	
22. KK011123_ <i>P. brassicae</i> y9	
23. KK011124_ <i>P. brassicae</i> Lilly-1	
24. KK011125_ <i>P. brassicae</i> F290	
25. KK011126_ <i>P. brassicae</i> Leduc-SS2	
26. KK011127_ <i>P. brassicae</i> P5	
27. KK011128_ <i>P. brassicae</i> MB-2	
28. KK011129_ <i>P. brassicae</i> ON-2	
29. KK011130_ <i>P. brassicae</i> P6	
30. KK011131_ <i>P. brassicae</i> P2	
31. KK011132_ <i>P. brassicae</i> QB	
32. KK011133_ <i>P. brassicae</i> C1	
33. KK011134_ <i>P. brassicae</i> C2	

Figure S4. Cont.

**Figure S4. Cont.**

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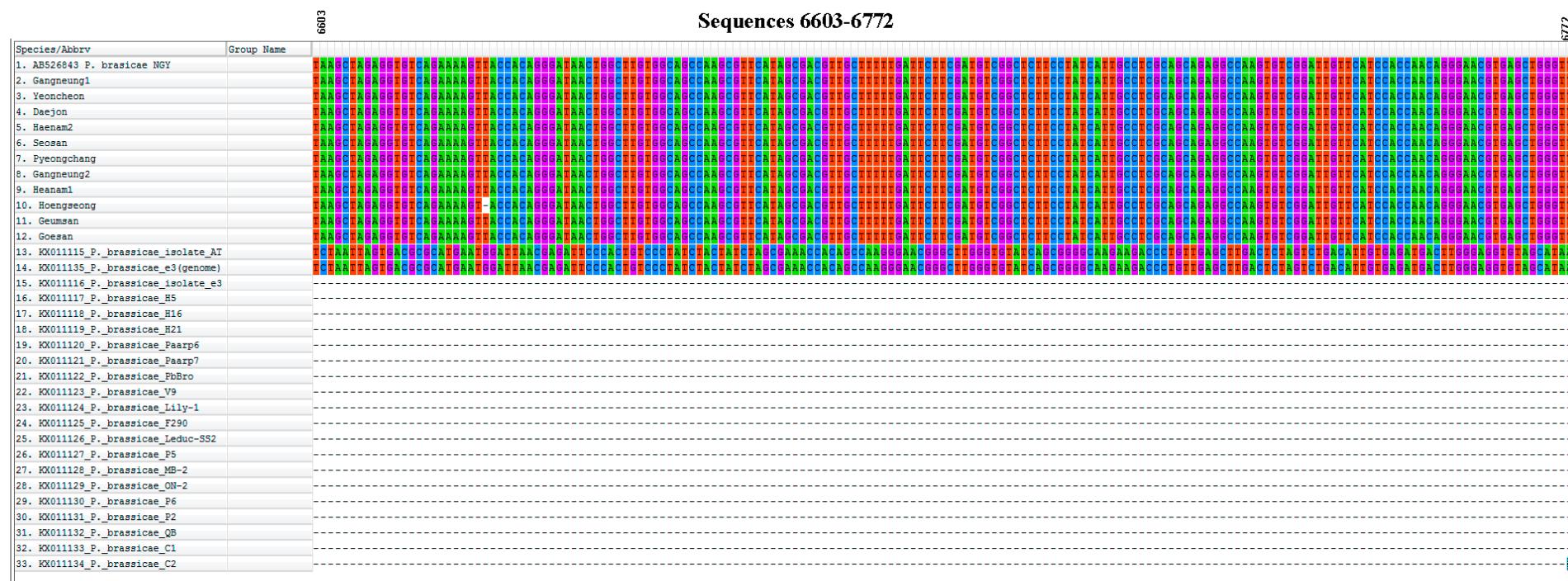


Figure S4. Cont.

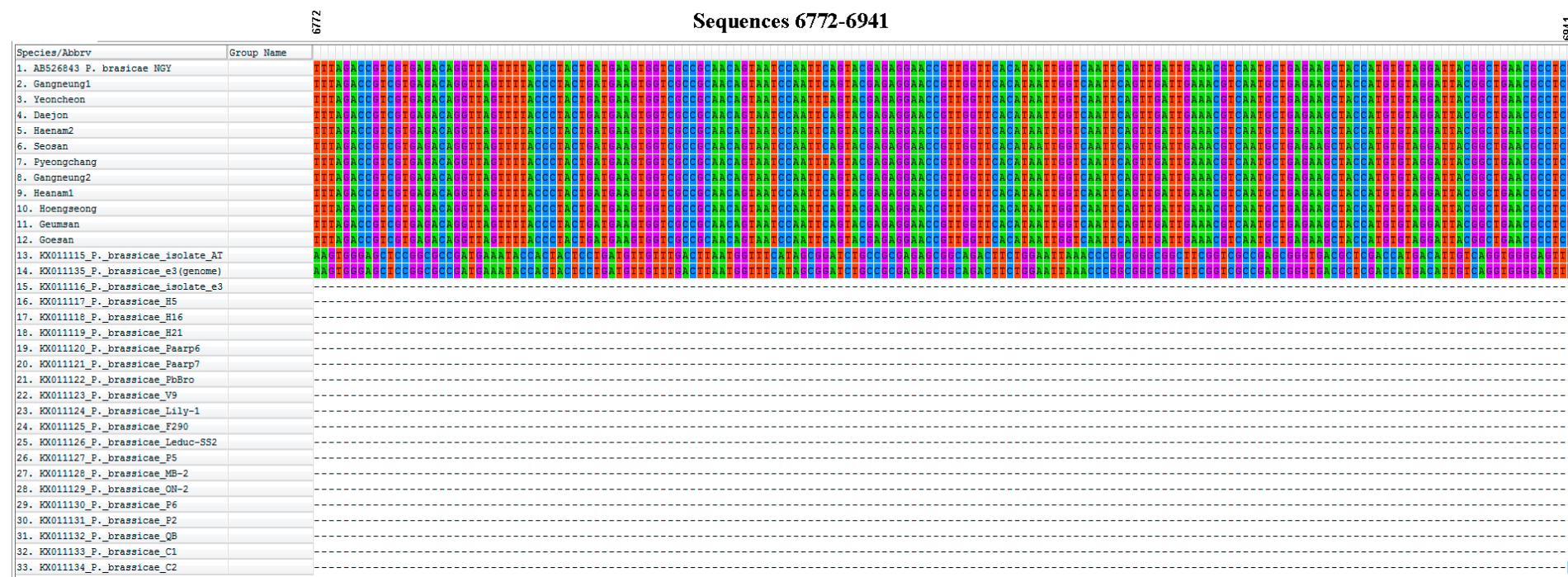
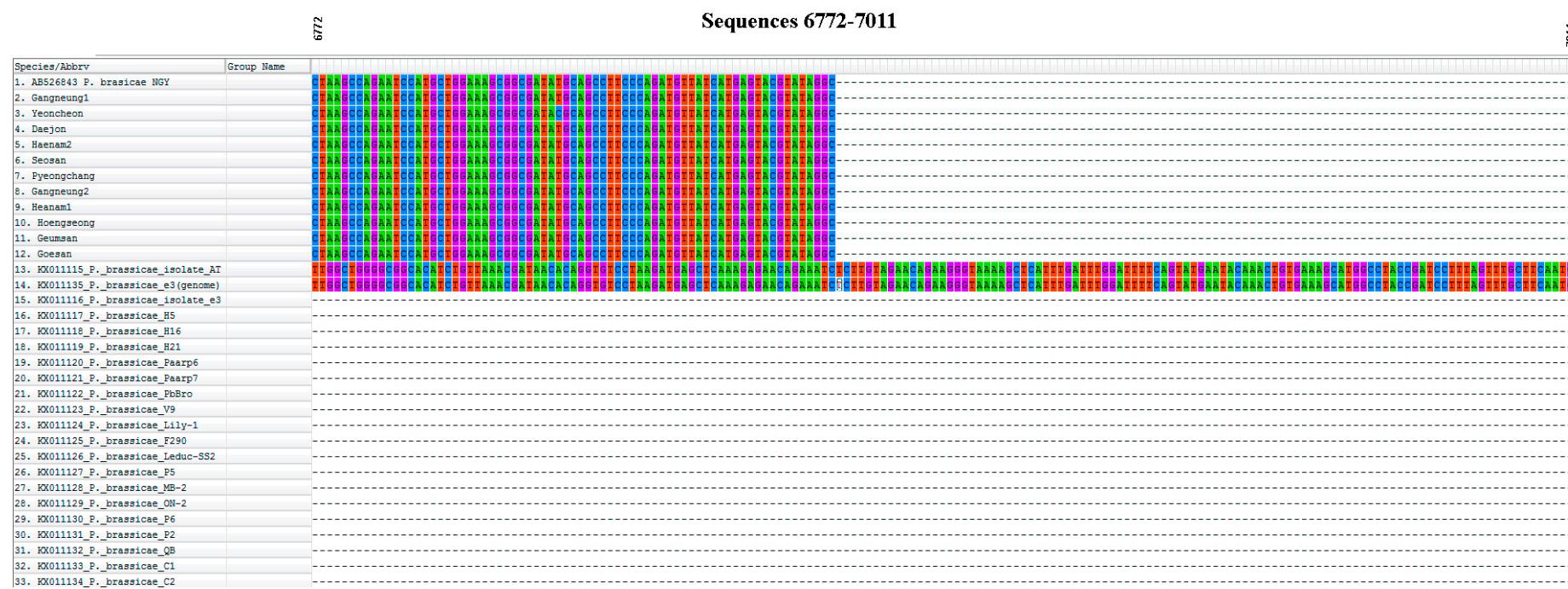


Figure S4. *Cont.*



Figures S4. LSU sequence variation in Korean *P. brassicae* isolates compared to reference sequences. Green, red, purple and blue colors represent A, T, G and C residues.

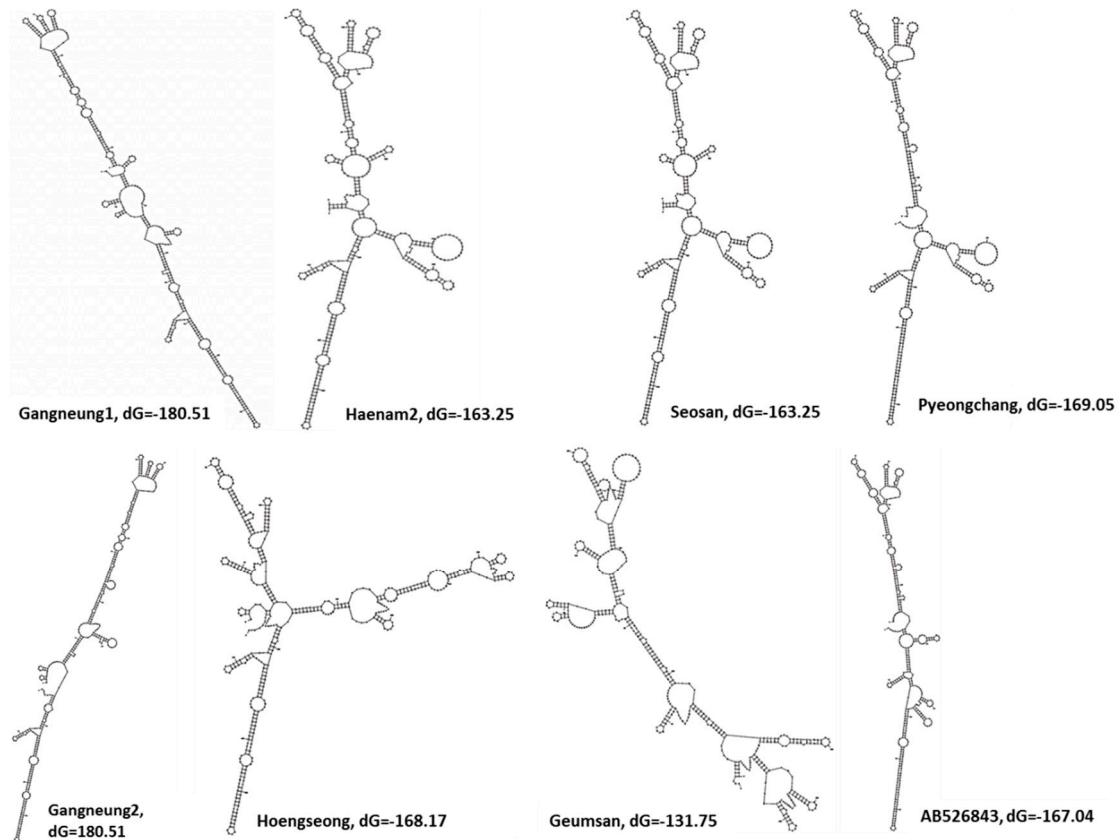


Figure S5. Predicted secondary structures. dG estimates free-energy in kcal·mol⁻¹.

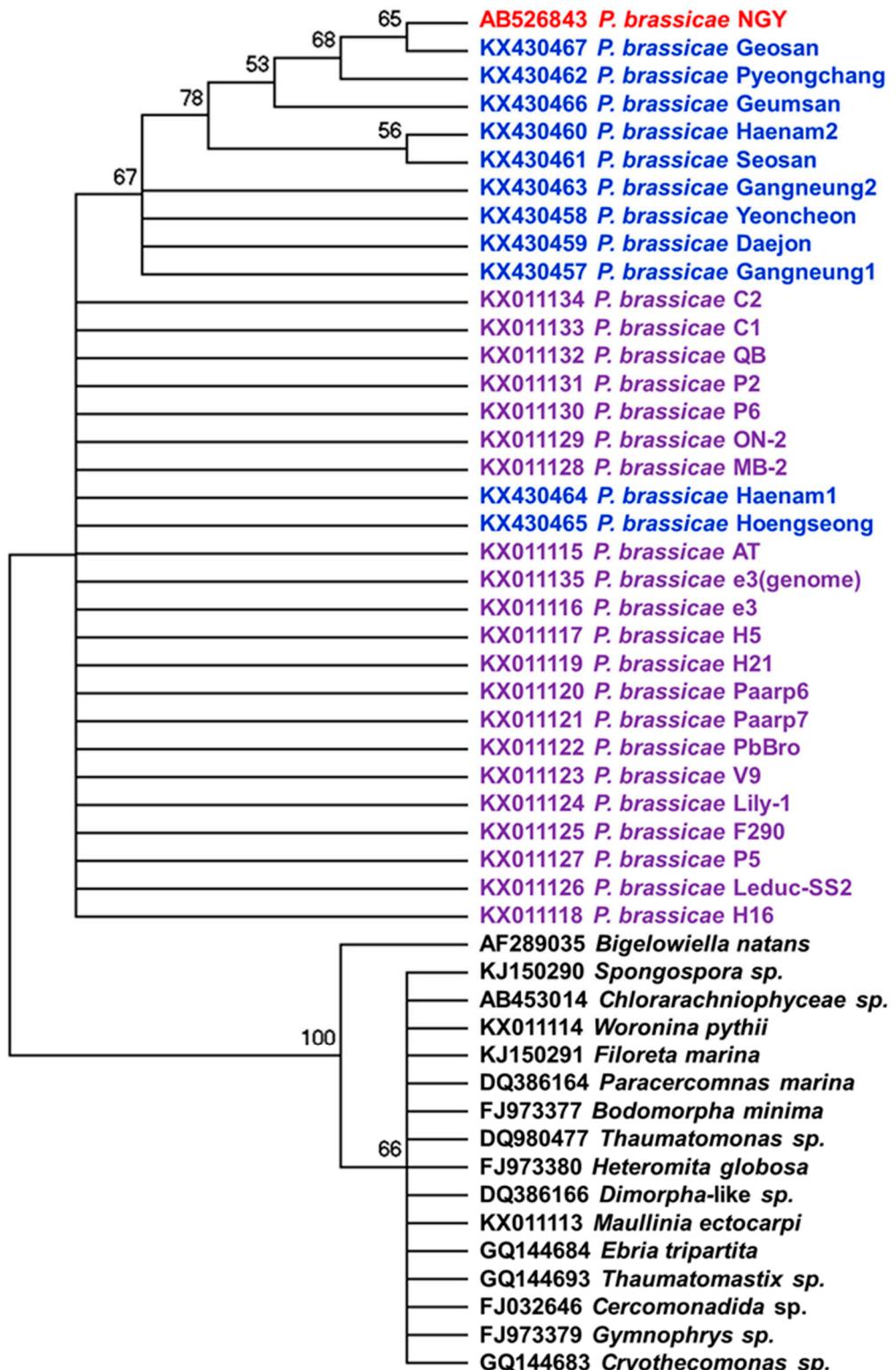


Figure S6. Cont.

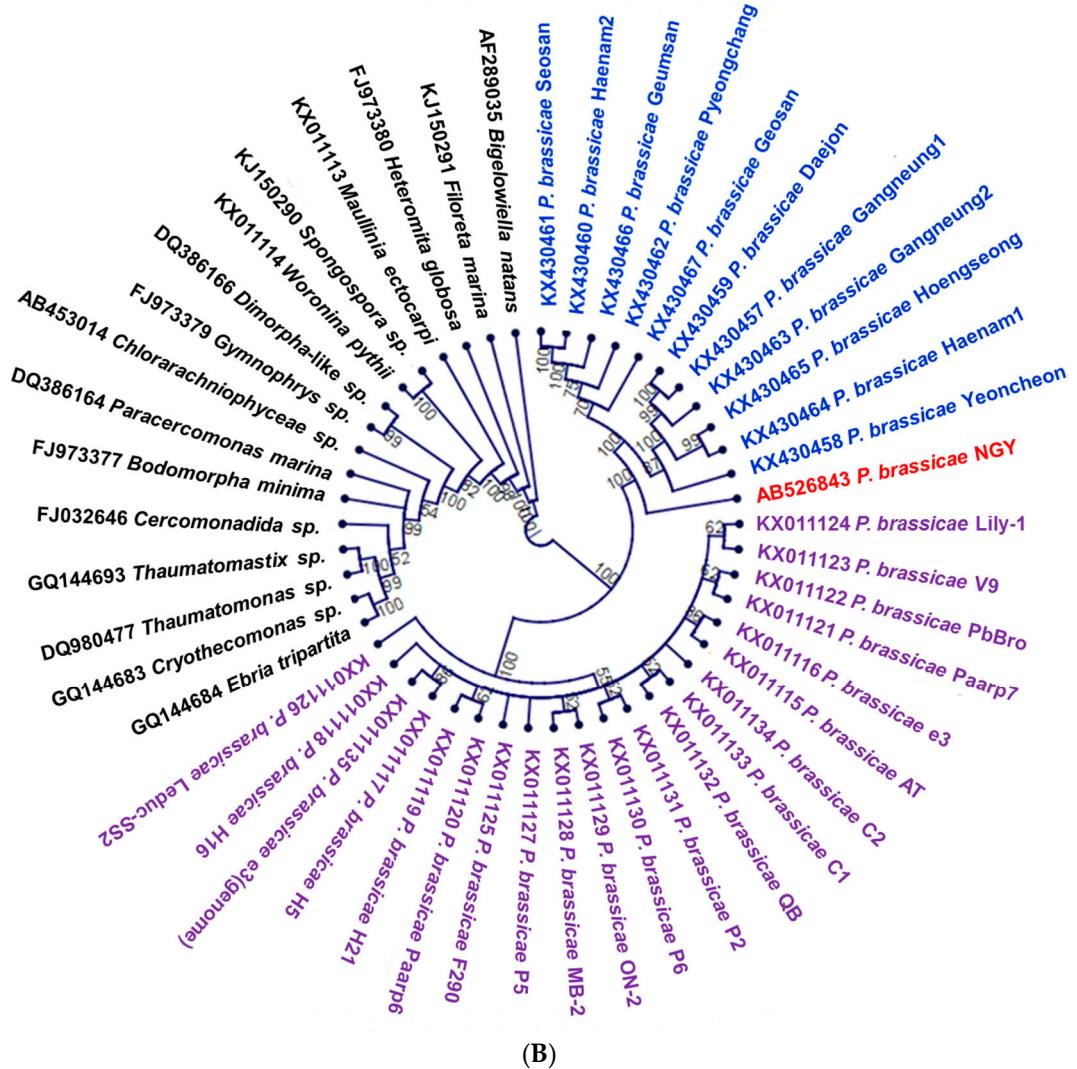


Figure S6. Phylogenetic classification of *P. brassicae* isolates and other cercozoa species based on variations in the nucleotide sequences of rDNA. Purple, red and blue colors indicate *P. brassicae* rDNA sequences obtained from Schwelm et al. [32], Niwa et al. [31] and this study. Black colors indicate rDNA sequences from cercozoa species. Complete rDNA, if available or LSU sequences were used. (A) Phylogenetic tree constructed following the Neighbour-Joining method and Maximum Composite Likelihood model in Mega6.06 software and (B) Circular cladogram constructed following the UPGMA method and Kimura 80 nucleotide distance measure method in CLC Main Workbench version 7.

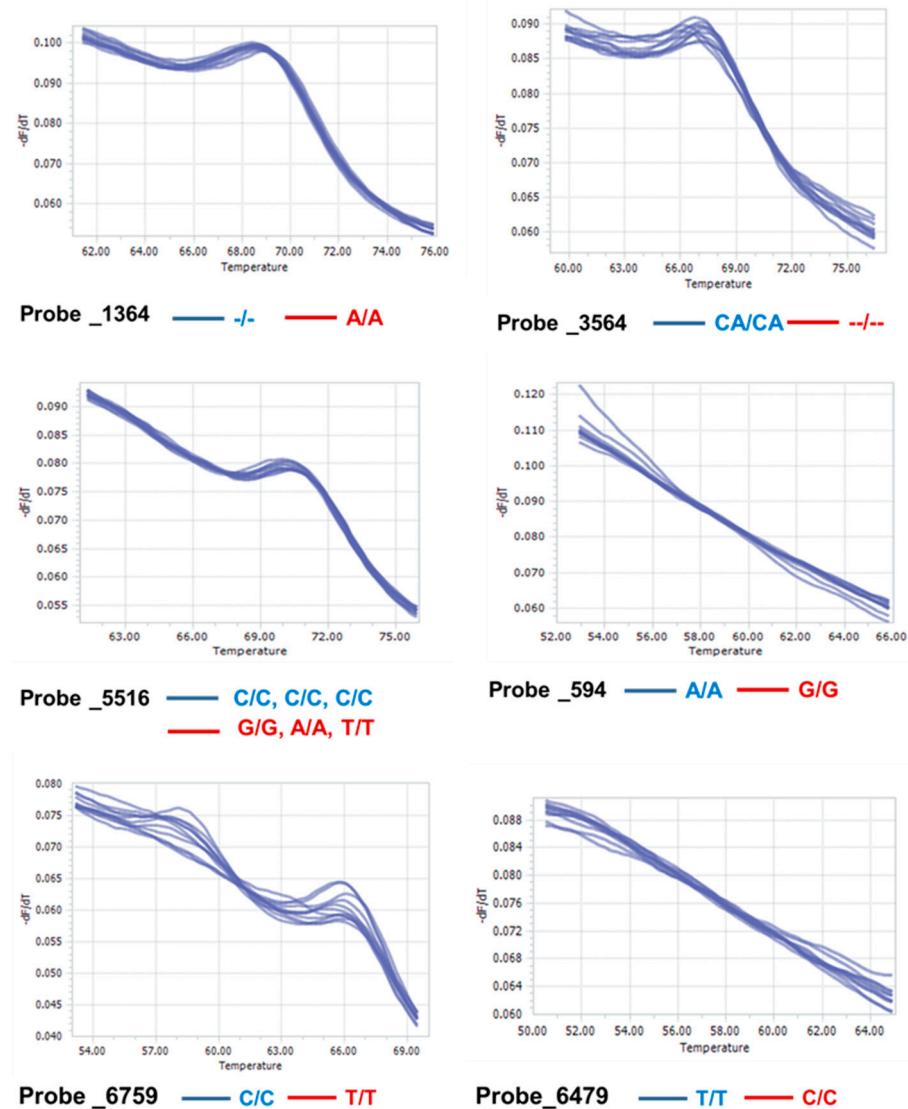


Figure S7. Absence of functional polymorphism (absence of red lines) between Korean *P. brassicae* isolates. Melting temperatures are shown for probes (single, oligo and multiple-single nucleotide polymorphism and InDel) designed at the LSU after high-resolution melting analysis in a Roche light cycler.

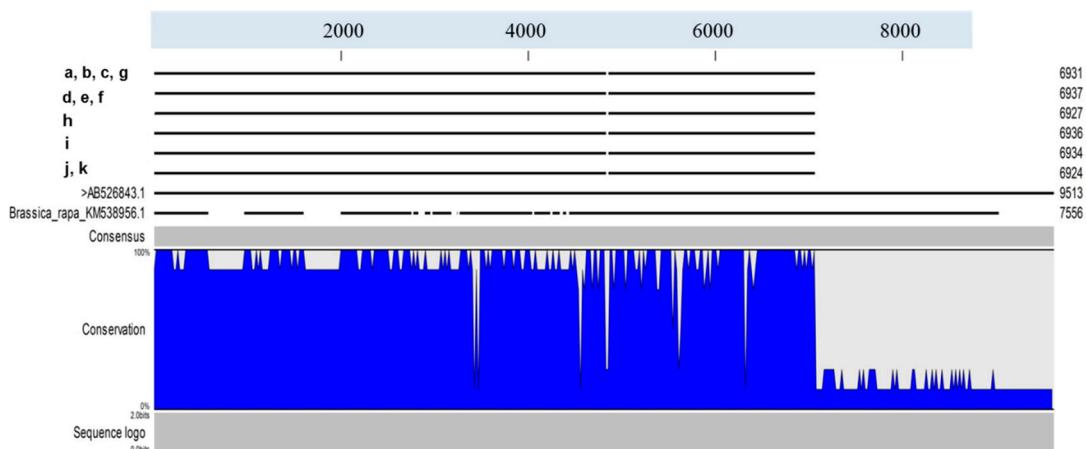


Figure S8. Variation in annotated sequences between *Plasmochiphora brassicae* and *Brassica rapa* larger subunit (LSU) rDNA sequences.



Figure S9. Variation in gall size produced by Korean *P. brassicae* isolates Daejon and Seosan, 28 days after inoculation. Scale = 0.5 cm.