

S1A

	1	40	60	80	100
DW30	TTTAATTTTAGAAGAAATAAAAGTACGTACGTAATTTTTTTTGACTTAGACTTGCTTTTGTGTTCTTCGAATTATATCAACATTGCACCTCTAACAATTAC				
DW28T.....T.....				
DW33T.....T.....				
DW36T.....T.....				
DW37T.....T.....				
DW39T.....T.....				
DW40T.....T.....				
DW75T.....T.....				
DW78T.....T.....				
DW96T.....T.....				
DW98T.....T.....				
DW100T.....T.....				
K40T.....T.....				
K42T.....T.....				
K47T.....T.....				
RDSC 5545T.....T.....				
RDSC 5546T.....T.....				
RDSC 5547T.....T.....				
RDSC 5548T.....T.....				
NB0003T.....T.....				
NB0004T.....T.....				
NB0093T.....T.....				
G2T.....T.....				
H1T.....T.....				
I1T.....T.....				
J1T.....T.....				
L1T.....T.....				
O1T.....T.....				
Ya1T.....T.....				
RDSC 2014T.....T.....				
MN419335T.....T.....				
GU454201T.....T.....				
GU454202T.....T.....				
GU454203T.....T.....				
GU454204T.....T.....				
GU454205T.....T.....				
GU454206T.....T.....				
GU454208T.....T.....				
	120	140	160	180	200
DW30	TTATTCGTTGAGAGAATACCTCCGGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTCTTCCTTCCCGTTTTTATGTTCTTAGTATAA				
DW28T.....T.....				
DW33T.....T.....				
DW36T.....T.....				
DW37T.....T.....				
DW39T.....T.....				
DW40T.....T.....				
DW75T.....T.....				
DW78T.....T.....				
DW96T.....T.....				
DW98T.....T.....				
DW100T.....T.....				
K40T.....T.....				
K42T.....T.....				
K47T.....T.....				
RDSC 5545T.....T.....				
RDSC 5546T.....T.....				
RDSC 5547T.....T.....				
RDSC 5548T.....T.....				
NB0003T.....T.....				
NB0004T.....T.....				
NB0093T.....T.....				
G2T.....T.....				
H1T.....T.....				
I1T.....T.....				
J1T.....T.....				
L1T.....T.....				
O1T.....T.....				
Ya1T.....T.....				
RDSC 2014T.....T.....				
MN419335T.....T.....				
GU454201T.....T.....				
GU454202T.....T.....				
GU454203T.....T.....				
GU454204T.....T.....				
GU454205T.....T.....				
GU454206T.....T.....				
GU454208T.....T.....				

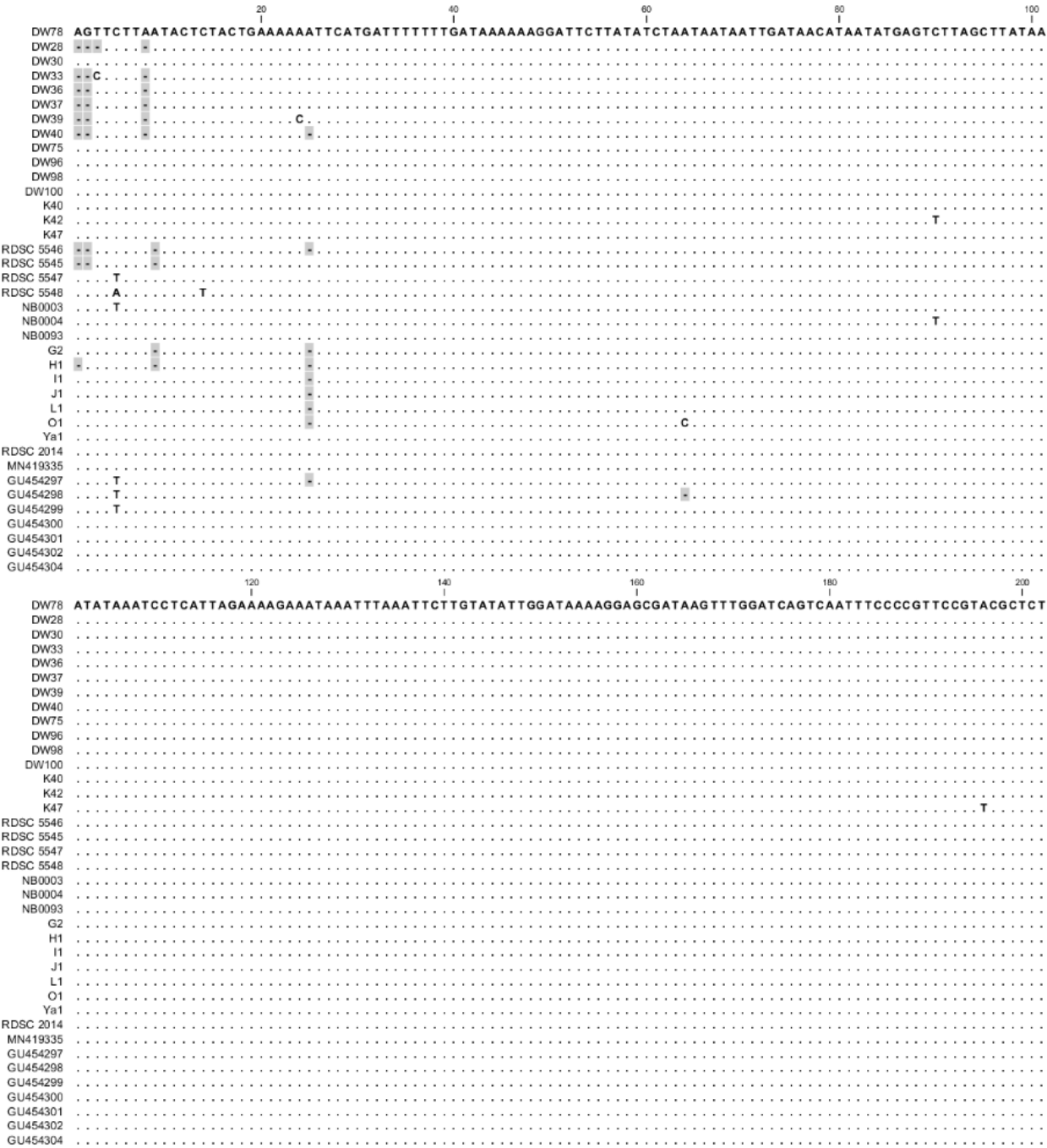
S1A

		220	240	260	280	300
DW30	TGTAACGGAAACCTTTT	TTTGTATGCGTTGCAACGCAACAAACAAGGTATTTATCAATTGACAAAAATACCCAGGACCTAACCCAATAAGTATCTTCTTGT				
DW28						T..T
DW33						T..T
DW36						T..T
DW37						T..T
DW39						T..T
DW40						T..T
DW75						
DW78						
DW96						
DW98						
DW100						
K40						
K42						
K47						
RDSC 5545						T..T
RDSC 5546	A..					T..T
RDSC 5547						
RDSC 5548						
NB0003						
NB0004						
NB0093						
G2						T..T
H1						
I1						
J1						
L1						
O1						
Ya1						
RDSC 2014						
MN419335						
GU454201						
GU454202						
GU454203						
GU454204						
GU454205						
GU454206						
GU454208						
		320	340	360	380	400
DW30	AAACTTTAATTTAATTAGAAATAAAATTATAAAATTAAGTTCTCAATTAAATTAATTGATTTAATCTATTCCATTAAAAAATCCCATAAAAA					AGAA
DW28						T..T
DW33						T..T
DW36						T..T
DW37						T..T
DW39						T..T
DW40						T..T
DW75						
DW78						
DW96						
DW98						
DW100						
K40						
K42						
K47						
RDSC 5545						T..T
RDSC 5546						
RDSC 5547						
RDSC 5548						
NB0003						
NB0004						
NB0093						
G2						T..T
H1						
I1						
J1						
L1						
O1						
Ya1						
RDSC 2014						
MN419335						
GU454201						
GU454202						
GU454203						
GU454204						
GU454205						
GU454206						
GU454208						

S1A

		420		440		460
DW30	AATCAACCAAAAAAGGGGCGAAGTGATACAAAAAGAACTCTGTTCTTTGTTAGTCCTATCTATAAGAGGAGAGTAT					
DW28					
DW33					
DW36					
DW37					
DW39					
DW40					
DW75					
DW78					
DW96					
DW98					
DW100					
K40					
K42					
K47					
RDSC 5545					
RDSC 5546					
RDSC 5547					
RDSC 5548					
NB0003					
NB0004					
NB0093					
G2					
H1					
I1					
J1					
L1					
O1					
Ya1					
RDSC 2014					
MN419335					
GU454201					
GU454202					
GU454203					
GU454204					
GU454205					
GU454206					
GU454208					

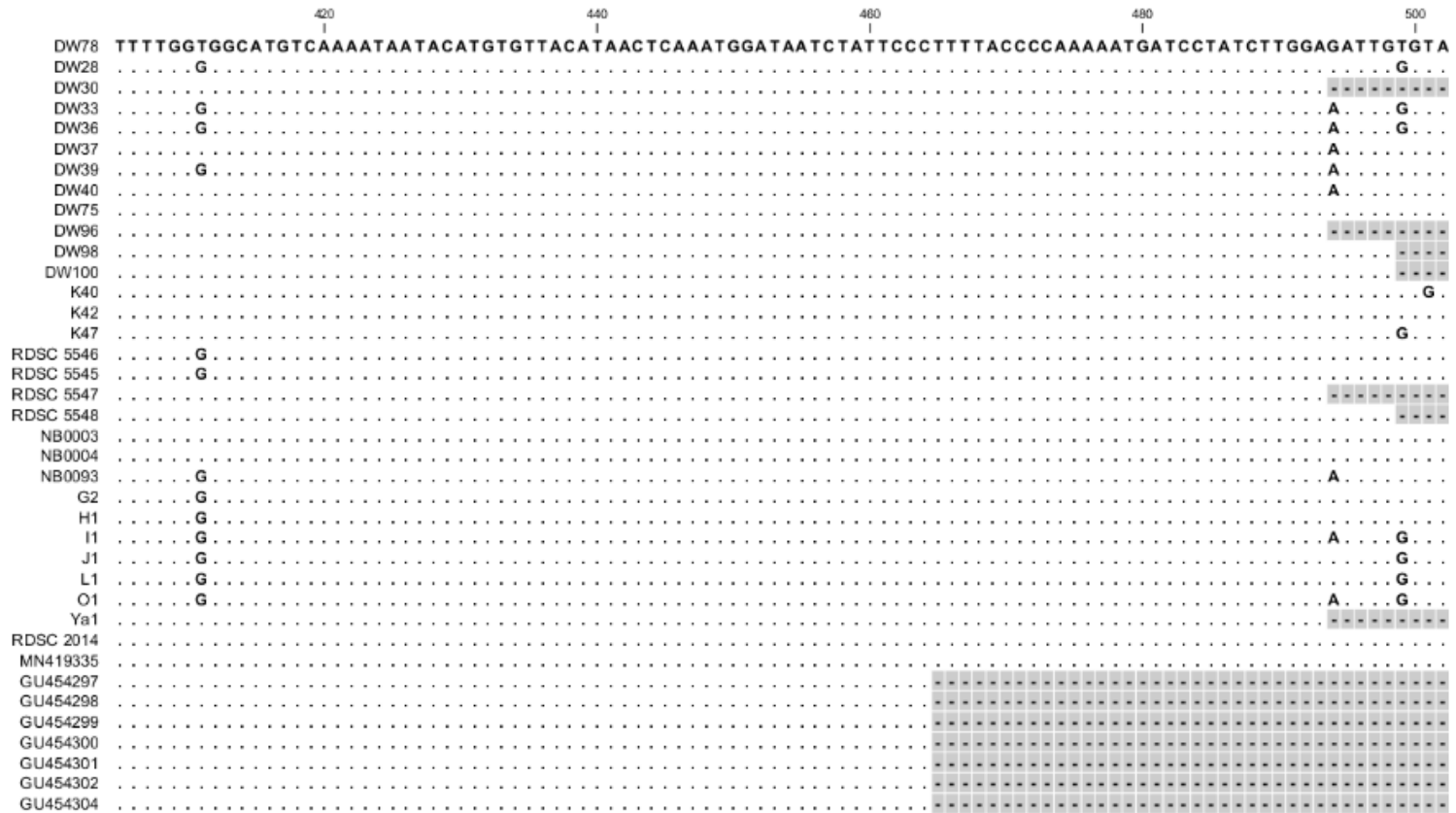
S1B



S1B

		220	240	260	280	300	
DW78	TCCAGTGAGCAAGTACTTTCTTTATTAGCTTATGTTTTTCCACAATACTTTATGTTAAATATTAGAATAACCATTTTGGTAACGAACAAATCATAATCTTA						
DW28							
DW30							
DW33							
DW36							
DW37							
DW39							
DW40							
DW75							
DW96							
DW98							
DW100							
K40							T
K42							
K47							
RDSC 5546							
RDSC 5545							
RDSC 5547							
RDSC 5548							
NB0003							
NB0004							T
NB0093							
G2							
H1							
I1							
J1							
L1							
O1							
Ya1							
RDSC 2014							
MN419335							
GU454297							Y . W . Y .
GU454298							
GU454299							
GU454300							
GU454301							
GU454302							
GU454304							
		320	340	360	380	400	
DW78	ATTTTCAGAAAAAAATTCATGAATTTGAAAAATTCAGTTTTTTTAGAAAAAAACACTTAATTAAAAAAATTTGTTCTTTATTTTTTCATATTTTTTTTTTGT						
DW28							
DW30							
DW33							
DW36							
DW37							
DW39							
DW40							
DW75							
DW96							
DW98							
DW100							
K40							
K42							
K47							
RDSC 5546							
RDSC 5545							
RDSC 5547							
RDSC 5548							
NB0003							
NB0004							
NB0093							
G2							
H1							
I1							
J1							
L1							
O1							
Ya1							
RDSC 2014							
MN419335							
GU454297							
GU454298							
GU454299							
GU454300							
GU454301							
GU454302							
GU454304							

S1B



Supplemental Figure S1. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers sequences of *Spirodela polyrrhiza* collected in Ukraine and China (for ecotype details see supplemental Table 2). Matching residues are shown as dots.

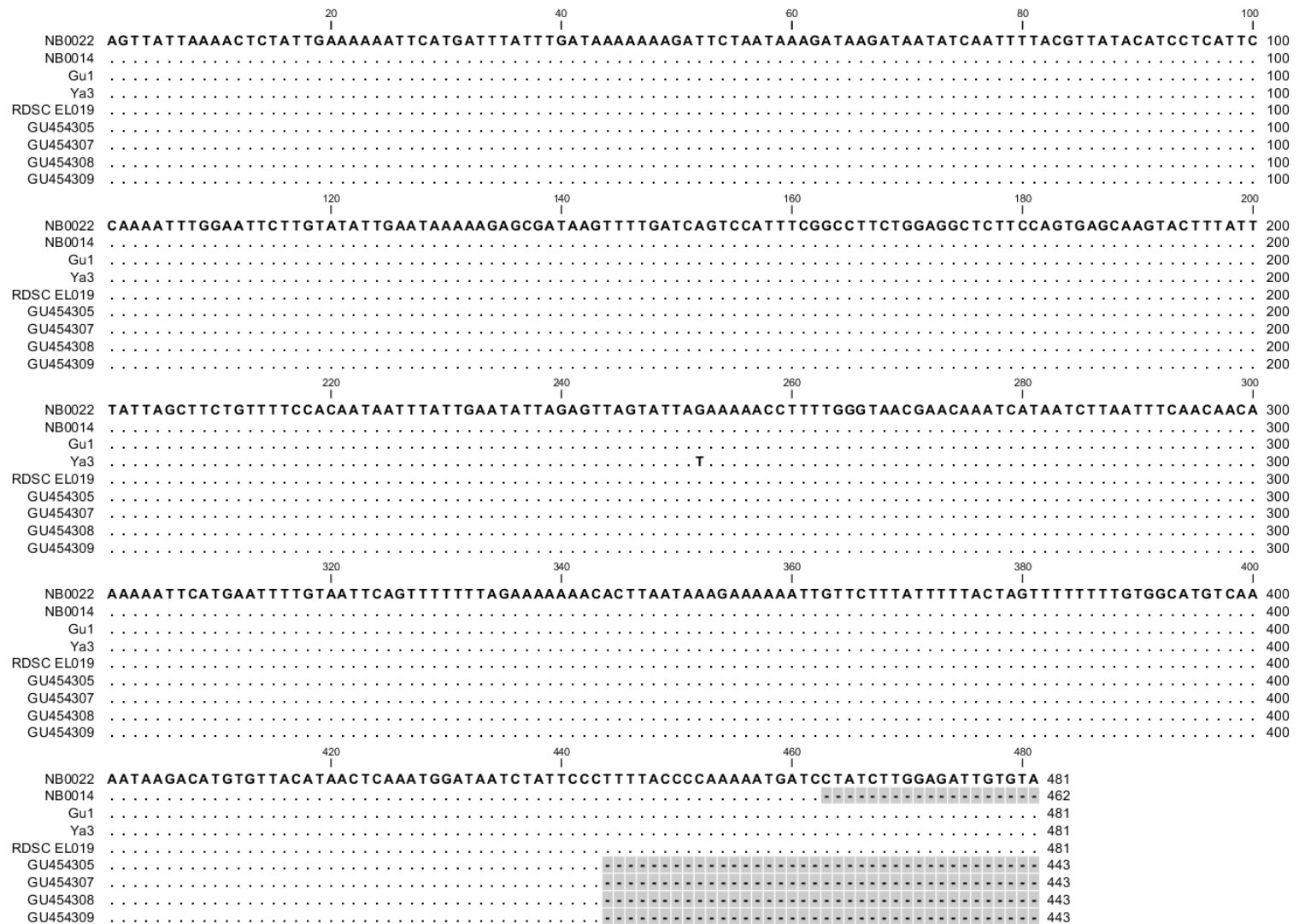
A. Nucleotide alignment of *atpH*–*atpF* barcodes including representative sequences of *S. polyrhiza* specimens available in GenBank: MN419335, USA; GU454201, Hong Kong; GU454202, India; GU454203, Malaysia; GU454204, USA; GU454205, Mexico; GU454206, Canada; GU454208, Europe.

B. Nucleotide alignment of *psbK-psbI* barcodes including representative sequences of *S. polyrhiza* specimens available in GenBank: MN419335, USA; GU454297, Hong Kong; GU454298, India; GU454299, Malaysia; GU454300, USA; GU454301, Mexico; GU454302, Canada; GU454304, Europe.

S2A

		20	40	60	80	100
NB0014		TTCTATAAGAAAAAGTACATAATAGACTTTTTTTACTTAGACTTGTTTTCTGCTTCTTCGAATTATATCAACATTGCACTCTAACAATTACTTTAGT				
NB0022	
Gu1	
Ya3	
RDSC EL019	
GU454209	
GU454211	
GU454212	
GU454213	
		120	140	160	180	200
NB0014		TGATAGAATACCTCCGGGAAGGACTGATTTTAGGATTAGTAATTAGGAGATCCTCTCGCTTTCTTCCTTCCCGTTTTTAGTTCTTAGTATAATGGAAACC				
NB0022	
Gu1	
Ya3	
RDSC EL019	
GU454209	
GU454211	
GU454212	
GU454213	
		220	240	260	280	300
NB0014		TTTTTTTAGTATGCGTTGCAACGCAACAAACAAGGTATTTATCAATTGACAAAATACCCAGGACCTAACCCAATAAGTATCTTCTTGTAATTGTAACTT				
NB0022	
Gu1	
Ya3	
RDSC EL019	
GU454209	
GU454211	
GU454212	
GU454213	
		320	340	360	380	400
NB0014		TAATTTAATTAGAATATTTAATTTAGAATATTTAATTATTATAAAATAATAAATAAATTAAGTTCTCAATTAATTAATTCAATATATTCCATTTTAA				
NB0022	
Gu1	
Ya3	
RDSC EL019	
GU454209	
GU454211	
GU454212	
GU454213	
		420	440	460	480	
NB0014		AATCCCATACCATAAAAAAAAAAGAAATCAACCAAAGGGGGCGAAGTAATACAAAAGAACTCTGTTCTTTGTTAGTCCTATCTATAAGAGGAGAGTAT				
NB0022	
Gu1	
Ya3	
RDSC EL019	
GU454209	
GU454211	
GU454212	
GU454213	

S2B



Supplemental Figure S2. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Landoltia punctata* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

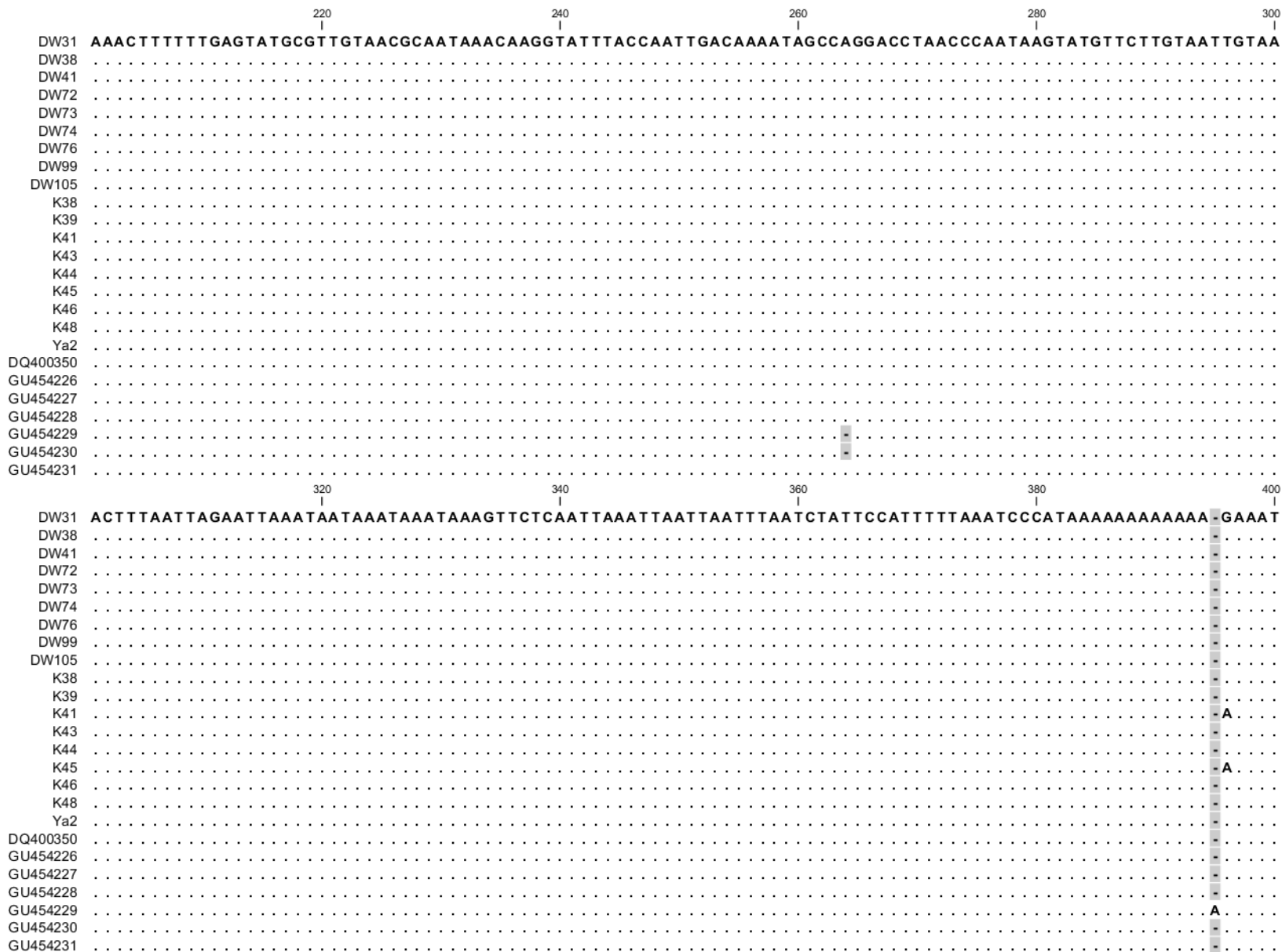
A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *La. punctata* from different parts of the world available in the GenBank: GU454209, South Africa; GU454211, India; GU454212, USA; GU454213, Australia.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *La. punctata* from different parts of the world available in the GenBank: GU454305, South Africa; GU454307, India; GU454308, USA; GU454309, Australia.

S3A

		20	40	60	80	100
DW31	TTCTAGAATAAAAAAGTACGTAATAGACTTTTGGACTTTGCTTTTCTTCGAATTATATCAACATTGTACTCTAACAATTACTTATTCGTT					
DW38					
DW41					
DW72					
DW73					
DW74					
DW76					
DW99					
DW105					
K38					
K39					
K41					
K43					
K44					
K45					
K46					
K48					
Ya2					
DQ400350					
GU454226					
GU454227					
GU454228					
GU454229					
GU454230					
GU454231					
		120	140	160	180	200
DW31	GAGAGAATACCTCCGGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTCTTCTCCGTTTTTCAGTTCTTAGTATAATGTAATGCCA					
DW38					
DW41					
DW72					
DW73					
DW74					
DW76					
DW99					
DW105					
K38					
K39					
K41					
K43					
K44					
K45					
K46					
K48					
Ya2					
DQ400350					
GU454226					
GU454227					
GU454228					
GU454229					
GU454230					
GU454231					

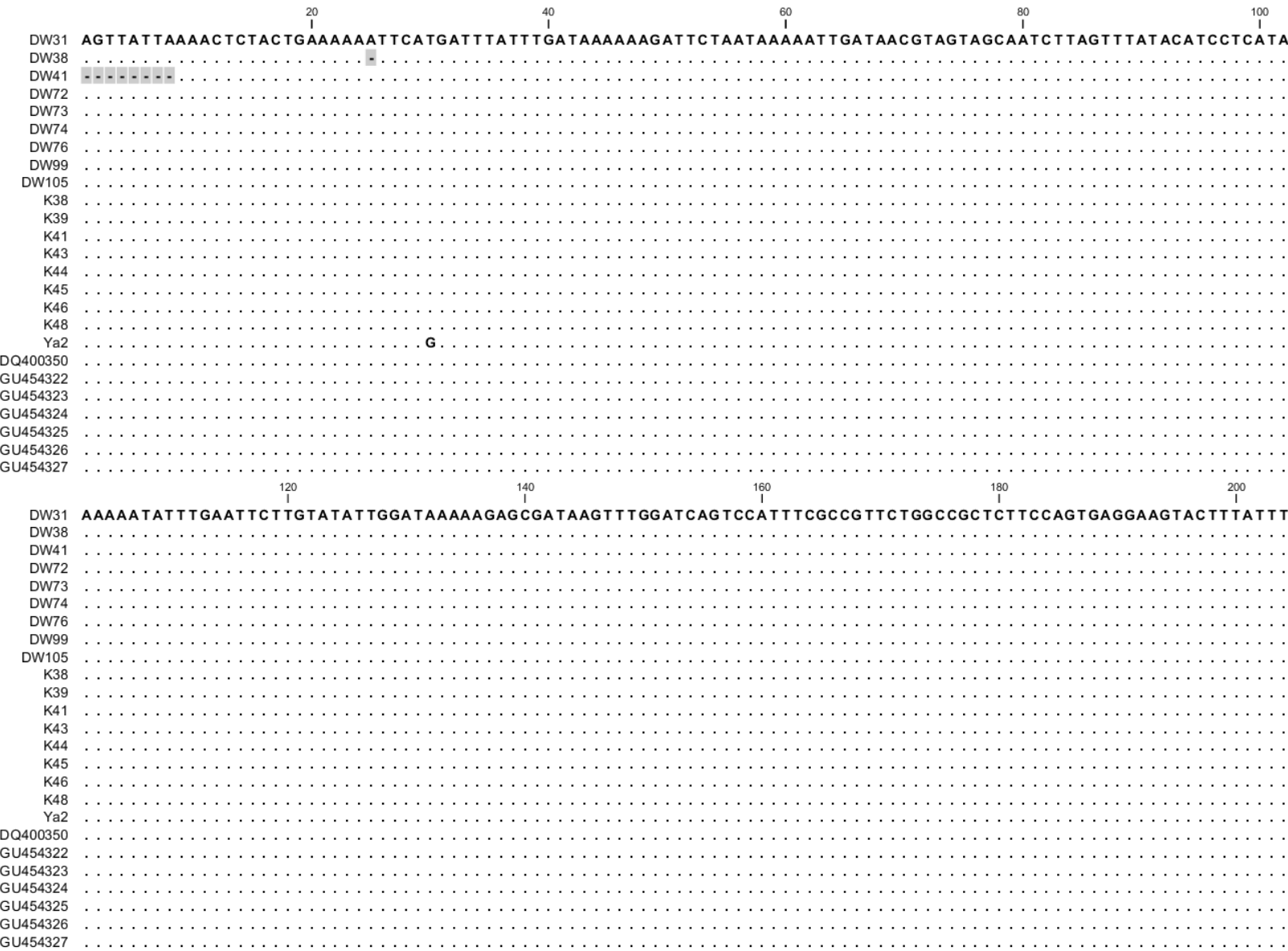
S3A



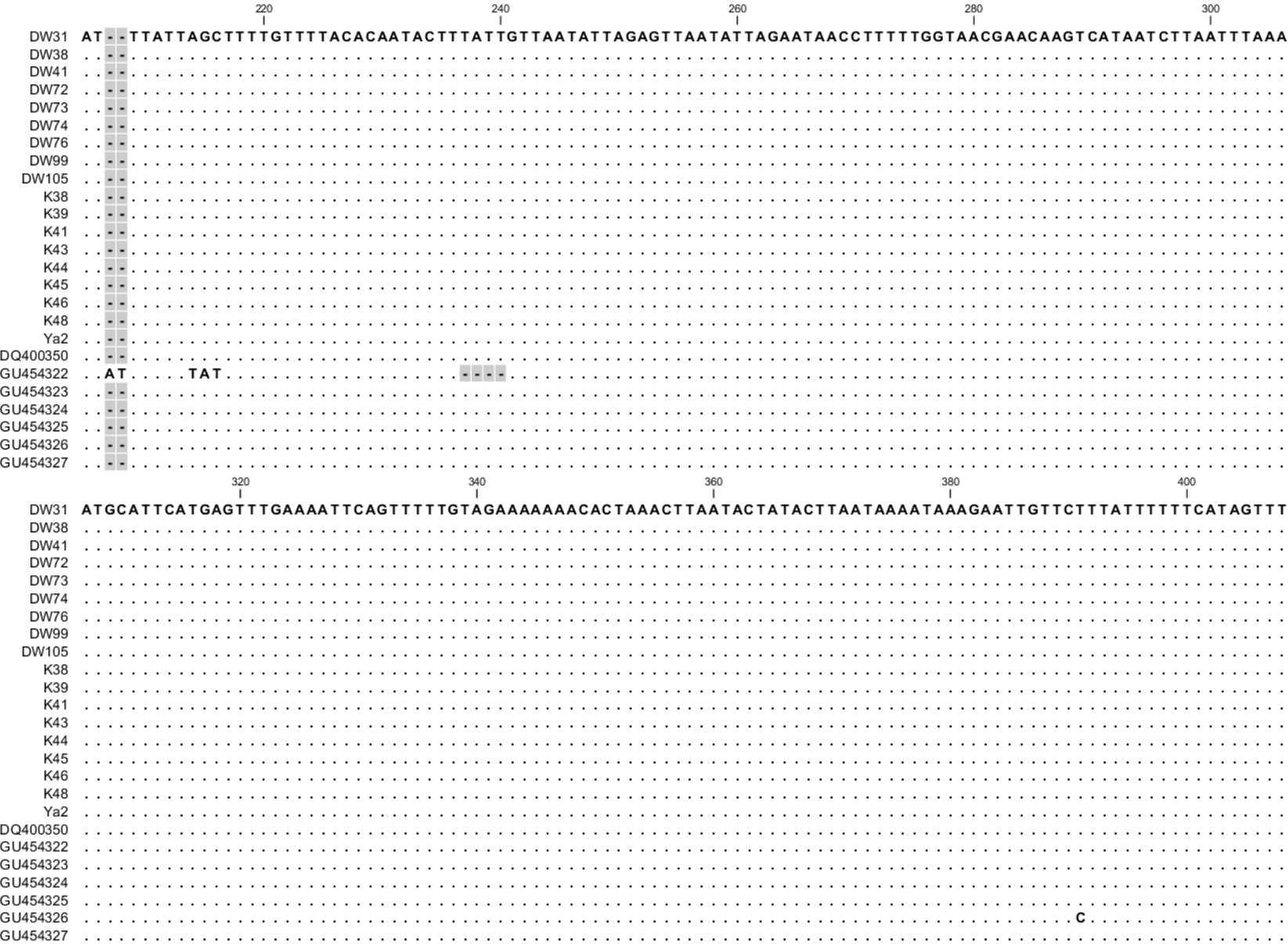
S3A

		420		440		460	
DW31	CAAACAAAGGGGGCGAAGTAATACAAAAGGA	CTCTGTTCTTTTTTAGTCCTATCTATAAGAGGAGAGTAT	470				
DW38	470
DW41	470
DW72	470
DW73	470
DW74	470
DW76	470
DW99	470
DW105	470
K38	470
K39	A.	470
K41	470
K43	470
K44	470
K45	A.	470
K46	470
K48	.	.	G.	.	.	A.	470
Ya2	470
DQ400350	470
GU454226	470
GU454227	470
GU454228	470
GU454229	470
GU454230	469
GU454231	470

S3B



S3B



S3B



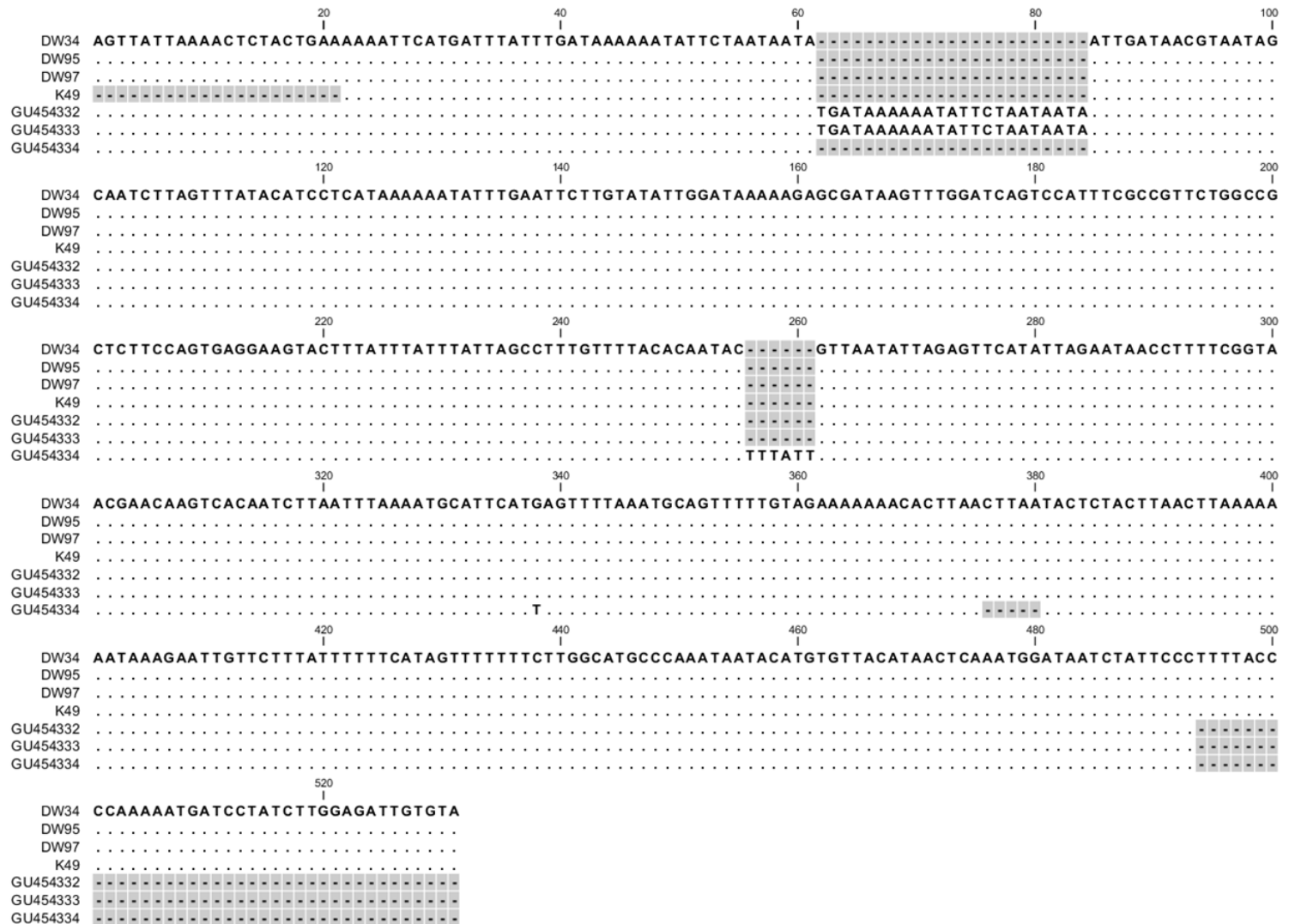
Supplemental Figure S3. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Lemna minor* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

- A.** Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *Le. minor* from different parts of the world available in the GenBank: DQ400350, Russia; GU454226, Turkey; GU454227, USA; GU454228, South Africa; GU454229, Japan; GU454230, Finland; GU454231, Germany.
- B.** Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *Le. minor* from different parts of the world available in the GenBank: DQ400350, Russia; GU454322, Turkey; GU454323, USA; GU454324, South Africa; GU454325, Japan; GU454326, Finland; GU454327, Germany.

S4A

DW34 **TTCTAGAATAAAAAAGTACGTCATAGACTTTTTGACTTAGACTTGCTTTTTGCTTCTTCGAATTATATCAAGATTGTACTCTAACAATTACTTATTCGTT**
 DW95
 DW97
 K49
 GU454236
 GU454237
 GU454238
 DW34 **GAGAGAATACCTCCGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTTCTTCCTTCCCGTTTTTCAGTTCTTAGTATAATGTAATGCA**
 DW95
 DW97
 K49
 GU454236
 GU454237
 GU454238
 DW34 **AAACTTTTTTGAGTATGCGTTGTAACGCAACAAACAAAGTATTTATCAATTGACAAAATAGCCAGGACCTAACCCAATAAGTATGTTCTTGTAATTGTAA**
 DW95
 DW97
 K49
 GU454236
 GU454237
 GU454238
 DW34 **ACTTTAATTAGAATTAATAATAATAAAAAAGTTCTCAATTAAATTAATTAATTTAATCTATTCCATTTTAAATCCCATAAAAAAAGAAATCAAACA**
 DW95
 DW97
 K49
 GU454236
 GU454237
 GU454238
 DW34 **AA--GGGGGCGAAGTAATACAAAAAGAACTCTGTTCTTTTTTAGTCCTATCTATAAGAGGAGAGTAT**
 DW95
 DW97
 K49
 GU454236
 GU454237
 GU454238 **CAAA**

S4B



Supplemental Figure S4. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Lemna trisulca* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *Le. trisulca* from different parts of the world available in the GenBank: GU454236, Canada; GU454237, USA; GU454237, UTCC 399.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *Le. trisulca* from different parts of the world available in the GenBank: GU454332, Canada; GU454333, USA; GU454334, UTCC 399.

S5A

DW101 **TTCTAGAATAAAAAAGTACGTAATAGACTTTTTGACTTAGACTTGCTTTTTGCTTCTTCGAATTATATCAAGATTGTACTCTAACAATTACTTTATTCGTT**
 NB0013
 P2
 KF726146
 MG000422
 GU454240

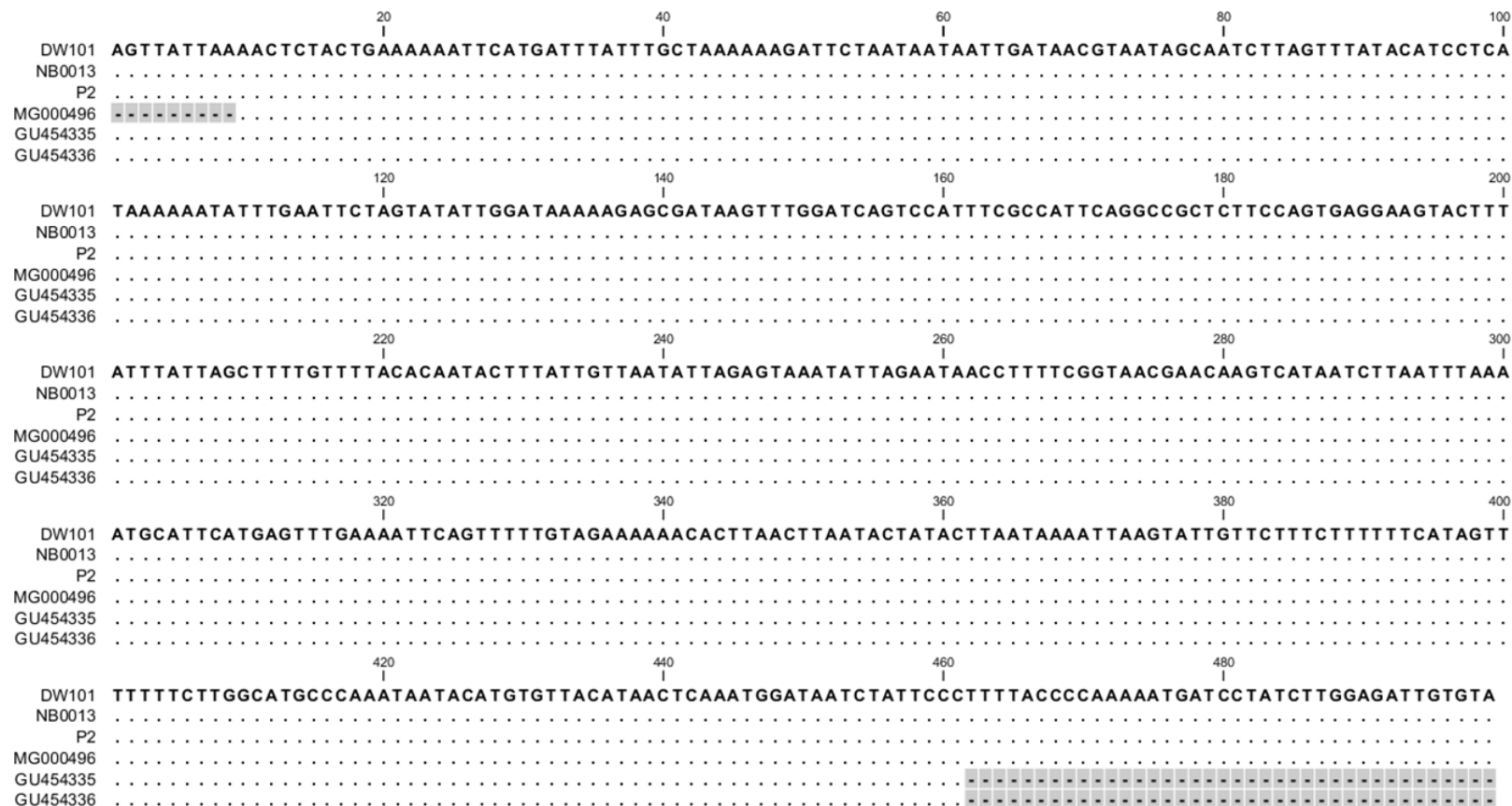
DW101 **GAGAGAATACCTCCGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTTCTTCTTCCGTTTTTCAGTTCTTAGTATAATGTAATGCA**
 NB0013
 P2
 KF726146
 MG000422
 GU454240

DW101 **AAACTTTTTTTGAGTATGCGTTGTAACGCAACAAACAAGGTATTTATCAATTGACAAAATAGCCAGGATCTAACCCAATAAGTATGTTCTTGAATTATA**
 NB0013
 P2
 KF726146
 MG000422
 GU454240

DW101 **AACTTTAATTAGAATTAATAATAAATAAAAAAGTTCTCAATTAAATTAATTAATTAATCTATTCCATTTAAAAATCCCATAAAAAAAAGAAATCAAAAC**
 NB0013
 P2
 KF726146
 MG000422
 GU454240

DW101 **AAAGGGGGCGAAGTAATACAAAAAGAACTCTGTTCTTTTTTAGTCCTATCTATAAGAGGAGAGTAT**
 NB0013
 P2
 KF726146
 MG000422
 GU454240

S5B



Supplemental Figure S5. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Lemna turionifera* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *Le. turionifera* from different parts of the world available in the GenBank: KF726146, China; MG000422, Canada; GU454240, Czech.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *Le. turionifera* from different parts of the world available in the GenBank: MG000496, Canada; GU454335, China; GU454336, Czech.

S6A

DW102 **TTT**TAGAATCAAAAAAGTACGTAATAGACTTTTTGACTTAGACTTGCTTTTTGCTTCTTCGAATTATATCAACATTGTACTCTAACAATTACTTTATTCG
 KX212889 . . **C**
 GU454219 . . **C**
 GU454220 . . **C**
 GU454221 . . **C**
 GU454222 . . **C**

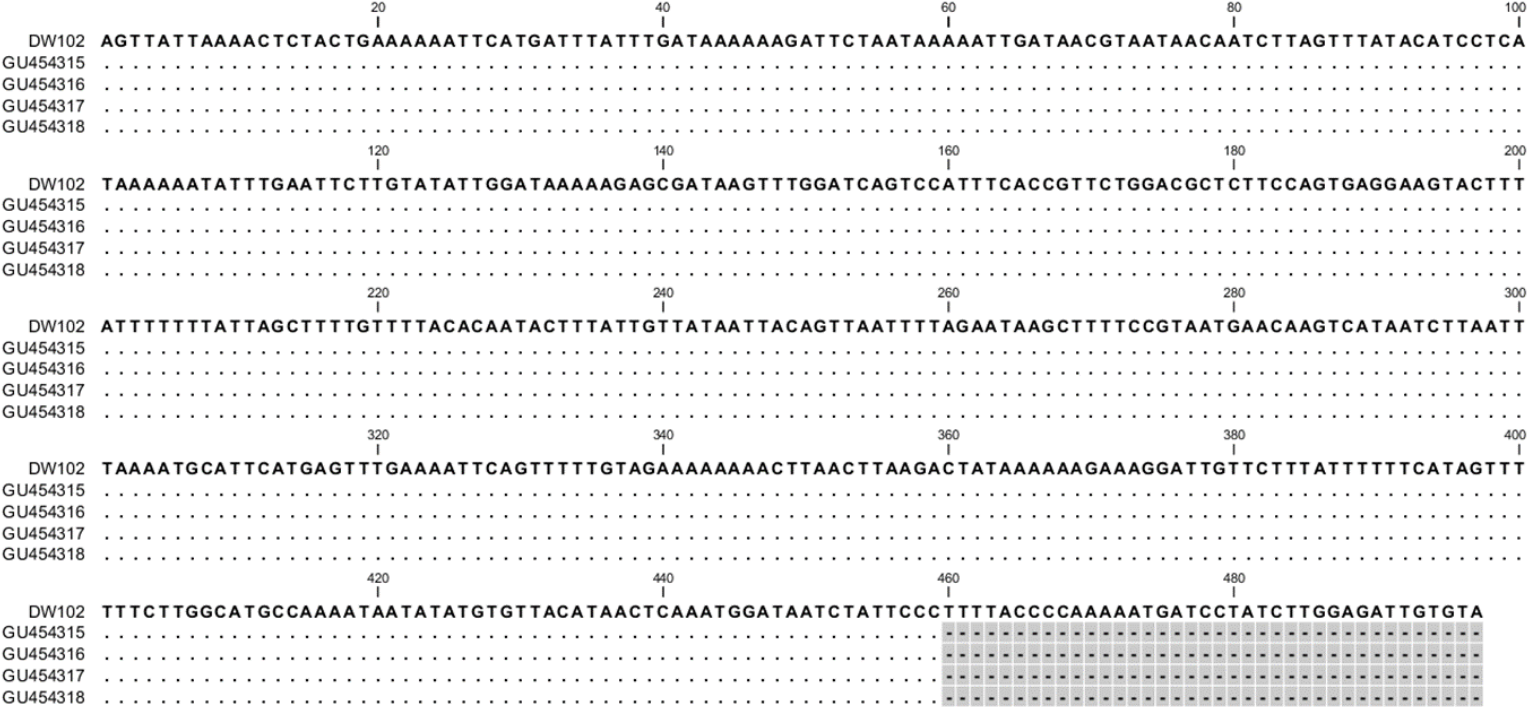
DW102 **TTG**AGAGAATACCTCCGGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTCTTCTCCTTCCCGTTTTTCAGTTCTTAGTATAATGTAATG
 KX212889
 GU454219
 GU454220
 GU454221
 GU454222

DW102 **CAAA**ATTTTTTAGAGTATGCGTTGTAACGCAATAAACAAGGTATTTACCAATTGACAAAAATAGCCAGGACCTAACCCAATAAGTATGTTCTTGTAAATTGT
 KX212889
 GU454219
 GU454220
 GU454221
 GU454222

DW102 **AAAC**TTTAATTAGAAATTAATAATAAATAAAAAAGTTCTCAATTAAATTAATTAATTTAATCTATTCCATTTTAAAATCCCATAAAAAAAAGAAATCAAA
 KX212889
 GU454219
 GU454220
 GU454221
 GU454222

DW102 **ACA**AAGGGGGCGAAGTAATACAAAAAGAACAGAACCTCTGTTCTTTTTTAGTCCTATCTATAAGAGGAGAGTAT
 KX212889
 GU454219
 GU454220
 GU454221
 GU454222

S6B

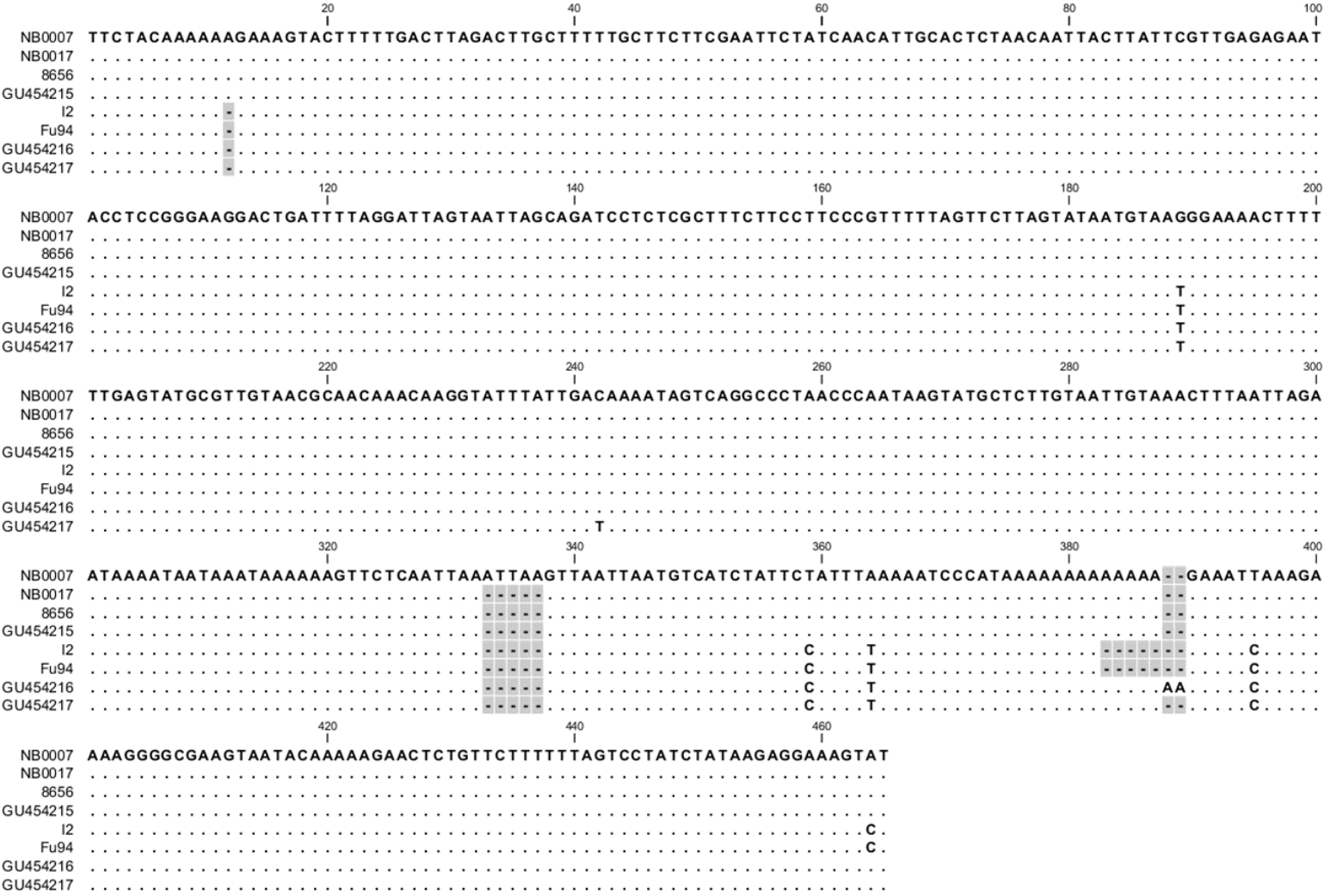


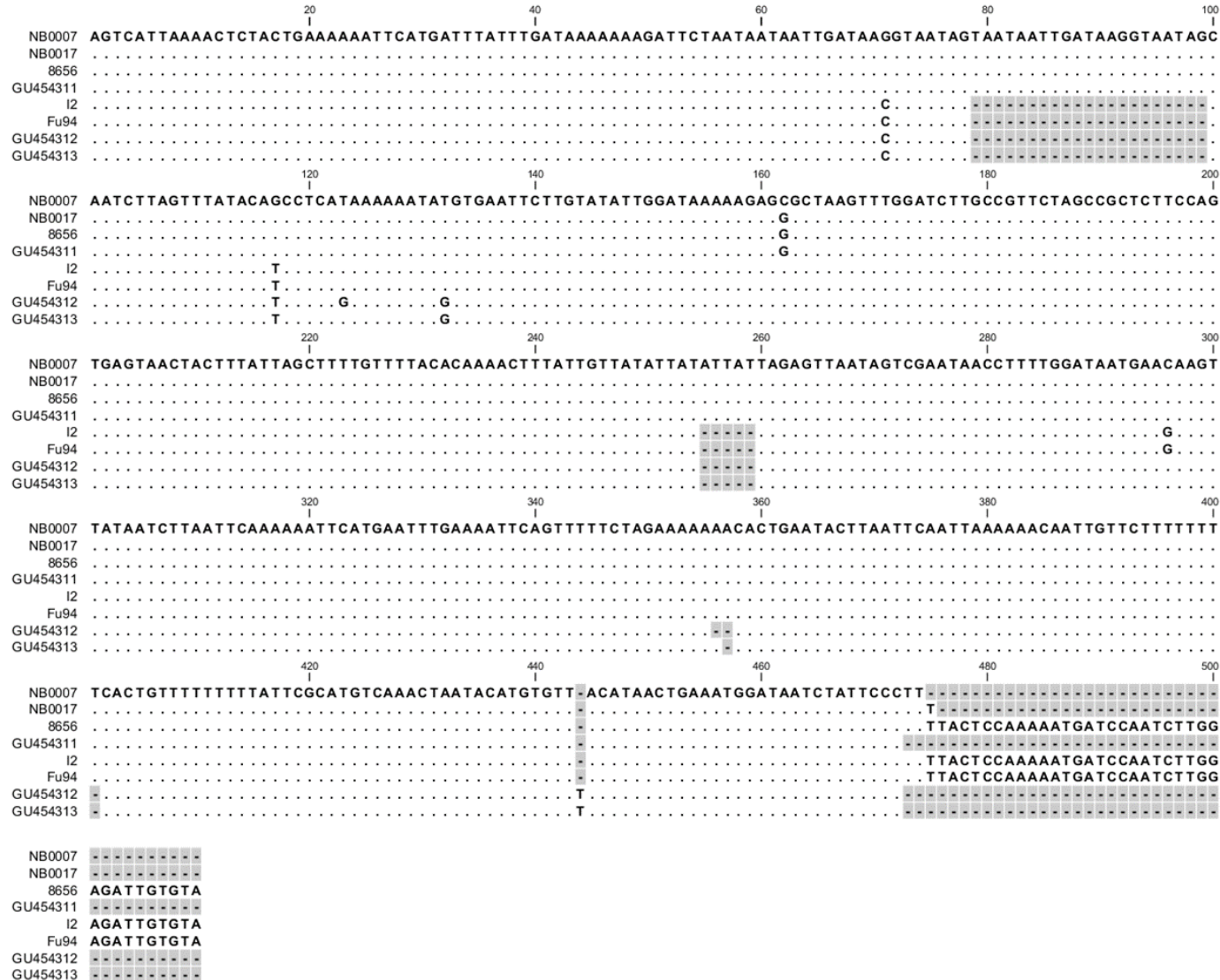
Supplemental Figure S6. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Lemna gibba*, ecotype DW102 (Supplemental Table 2). Matching residues are shown as dots.

A. Nucleotide alignment of the DW102 *atpH-atpF* barcode with the representative sequences of *Le. gibba* from different parts of the world available in the GenBank: KX212889, China; GU454219, USA; GU454220, Italy; GU454221, Ethiopia; GU454222, Japan.

B. Nucleotide alignment of the DW102 *psbK-psbI* barcode with the representative sequences of *Le. gibba* from different parts of the world available in the GenBank: GU454315, USA; GU454316, Italy; GU454317, Ethiopia; GU454318, Japan.

S7A





Supplemental Figure S7. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Lemna aequinoctialis* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

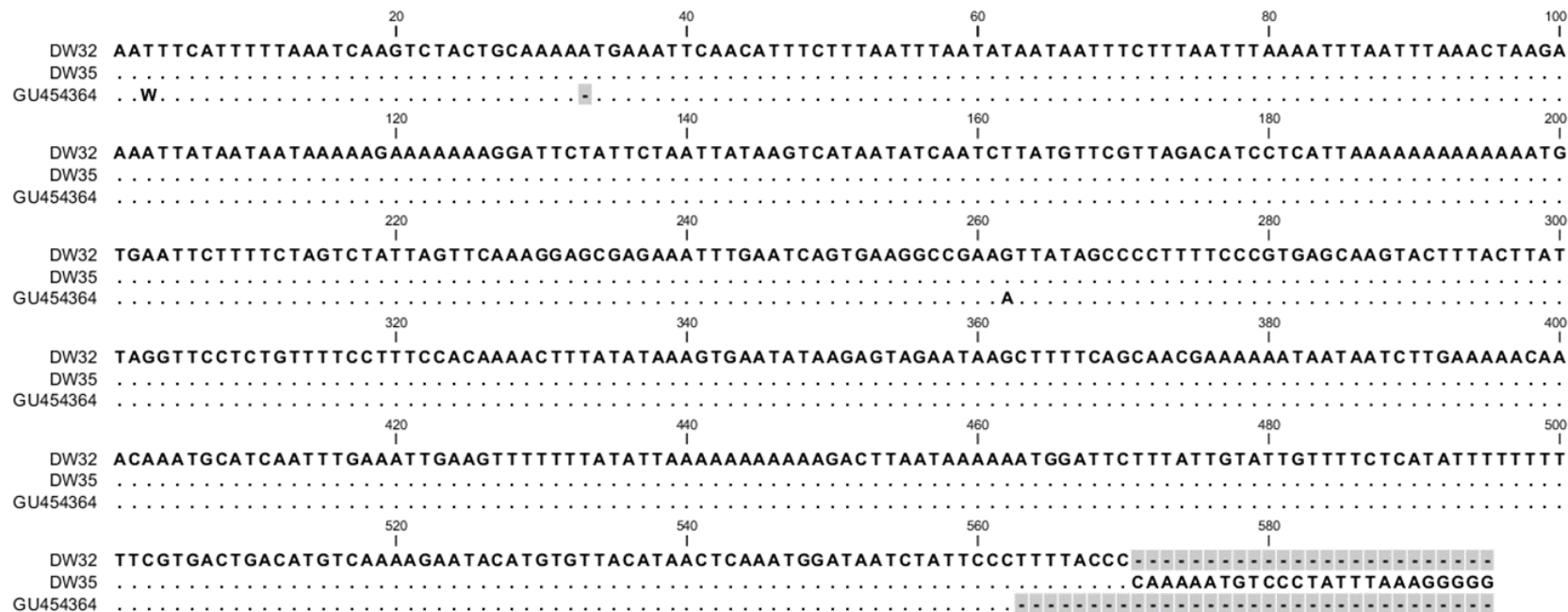
A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *Le. aequinoctialis* from different parts of the world available in the GenBank: GU454215, USA, California, Centerville; GU454216, USA, California, Plainsburg; GU454217, USA, Texas, Austin.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *Le. aequinoctialis* from different parts of the world available in the GenBank: GU454311, USA, California, Centerville; GU454312, USA, California, Plainsburg; GU454313, USA, Texas, Austin.

S8A

DW32 TTCTCGAATAAAAAAGTACGTCATAGTGTTTTGACTTAGACTTGCTTTTTGCTTGTTTCGAATTATCTCTAAATTGCACCTATAACAATTACTTATTCGTT
 DW35
 MG775412
 MG775413
 MG812317
 DW32 GAGAGAATACCTCCGGAAGGACTGATTTTAGGATTAGTAATTAGCAGATCCTCTCGCTTTCTTCCTCCCGTTTTTAGTTTCGTAGTcTAATGGAAACCT
 DW35
 MG775412
 MG775413
 MG812317
 DW32 TTTTLAGTATGCGTTGCAACGCAACAAACAAGGTAGTTATCAATTGACAAAATACCCAGGACCTAACCCAATAAGTAGATTCTTGTAATTGTAAACTTTA
 DW35
 MG775412
 MG775413
 MG812317
 DW32 ATTTGTTTTTTTTTATAAAAAATAAAA - GTTTCTCAATTAAATTAATTAATCGATTAAAAATAAAAAATCCCACAAAAAAA - GAAATCAACCAAAGC
 DW35
 MG775412
 MG775413
 MG812317
 DW32 AAAGGGGGGG - AGTAATACAAAAAGAACTCTGTTCTTTGTTAGTCCTATCTATAAGAGGAGAGTAT
 DW35
 MG775412
 MG775413
 MG812317

S8B

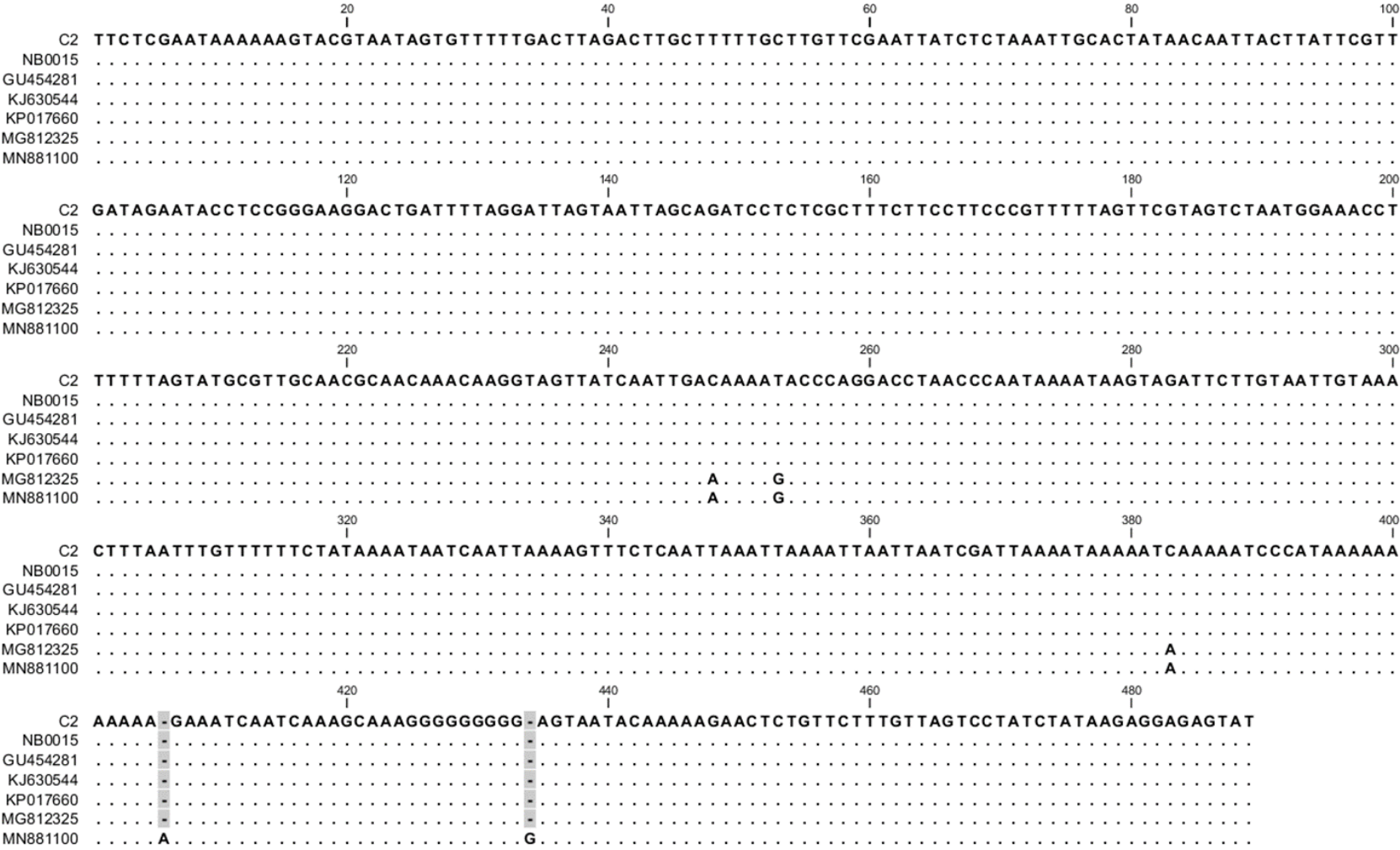


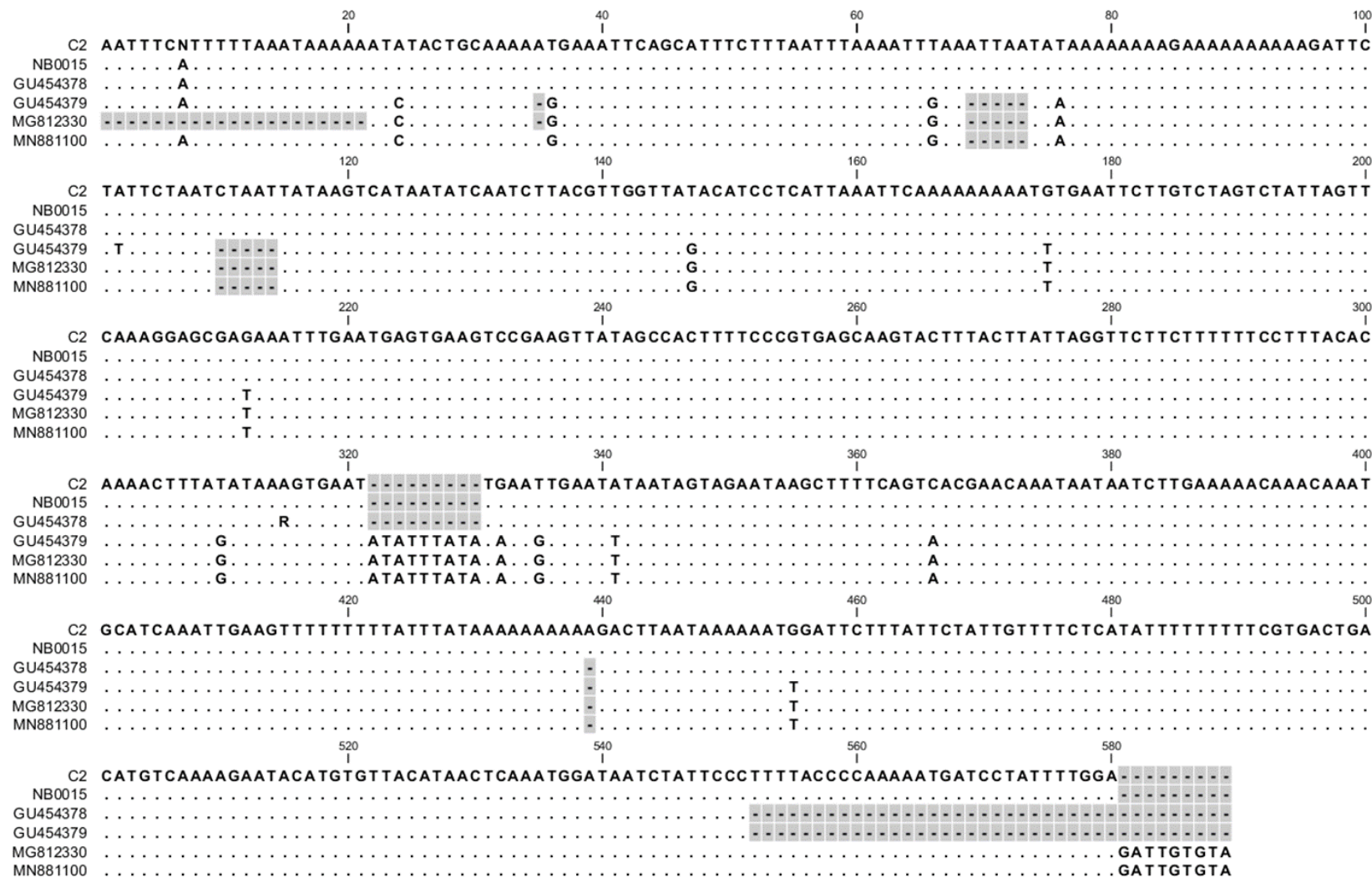
Supplemental Figure S8. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Wolffia arrhiza* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *W. arrhiza* from different parts of the world available in the GenBank: MG812317, Kenya; MG775412, Italy; MG775413, Brazil.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequence of *W. arrhiza* available in the GenBank: GU454364, Hungary.

S9A





Supplemental Figure S9. Nucleotide alignment of *atpH-atpF* and *psbK-psbI* spacers of *Wolffia globosa* (for ecotypes details see supplemental Table 2). Matching residues are shown as dots.

A. Nucleotide alignment of *atpH-atpF* barcodes including the representative sequences of *W. globosa* from different parts of the world available in the GenBank: GU454281, USA; KJ630544, China; KP017660, China; MG812325, India; MN881100, Japan.

B. Nucleotide alignment of *psbK-psbI* barcodes including the representative sequences of *W. globosa* from different parts of the world available in the GenBank: GU454378, USA; GU454379, Thailand; MG812330, India; MN881100, Japan.