

1 **TITLE**

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3 Phylogenetic analysis and development of molecular markers for five medicinal
4 *Alpinia* species based on complete plastome sequences

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6 **AUTHOR LIST**

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30 **Supplementary tables**

31 **Table S1. Base composition in the plastomes of the four *Alpinia* species.**

32 **Table S2. List of genes annotated in the plastome of *A. galanga*. Numbers in parentheses**
33 **represented the repetition of genes. Superscript T: trans-splicing gene.**

34 **Table S3. List of genes annotated in the plastome of *A. nigra*. Numbers in parentheses**
35 **represented the copy number of genes. Superscript T: trans-splicing gene.**

36 **Table S4. List of genes annotated in the plastome of *A. officinarum*. Numbers in parentheses**
37 **represented the repetition of genes. Superscript T: trans-splicing gene.**

38 **Table S5. List of genes annotated in the plastome of *A. oxyphylla*. Numbers in parentheses**
39 **represented the repetition of genes. Superscript T: trans-splicing gene.**

40 **Table S6. The length of introns and exons for the splitting genes in the plastome of *A. galanga*.**
41 **The gene *rps12* was a trans-splicing gene.**

42 **Table S7. The length of introns and exons for the splitting genes in the plastome of *A. nigra*.**
43 **The gene *rps12* was a trans-splicing gene.**

44 **Table S8. The length of introns and exons for the splitting genes in the plastome of *A.***
45 ***officinarum*. The gene *rps12* was a trans-splicing gene.**

46 **Table S9. The length of introns and exons for the splitting genes in the plastome of *A.***
47 ***oxyphylla*. The gene *rps12* was a trans-splicing gene.**

48 **Table S10. SSR identified in the plastome of *A. galanga*. P1 = Mononucleotide; P2 = Di**
49 **nucleotide; P3 = Tri nucleotide; P4 = Tetra nucleotide; P5 = Penta nucleotide; 6 = Hexa**
50 **nucleotide repeats and c = Compound repeat microsatellites.**

51 **Table S11. SSR identified in the plastome of *A. nigra*. P1 = Mononucleotide; P2 = Di nucleotide;**
52 **P3 = Tri nucleotide; P4 = Tetra nucleotide; P5 = Penta nucleotide; 6 = Hexa nucleotide repeats**
53 **and c = Compound repeat microsatellites.**

54 **Table S12. SSR identified in the plastome of *A. officinarum*. P1 = Mononucleotide; P2 = Di**
55 **nucleotide; P3 = Tri nucleotide; P4 = Tetra nucleotide; P5 = Penta nucleotide; 6 = Hexa**
56 **nucleotide repeats and c = Compound repeat microsatellites.**

57 **Table S13. SSR identified in the plastome of *A. oxyphylla*. P1 = Mononucleotide; P2 = Di**
58 **nucleotide; P3 = Tri nucleotide; P4 = Tetra nucleotide; P5 = Penta nucleotide; 6 = Hexa**
59 **nucleotide repeats and c = Compound repeat microsatellites.**

60 **Table S14. Comparison of SSR markers found among four *Alpinia* species and one outgroup**
61 **species of *Zingiber spectabile*. Zisp: *Zingiber spectabile*; Alga: *Alpinia galanga*; Alni: *Alpinia***
62 ***nigra*; Aloh: *Alpinia officinarum*; Alox: *Alpinia oxyphylla*.**

63 **Table S15. Dispersed repeat sequences in the plastome of *A. galanga*.**

64 **Table S16. Dispersed repeat sequences in the plastome of *A. nigra*.**

65 **Table S17. Dispersed repeat sequences in the plastome of *A. officinarum*.**

66 **Table S18. Dispersed repeat sequences in the plastome of *A. oxyphylla*.**

67 **Table S19. Tandem repeat sequences identified in the plastome of *A. galanga*. a: coding**
68 **sequences; b: intergenic spacers.**

69 **Table S20. Tandem repeat sequences identified in the plastome of *A. nigra*. a: coding**
70 **sequences; b: intergenic spacers.**

71 **Table S21. Tandem repeat sequences identified in the plastome of *A. officinarum*. a: coding**
72 **sequences; b: intergenic spacers.**

73 **Table S22. Tandem repeat sequences identified in the plastome of *A. oxyphylla*. a: coding**
74 **sequences; b: intergenic spacers.**

75 **Table S23. The distances among the shared intergenic spacer (IGS) regions from the five**
76 ***Alpinia* plastomes. Alga: *Alpinia galanga*; Alha: *Alpinia hainanensis*; Alni: *Alpinia nigra*; Aloh:**
77 ***Alpinia officinarum*; Alox: *Alpinia oxyphylla*.**

78 **Table S24. The list of accession numbers of the plastome sequences used in the phylogenetic**
79 **analyses of the Zingiberaceae.**

80 **Table S25. The dN, dS, and dN/dS (ω) value of 77 common protein-coding genes from**
81 **plastomes of 21 *Alpinia* species.**

82 **Table S26. The two pairs of primers for the amplification of DNA barcodes.**

83 **Table S27. The list of sample numbers of the samples used in the species discrimination**
84 **analyses of the *Alpinia*.**

85

86 **Figure S1. Schematic representation of the *A. nigra* plastome features.**

87 **Figure S2. Schematic representation of the *A. officinarum* plastome features.**

88 **Figure S3. Schematic representation of the *A. oxyphylla* plastome features.**

89 **Figure S4. The schematic diagram of position and length of introns and exons for the splitting**

90 **genes in the plastome of *A. galanga*. The gene *rps12* was a trans-splicing gene.**

91 **Figure S5. The schematic diagram of position and length of introns and exons for the splitting**

92 **genes in the plastome of *A. nigra*. The gene *rps12* was a trans-splicing gene.**

93 **Figure S6. The schematic diagram of position and length of introns and exons for the splitting**

94 **genes in the plastome of *A. officinarum*. The gene *rps12* was a trans-splicing gene.**

95 **Figure S7. The schematic diagram of position and length of introns and exons for the splitting**

96 **genes in the plastome of *A. oxyphylla*. The gene *rps12* was a trans-splicing gene.**

97 **Figure S8. The VCF output for the *A. officinarum*.**

98 **Figure S9. The VCF output for the *A. oxyphylla*.**

99 **Figure S10. The VCF output for the *A. oxyphylla*.**

100 **Figure S11. The VCF output for the *A. nigra*.**

101 **Figure S12. The original and full-length gel electrophoresis results of the amplification of DNA**

102 **barcodes using designed primers.**

103 **Figure S13. The alignment of amplicons produced by designed Alpp primers.**

104 **Figure S14. The alignment of amplicons produced by designed Alpr primers.**

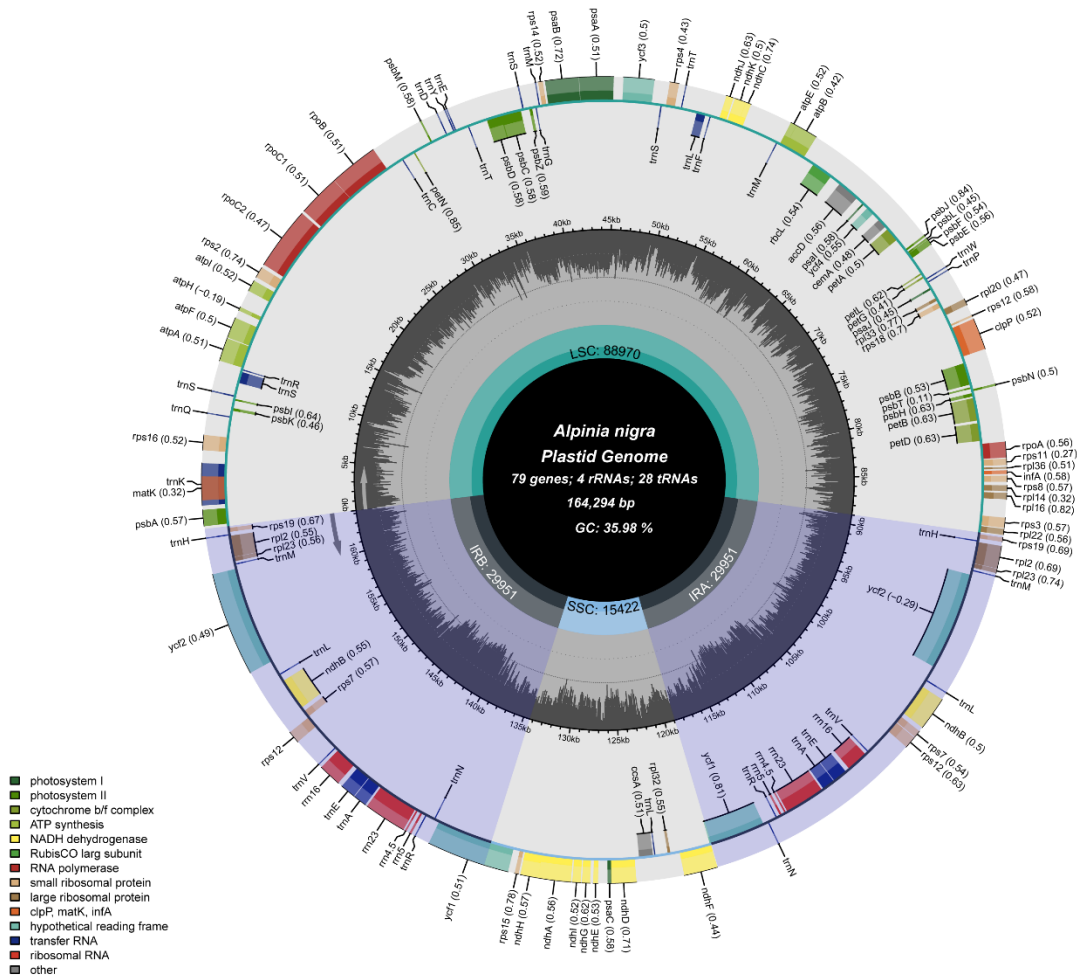
105 **Figure S15. The alignment of amplicons in 10 *Alpinia* plastomes produced by designed Alpp**

106 **primers in silico.**

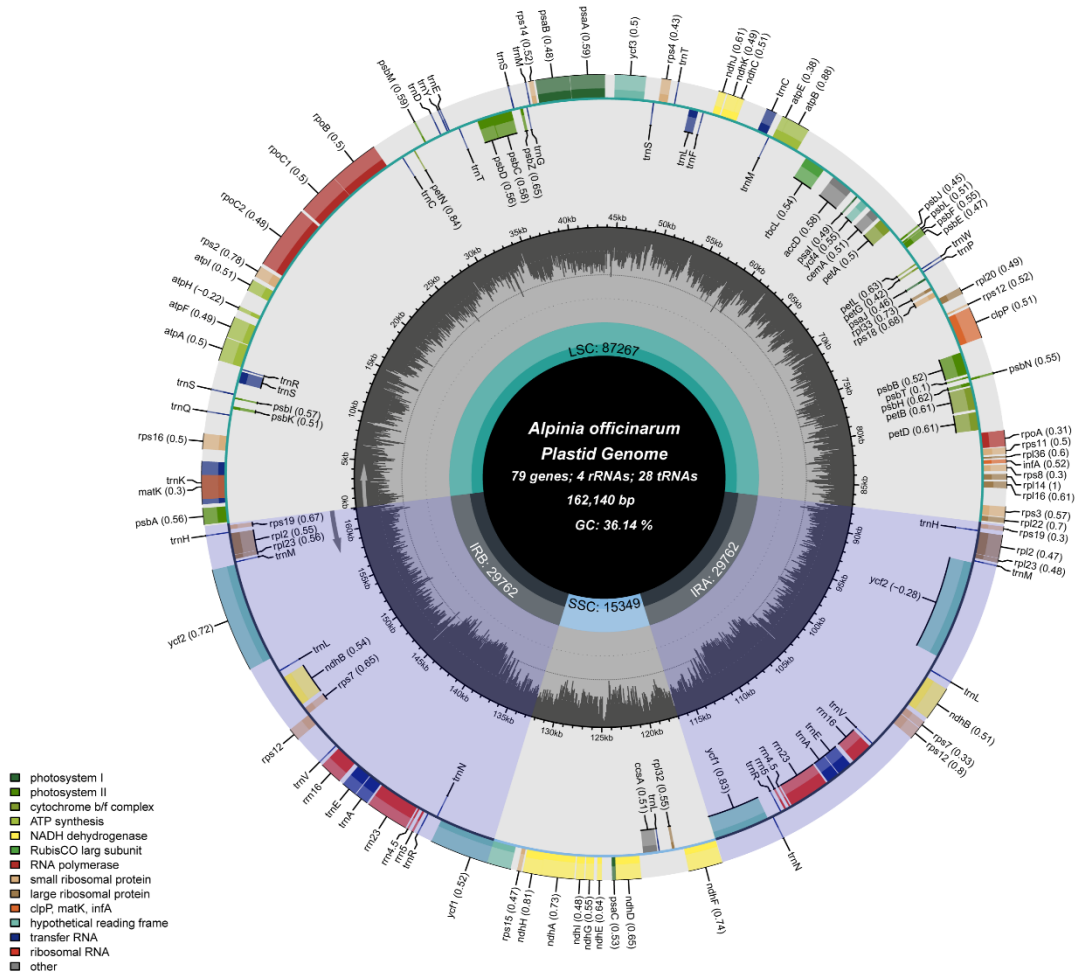
107 **Figure S16. The alignment of amplicons in 10 *Alpinia* plastomes produced by designed Alpp**

108 **primers in silico.**

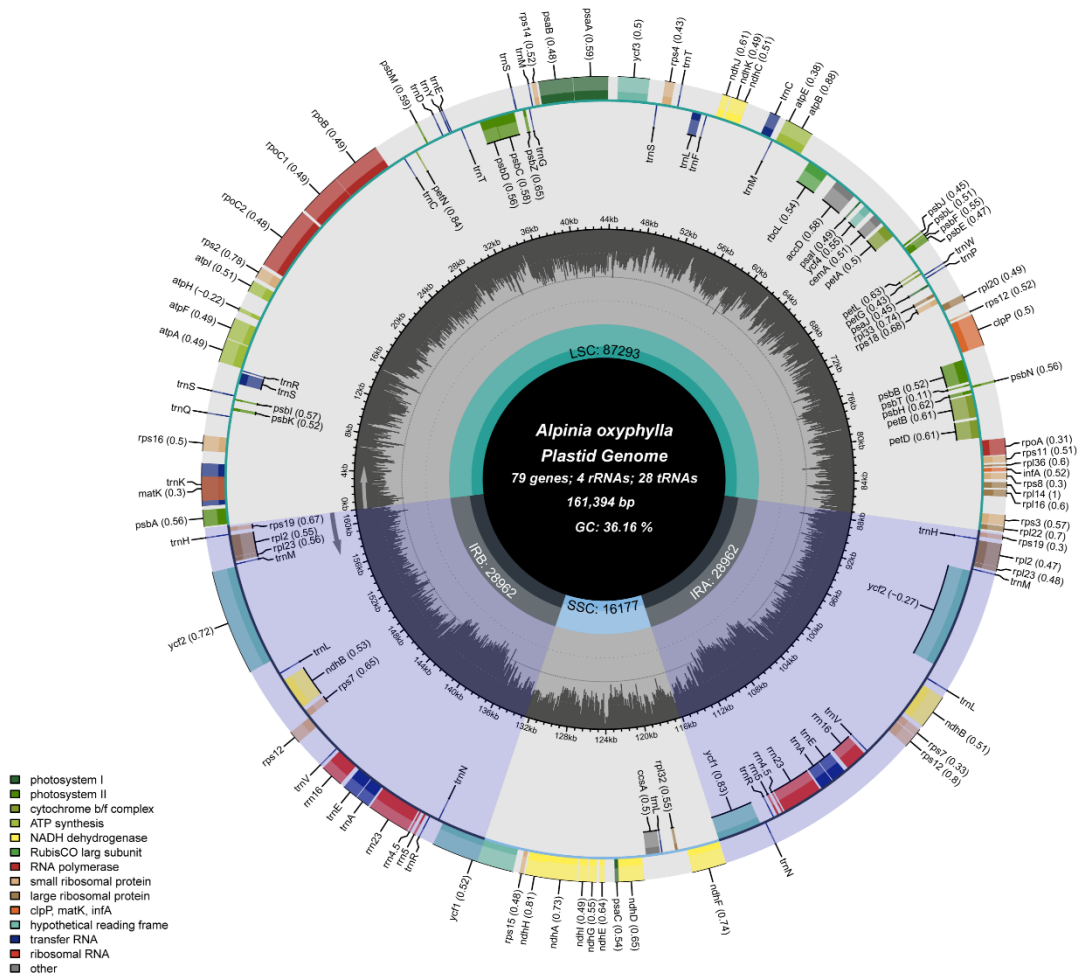
109 **Figure S1. Schematic representation of the *A. nigra* plastome features.**
 110 From the center going outward, the first circle shows the species name and specific information
 111 regarding the genome (length, GC content, and the number of genes). The optional GC content is
 112 depicted as the proportion of the shaded parts of each section and the length of the corresponding
 113 single short copy (SSC), inverted repeat (IRa and IRb), and large single-copy (LSC) regions are also
 114 given in this circle. The outer circle shows the gene names and their optional codon usage bias. The
 115 genes are colored based on their functional categories. Genes inside and outside of the circle are
 116 transcribed in clockwise and counterclockwise directions, represented with arrows. The optional
 117 shaded area stretching from the inner sphere toward the outer circle marks the IR regions.



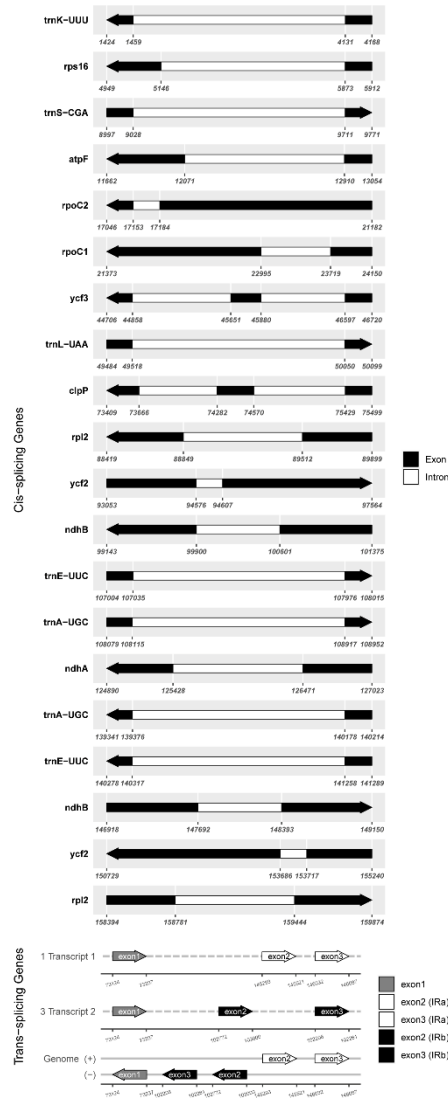
119 **Figure S2. Schematic representation of the *A. officinarum* plastome features.**
 120 From the center going outward, the first circle shows the species name and specific information
 121 regarding the genome (length, GC content, and the number of genes). The optional GC content is
 122 depicted as the proportion of the shaded parts of each section and the length of the corresponding
 123 single short copy (SSC), inverted repeat (IRa and IRb), and large single-copy (LSC) regions are also
 124 given in this circle. The outer circle shows the gene names and their optional codon usage bias. The
 125 genes are colored based on their functional categories. Genes inside and outside of the circle are
 126 transcribed in clockwise and counterclockwise directions, represented with arrows. The optional
 127 shaded area stretching from the inner sphere toward the outer circle marks the IR regions.



129 **Figure S3. Schematic representation of the *A. oxyphylla* plastome features.**
 130 From the center going outward, the first circle shows the species name and specific information
 131 regarding the genome (length, GC content, and the number of genes). The optional GC content is
 132 depicted as the proportion of the shaded parts of each section and the length of the corresponding
 133 single short copy (SSC), inverted repeat (IRa and IRb), and large single-copy (LSC) regions are also
 134 given in this circle. The outer circle shows the gene names and their optional codon usage bias. The
 135 genes are colored based on their functional categories. Genes inside and outside of the circle are
 136 transcribed in clockwise and counterclockwise directions, represented with arrows. The optional
 137 shaded area stretching from the inner sphere toward the outer circle marks the IR regions.

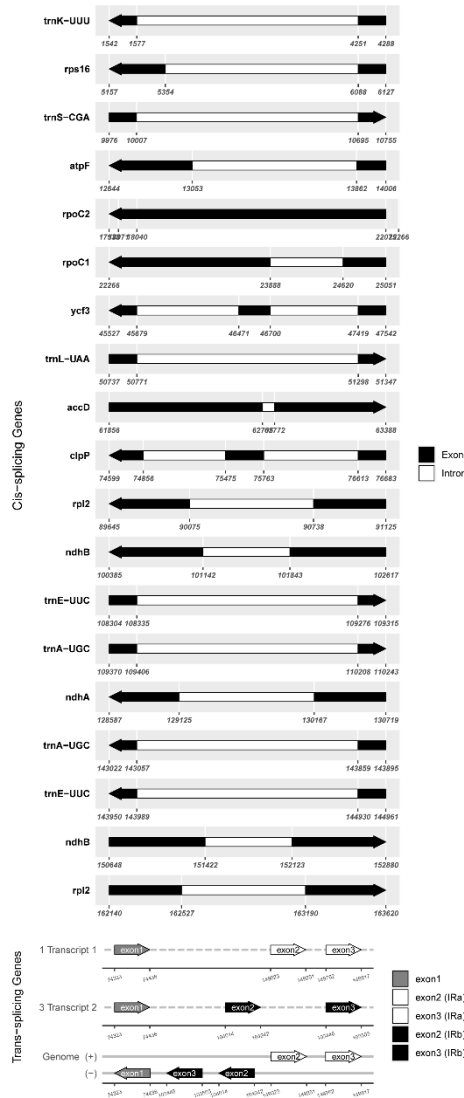


139 **Figure S4. The schematic diagram of position and length of introns and exons for**
 140 **the splitting genes in the plastome of *A. galanga*. The gene *rps12* was a trans-**
 141 **splicing gene.**



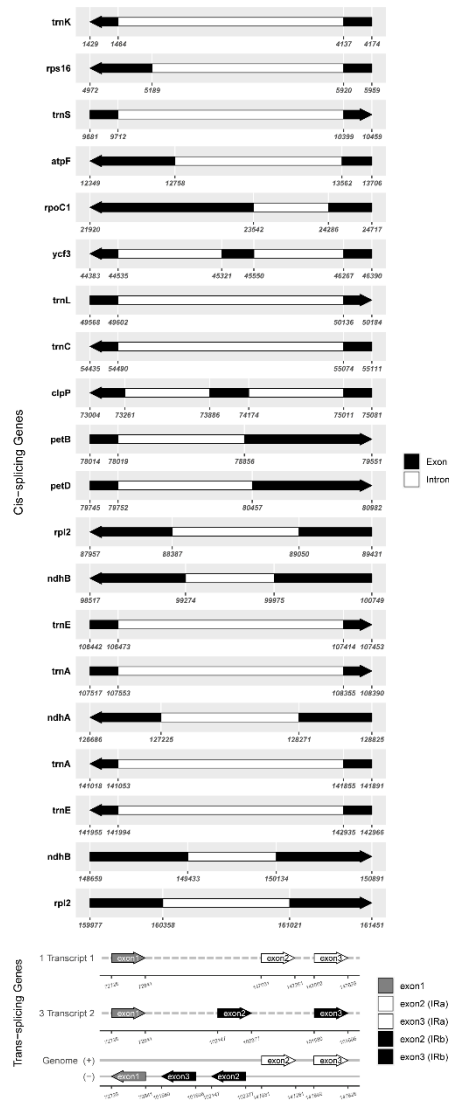
142

143 **FigureS5. The schematic diagram of position and length of introns and exons for**
 144 **the splitting genes in the plastome of *A. nigra*. The gene *rps12* was a trans-**
 145 **splicing gene.**



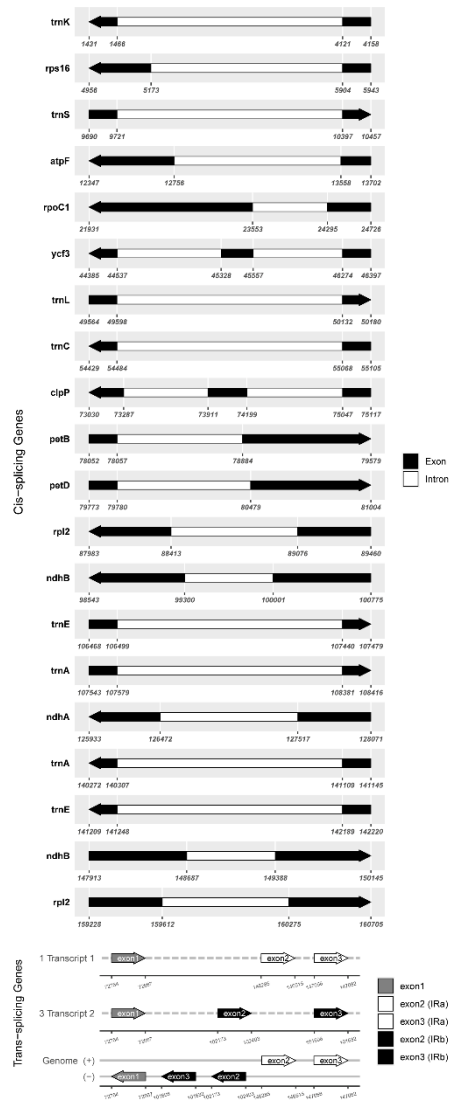
146

147 **Figure S6. The schematic diagram of position and length of introns and exons**
 148 **for the splitting genes in the plastome of *A. officinarum*. The gene *rps12* was a**
 149 **trans-splicing gene.**



150

151 **FigureS7. The schematic diagram of position and length of introns and exons for**
 152 **the splitting genes in the plastome of *A. oxyphylla*. The gene *rps12* was a trans-**
 153 **splicing gene.**



154

155 **Figure S8. The VCF output for the *A. officinarum*.**

156 The VCF file with all the detected intra-individual polymorphism outputed by the heteroplasmy mode
157 of NOVOPLasty. The allele frequency (AF), depth of coverage (DP) are given as additional info. FR
158 indicates if the polymorphism was detected on the forward and/or reverse strand. LCR will indicate if
159 the polymorphism is situated near a low-complexity region; SNR stands for single nucleotide repeat.

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160 ##fileformat=VCFv4.0
161 ##fileDate=20210531
162 ##reference=/home/zhangh/my_apps/HybPiper-master/MK940823.fasta
163 ##INFO=<ID=AF,Number=1,Type=Float,Description="Allele Frequency">
164 ##INFO=<ID=DP,Number=1,Type=Integer,Description="Raw Depth">
165 ##INFO=<ID=FR,Number=1,Type=Flag,Description="Detected on the forward(F) and/or reverse(R) strand">
166 ##INFO=<ID=LCR,Number=1,Type=String,Description="Low Complexity Region">
167 #CHROM POS ID REF ALT QUALFILTER INFO
168 cp 87674 . A . . AF=;DP=129;FR=R;LCR=SNR
169 cp 87680 . A . . AF=;DP=125;FR=R;LCR=SNR
170
```

171 **Figure S9. The VCF output for the *A. oxyphylla*.**

172 The VCF file with all the detected intra-individual polymorphism outputed by the heteroplasmy mode
173 of NOVOPLasty. The allele frequency (AF), depth of coverage (DP) are given as additional info. FR
174 indicates if the polymorphism was detected on the forward and/or reverse strand. LCR will indicate if
175 the polymorphism is situated near a low-complexity region; SNR stands for single nucleotide repeat.

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176 ##fileformat=VCFv4.0
177 ##fileDate=14:13:3606
178 ##reference=/home/zhangh/my_apps/HybPiper-master/MK940824.fasta
179 ##INFO=<ID=AF,Number=1,Type=Float,Description="Allele Frequency">
180 ##INFO=<ID=DP,Number=1,Type=Integer,Description="Raw Depth">
181 ##INFO=<ID=FR,Number=1,Type=Flag,Description="Detected on the forward(F) and/or reverse(R) strand">
182 ##INFO=<ID=LCR,Number=1,Type=String,Description="Low Complexity Region">
183 #CHROM POS ID REF ALT QUALFILTER INFO
184 cp 89024 . T G . . AF=0.949;DP=39;FR=R;LCR=SNR
185 cp 89039 . T A,C . . AF=0.976;DP=41;FR=R;LCR=
186 cp 89040 . A G,T . . AF=0.976;DP=41;FR=R;LCR=
187 cp 89195 . T A . . AF=0.0511;DP=39;FR=R;LCR=
188 cp 89197 . C A . . AF=0.0511;DP=39;FR=R;LCR=
189 cp 89327 . T G . . AF=0.0447;DP=44;FR=R;LCR=
190 cp 89457 . A C . . AF=0.0761;DP=39;FR=R;LCR=
191 cp 89630 . A C . . AF=0.0403;DP=49;FR=R;LCR=
192 cp 90064 . A T . . AF=0.0447;DP=44;FR=R;LCR=
193 cp 90409 . CAATTATA C . . AF=0.0364;DP=55;FR=R;LCR=
194 cp 90494 . G T . . AF=0.048;DP=41;FR=R;LCR=
195 cp 90510 . T A . . AF=0.0505;DP=39;FR=R;LCR=
196 cp 90524 . A G,T . . AF=0.952;DP=41;FR=R;LCR=
197 cp 90525 .
198 A,C . . AF=0.977;DP=43;FR=R;LCR=
199 cp 91306 .
200 C,A . . AF=0.965;DP=56;FR=R;LCR=
201 cp 92629 . G T . . AF=0.0322;DP=62;FR=R;LCR=
202 cp 93100 . T A . . AF=0.0214;DP=46;FR=R;LCR=
203 cp 93468 . T A . . AF=0.0286;DP=35;FR=R;LCR=
204 cp 93769 . C A . . AF=0.0176;DP=56;FR=R;LCR=
205 cp 93821 . G T . . AF=0.0169;DP=59;FR=R;LCR=
206 cp 93848 . A C . . AF=0.0327;DP=61;FR=R;LCR=
207 cp 93894 . A T . . AF=0.0605;DP=49;FR=R;LCR=
208 cp 94060 . C T . . AF=0.0214;DP=46;FR=R;LCR=
209 cp 94062 . C T . . AF=0.0429;DP=46;FR=R;LCR=
210 cp 94884 . G T . . AF=0.0196;DP=51;FR=F;LCR=
211 cp 96369 . T G . . AF=0.0435;DP=46;FR=F;LCR=
212 cp 96467 . A T . . AF=0.0351;DP=57;FR=F;LCR=
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213 cp 96534 . T A . . AF=0.0358;DP=55;FR=F;LCR=
214 cp 97616 . G A . . AF=0.0402;DP=49;FR=R;LCR=
215 cp 97916 . C A . . AF=0.0428;DP=92;FR=FR;LCR=
216 cp 98809 . A C . . AF=0.0455;DP=44;FR=R;LCR=
217 cp 98951 . A C . . AF=0.0521;DP=38;FR=R;LCR=
218 cp 100787 . C A . . AF=0.0306;DP=65;FR=F;LCR=
219 cp 100914 . A C . . AF=0.0278;DP=36;FR=F;LCR=
220 cp 101043 . G T . . AF=0.0182;DP=54;FR=F;LCR=
221 cp 101153 . G T . . AF=0.0217;DP=46;FR=R;LCR=
222 cp 101570 . C A . . AF=0.0698;DP=43;FR=F;LCR=
223 cp 101632 . G T . . AF=0.0836;DP=47;FR=F;LCR=
224 cp 101633 . A T . . AF=0.0627;DP=47;FR=F;LCR=
225 cp 101634 . A T . . AF=0.0627;DP=47;FR=F;LCR=
226 cp 101657 . A C . . AF=0.0393;DP=50;FR=F;LCR=
227 cp 101775 . C A . . AF=0.0359;DP=55;FR=F;LCR=
228 cp 102204 . T G . . AF=0.0378;DP=52;FR=F;LCR=
229 cp 102454 .
230 C,T . . AF=0.898;DP=58;FR=F;LCR=
231 cp 102794 . T C . . AF=0.0408;DP=49;FR=F;LCR=
232 cp 102797 . A G . . AF=0.0408;DP=49;FR=F;LCR=
233 cp 102849 . C T . . AF=0.042;DP=47;FR=F;LCR=
234 cp 102870 . A T . . AF=0.044;DP=45;FR=F;LCR=
235 cp 103038 . A G . . AF=0.054;DP=37;FR=F;LCR=
236 cp 103221 . G T . . AF=0.0465;DP=43;FR=F;LCR=
237 cp 103385 . G A . . AF=0.0371;DP=53;FR=F;LCR=
238 cp 103401 . C T . . AF=0.0364;DP=54;FR=F;LCR=
239 cp 103533 . C A . . AF=0.0457;DP=43;FR=F;LCR=
240 cp 103963 . C T . . AF=0.0435;DP=46;FR=F;LCR=
241 cp 104003 . C A . . AF=0.0427;DP=46;FR=F;LCR=
242 cp 104432 . A C . . AF=0.0702;DP=28;FR=F;LCR=
243 cp 104713 . T G . . AF=0.0488;DP=41;FR=F;LCR=
244 cp 104762 . G T . . AF=0.0393;DP=50;FR=F;LCR=
245 cp 105233 . A T . . AF=0.127;DP=55;FR=F;LCR=
246

```

247 **Figure S10. The VCF output for the *A. galanga*.**

248 The VCF file with all the detected intra-individual polymorphism outputed by the heteroplasmy mode
249 of NOVOPLasty. The allele frequency (AF), depth of coverage (DP) are given as additional info. FR
250 indicates if the polymorphism was detected on the forward and/or reverse strand. LCR will indicate if
251 the polymorphism is situated near a low-complexity region; SNR stands for single nucleotide repeat.

```

252 ##fileformat=VCFv4.0
253 ##fileDate=11:36:2106
254 ##reference=/home/zhangh/my_apps/HybPiper-master/NC_035895.fasta
255 ##INFO=<ID=AF,Number=1,Type=Float,Description="Allele Frequency">
256 ##INFO=<ID=DP,Number=1,Type=Integer,Description="Raw Depth">
257 ##INFO=<ID=FR,Number=1,Type=Flag,Description="Detected on the forward(F) and/or reverse(R) strand">
258 ##INFO=<ID=LCR,Number=1,Type=String,Description="Low Complexity Region">
259 #CHROM POS ID REF ALT QUALFILTER INFO
260 cp 229 . T A . . AF=0.0111;DP=90;FR=R;LCR=
261 cp 234 . A C . . AF=0.0404;DP=74;FR=R;LCR=
262

```

263 **Figure S11. The VCF output for the *A. nigra*.**

264 The VCF file with all the detected intra-individual polymorphism outputed by the heteroplasmy mode
265 of NOVOPLasty. The allele frequency (AF), depth of coverage (DP) are given as additional info. FR
266 indicates if the polymorphism was detected on the forward and/or reverse strand. LCR will indicate if
267 the polymorphism is situated near a low-complexity region; SNR stands for single nucleotide repeat.

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268 ##fileformat=VCFv4.0
269 ##fileDate=19:46:5906
270 ##reference=/home/zhangh/my_apps/HybPiper-master/MK940825.fasta

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273 ##INFO=<ID=FR,Number=1,Type=Flag,Description="Detected on the forward(F) and/or reverse(R) strand">
274 ##INFO=<ID=LCR,Number=1,Type=String,Description="Low Complexity Region">
275 #CHROM POS ID REF ALT QUALFILTER INFO
276 cp 89413 . A T . . AF=0.0184;DP=162;FR=R;LCR=SNR
277 cp 89452 .
278 C,A . . AF=0.988,;DP=162;FR=R;LCR=SNR
279 cp 89783 . C A . . AF=0.0311;DP=224;FR=R;LCR=SNR(T)
280 cp 89832 . G T . . AF=0.0135;DP=148;FR=R;LCR=
281 cp 89833 . G T . . AF=0.0128;DP=156;FR=R;LCR=
282 cp 89900 . A C . . AF=0.0185;DP=108;FR=R;LCR=
283 cp 89990 . C A . . AF=0.0167;DP=119;FR=R;LCR=
284 cp 90217 . C A . . AF=0.0129;DP=232;FR=R;LCR=
285 cp 90316 . T A . . AF=0.0133;DP=224;FR=R;LCR=
286 cp 90780 . C A . . AF=0.0173;DP=115;FR=R;LCR=
287 cp 90833 . C A . . AF=0.0185;DP=108;FR=R;LCR=
288 cp 91245 . C T . . AF=0.0217;DP=92;FR=R;LCR=
289 cp 91535 . C A . . AF=0.0156;DP=192;FR=R;LCR=
290 cp 92306 . C A . . AF=0.016;DP=124;FR=R;LCR=
291 cp 92564 . G T . . AF=0.0153;DP=130;FR=R;LCR=
292 cp 92743 . C A . . AF=0.0159;DP=126;FR=R;LCR=
293 cp 92819 . C A . . AF=0.0181;DP=110;FR=R;LCR=
294 cp 92859 . A G . . AF=0.0165;DP=120;FR=R;LCR=
295 cp 93059 . A G . . AF=0.0133;DP=150;FR=R;LCR=
296 cp 93379 . C A . . AF=0.0176;DP=113;FR=R;LCR=
297 cp 93769 . G T . . AF=0.0181;DP=110;FR=R;LCR=
298 cp 94088 . G T . . AF=0.0174;DP=114;FR=R;LCR=SNR
299 cp 94187 . G A . . AF=0.0159;DP=126;FR=R;LCR=
300 cp 94368 . G T . . AF=0.0115;DP=260;FR=R;LCR=
301 cp 94439 . C A . . AF=0.0146;DP=273;FR=R;LCR=
302 cp 94608 . C A . . AF=0.0167;DP=119;FR=R;LCR=SNR
303 cp 95000 . C A . . AF=0.0129;DP=155;FR=R;LCR=
304 cp 95112 .
305 . . AF=;DP=126;FR=R;LCR=
306 cp 96101 . C A . . AF=0.016;DP=124;FR=R;LCR=
307 cp 96495 . G C,T . . AF=0.0177,;DP=112;FR=R;LCR=
308 cp 96569 . C A . . AF=0.0157;DP=127;FR=R;LCR=
309 cp 96609 . G T . . AF=0.0156;DP=128;FR=R;LCR=
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313 cp 97234 . G T . . AF=0.0179;DP=111;FR=R;LCR=
314 cp 97385 . G T . . AF=0.0138;DP=289;FR=R;LCR=
315 cp 97880 . G T . . AF=0.0182;DP=110;FR=R;LCR=
316 cp 98283 . G T . . AF=0.0141;DP=142;FR=R;LCR=
317 cp 98365 . G T . . AF=0.0158;DP=126;FR=R;LCR=
318 cp 98384 . G T,C . . AF=0.0165,;DP=121;FR=R;LCR=
319 cp 98881 . G T . . AF=0.0186;DP=107;FR=R;LCR=
320 cp 98912 . G T . . AF=0.0192;DP=104;FR=R;LCR=
321 cp 99236 . G T . . AF=0.0178;DP=112;FR=R;LCR=
322 cp 99380 . C A . . AF=0.015;DP=133;FR=R;LCR=
323 cp 99693 . G T . . AF=0.017;DP=117;FR=R;LCR=
324 cp 99698 . C A . . AF=0.0183;DP=109;FR=R;LCR=
325 cp 99927 . G T . . AF=0.0152;DP=131;FR=R;LCR=
326 cp 100269 . A G . . AF=0.0113;DP=266;FR=R;LCR=
327 cp 100705 . G T . . AF=0.017;DP=117;FR=R;LCR=
328 cp 100788 . C A . . AF=0.01;DP=298;FR=R;LCR=
329 cp 100859 . C A . . AF=0.0158;DP=126;FR=R;LCR=
330 cp 101082 . T A,C . . AF=0.987,;DP=152;FR=R;LCR=

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331	cp	101367	.	C	A	.	.	AF=0.0234;DP=128;FR=R;LCR=
332	cp	101491	.	C	A	.	.	AF=0.0185;DP=108;FR=R;LCR=
333	cp	101718	.	G	T	.	.	AF=0.0155;DP=128;FR=R;LCR=
334	cp	101778	.	C	A	.	.	AF=0.0152;DP=131;FR=R;LCR=
335	cp	102454	.	G	A	.	.	AF=0.0125;DP=240;FR=R;LCR=
336	cp	102710	.	G	T	.	.	AF=0.0129;DP=155;FR=R;LCR=
337	cp	103144	.	T	C	.	.	AF=0.0175;DP=114;FR=R;LCR=
338	cp	103270	.	C	A	.	.	AF=0.0156;DP=128;FR=R;LCR=
339	cp	103433	.	A	C	.	.	AF=0.0155;DP=128;FR=R;LCR=
340	cp	103505	.	C	A	.	.	AF=0.0308;DP=97;FR=R;LCR=SNR(T)
341	cp	103686	.	CATATTGTAGGGTC	.	.	.	AF=0.0487;DP=308;FR=R;LCR=
342	cp	103993	.	G	T	.	.	AF=0.0113;DP=176;FR=R;LCR=
343	cp	104347	.	T	G	.	.	AF=0.0465;DP=129;FR=R;LCR=
344	cp	104484	.	G	T	.	.	AF=0.0177;DP=112;FR=R;LCR=
345	cp	105072
346		G,T	AF=0.984;DP=124;FR=R;LCR=
347	cp	105391	.	A	G,C	.	.	AF=0.908;DP=141;FR=R;LCR=
348	cp	105437
349		AF=;DP=133;FR=R;LCR=
350	cp	105853
351		G,T	AF=0.982;DP=112;FR=R;LCR=
352	cp	105854	.	A	C,G	.	.	AF=0.0177;DP=112;FR=R;LCR=
353	cp	105889	.	C	A	.	.	AF=0.0326;DP=92;FR=R;LCR=
354	cp	105912	.	G	C	.	.	AF=0.0326;DP=313;FR=R;LCR=
355	cp	105928	.	A	C,G	.	.	AF=0.966;DP=303;FR=R;LCR=
356	cp	106064	.	G	T	.	.	AF=0.0207;DP=145;FR=R;LCR=
357	cp	106226	.	C	A	.	.	AF=0.0129;DP=154;FR=R;LCR=
358	cp	106253	.	G	A	.	.	AF=0.941;DP=136;FR=R;LCR=
359	cp	106619	.	G	T	.	.	AF=0.0135;DP=147;FR=R;LCR=
360	cp	106757	.	A	G	.	.	AF=0.0179;DP=111;FR=R;LCR=
361	cp	107497	.	C	A	.	.	AF=0.016;DP=125;FR=R;LCR=
362	cp	107550	.	G	C	.	.	AF=0.0166;DP=120;FR=R;LCR=
363	cp	107819	.	G	T	.	.	AF=0.0177;DP=112;FR=R;LCR=
364	cp	108374	.	C	A	.	.	AF=0.0144;DP=138;FR=R;LCR=
365	cp	108429	.	C	A	.	.	AF=0.0171;DP=116;FR=R;LCR=
366	cp	108809	.	G	T	.	.	AF=0.0129;DP=154;FR=R;LCR=
367	cp	109167	.	C	A	.	.	AF=0.0147;DP=136;FR=R;LCR=
368	cp	109188	.	C	A	.	.	AF=0.0173;DP=115;FR=R;LCR=
369	cp	109459	.	C	A	.	.	AF=0.017;DP=117;FR=R;LCR=
370	cp	109852	.	C	A	.	.	AF=0.0191;DP=104;FR=R;LCR=
371	cp	110067	.	C	A	.	.	AF=0.0158;DP=126;FR=R;LCR=
372	cp	110534	.	A	G,T	.	.	AF=0.985;DP=132;FR=R;LCR=
373	cp	111499	.	C	A	.	.	AF=0.0155;DP=128;FR=R;LCR=
374	cp	111733	.	G	T	.	.	AF=0.0165;DP=120;FR=R;LCR=
375	cp	111765	.	G	T	.	.	AF=0.018;DP=111;FR=R;LCR=
376	cp	112099	.	A	G,T	.	.	AF=0.983;DP=116;FR=R;LCR=
377	cp	112260	.	G	C,T	.	.	AF=0.984;DP=126;FR=R;LCR=
378	cp	112403	.	C	A	.	.	AF=0.016;DP=124;FR=R;LCR=
379	cp	112442	.	C	A	.	.	AF=0.0176;DP=113;FR=R;LCR=
380	cp	113139	.	C	A	.	.	AF=0.0157;DP=127;FR=R;LCR=
381	cp	113146	.	C	A	.	.	AF=0.0174;DP=114;FR=R;LCR=
382	cp	113157	.	T	G	.	.	AF=0.0257;DP=116;FR=R;LCR=
383	cp	113194	.	T	G	.	.	AF=0.0264;DP=113;FR=R;LCR=
384	cp	113195	.	C	A	.	.	AF=0.0264;DP=113;FR=R;LCR=
385	cp	113274	.	G	C,T	.	.	AF=0.0272;DP=110;FR=R;LCR=
386	cp	113281	.	CATTAAAG C	.	.	.	AF=0.0174;DP=230;FR=R;LCR=
387	cp	113323	.	C	G	.	.	AF=0.0296;DP=135;FR=R;LCR=
388	cp	113330	.	G	T	.	.	AF=0.0142;DP=140;FR=R;LCR=
389	cp	113780	.	C	A	.	.	AF=0.0151;DP=132;FR=R;LCR=
390	cp	114159	.	G	T	.	.	AF=0.0156;DP=128;FR=R;LCR=

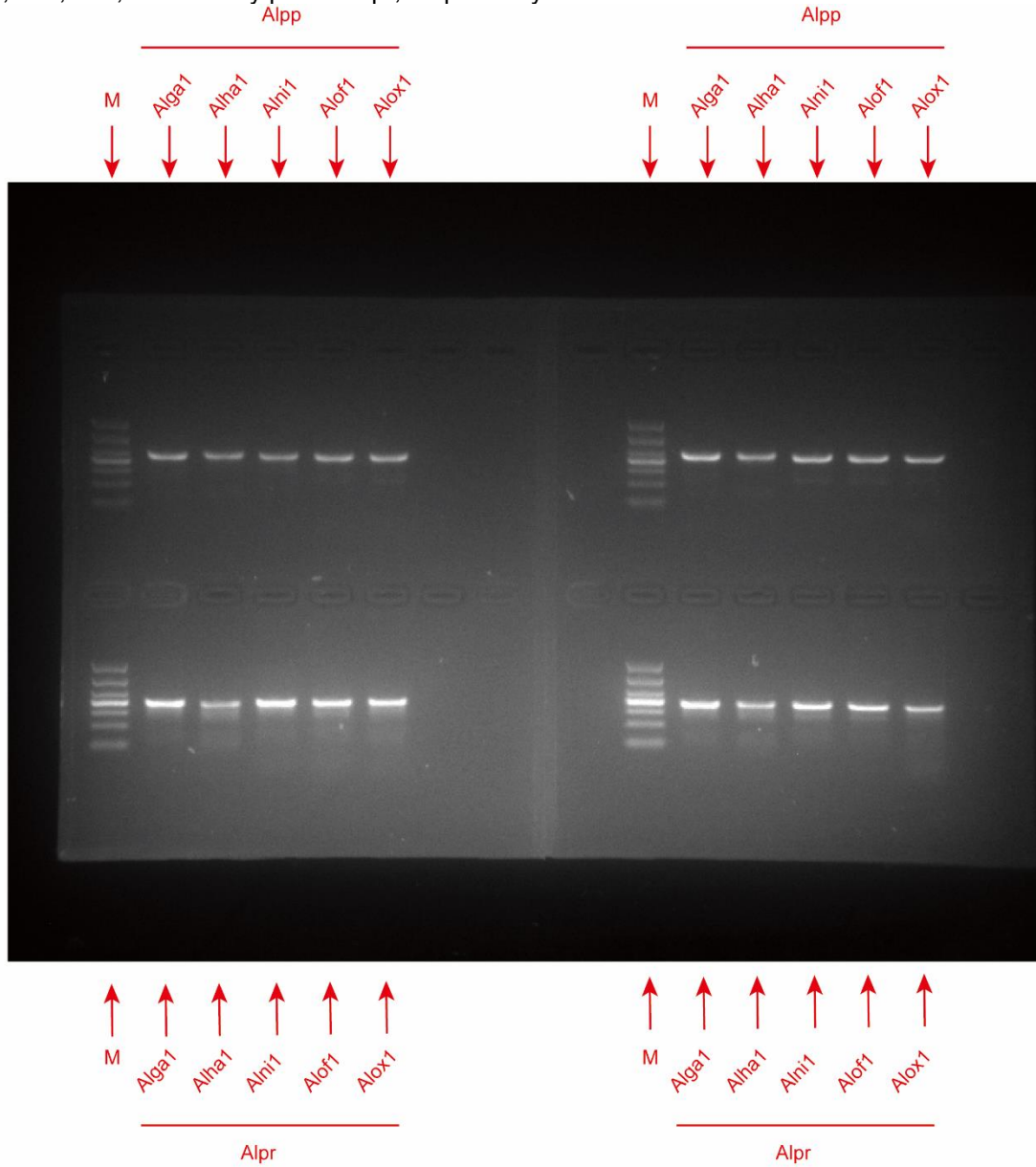
391	cp	114431	.	G	C	.	.	AF=0.964;DP=277;FR=R;LCR=
392	cp	114548	.	A	G	.	.	AF=0.97;DP=266;FR=R;LCR=SNR(T)
393	cp	114609	.	T	A	.	.	AF=0.978;DP=268;FR=R;LCR=
394	cp	114743	.	G	T	.	.	AF=0.0104;DP=288;FR=R;LCR=
395	cp	115064	.	T	C	.	.	AF=0.0561;DP=160;FR=R;LCR=
396	cp	115071	.	A	C	.	.	AF=0.0518;DP=154;FR=R;LCR=
397	cp	115341	.	T	C,A	.	.	AF=0.99;DP=193;FR=R;LCR=
398	cp	115358	.	A	.	.	.	AF=;DP=204;FR=R;LCR=
399	cp	115361	.	T	.	.	.	AF=;DP=204;FR=R;LCR=
400	cp	115379	.	A	G,T	.	.	AF=0.987;DP=157;FR=R;LCR=SNR(A)
401	cp	115814	.	C	A	.	.	AF=0.0267;DP=112;FR=R;LCR=
402	cp	115919	.	G	T	.	.	AF=0.017;DP=117;FR=R;LCR=
403	cp	115956	.	G	T	.	.	AF=0.0167;DP=119;FR=R;LCR=
404	cp	116186	.	G	T	.	.	AF=0.0162;DP=123;FR=R;LCR=
405	cp	116406	.	G	T	.	.	AF=0.0146;DP=136;FR=R;LCR=
406	cp	116975	.	C	A	.	.	AF=0.982;DP=111;FR=R;LCR=
407	cp	117009	.	A	G	.	.	AF=0.973;DP=111;FR=R;LCR=
408	cp	117047	.	C	T,G	.	.	AF=0.0171;DP=116;FR=R;LCR=
409	cp	132064	.	T	TTGATTG	.	.	AF=0.0101;DP=198;FR=R;LCR=
410	cp	132117	.	T	G	.	.	AF=0.971;DP=69;FR=R;LCR=SNR
411	cp	132323	.	G	T	.	.	AF=0.0262;DP=76;FR=R;LCR=SNR(T)
412	cp	132733	.	C	A	.	.	AF=0.018;DP=111;FR=R;LCR=
413	cp	132834	.	T	G,A	.	.	AF=0.988;DP=167;FR=R;LCR=
414	cp	132836	.	G	C	.	.	AF=0.0108;DP=184;FR=R;LCR=
415	cp	132894	.	AGA	A	.	.	AF=1;DP=195;FR=R;LCR=
416	cp	133034	.	T	TCTGTTTCATCA	.	.	AF=0.976;DP=168;FR=R;LCR=
417	cp	133069	.	A	G,T	.	.	AF=0.988;DP=258;FR=R;LCR=
418	cp	133077	.	G	T	.	.	AF=0.0123;DP=243;FR=R;LCR=
419	cp	133078	.	A	T	.	.	AF=0.0123;DP=243;FR=R;LCR=
420	cp	133678	.	G	T	.	.	AF=0.0118;DP=255;FR=R;LCR=
421	cp	133893	.	G	A	.	.	AF=0.0165;DP=120;FR=R;LCR=
422	cp	133938	.	A	G	.	.	AF=0.0192;DP=104;FR=R;LCR=
423	cp	134177	.	C	A	.	.	AF=0.0193;DP=155;FR=R;LCR=
424	cp	134440	.	T	C	.	.	AF=0.0152;DP=131;FR=R;LCR=
425	cp	134612	.	G	T	.	.	AF=0.0165;DP=120;FR=R;LCR=
426	cp	134726	.	A	T	.	.	AF=0.0101;DP=297;FR=R;LCR=SNR
427	cp	135016	.	C	A	.	.	AF=0.0186;DP=107;FR=R;LCR=SNR(T)
428	cp	137723	.	G	T	.	.	AF=0.0175;DP=114;FR=R;LCR=
429	cp	137835	.	C	G	.	.	AF=0.0112;DP=355;FR=R;LCR=
430	cp	137882	.	G	T	.	.	AF=0.0163;DP=122;FR=R;LCR=
431	cp	138049	.	C	A	.	.	AF=0.0144;DP=138;FR=R;LCR=
432	cp	138189	.	T	C	.	.	AF=0.016;DP=125;FR=R;LCR=
433	cp	138594	.	C	A	.	.	AF=0.0105;DP=286;FR=R;LCR=
434	cp	138801	.	G	T	.	.	AF=0.0134;DP=148;FR=R;LCR=
435	cp	139170	.	C	A	.	.	AF=0.0168;DP=118;FR=R;LCR=
436	cp	139329	.	G	T	.	.	AF=0.0191;DP=104;FR=R;LCR=
437	cp	139394	.	G	C	.	.	AF=0.0179;DP=111;FR=R;LCR=
438	cp	139966	.	C	A	.	.	AF=0.0196;DP=101;FR=R;LCR=
439	cp	140338	.	G	T	.	.	AF=0.016;DP=124;FR=R;LCR=
440	cp	140537	.	C	A	.	.	AF=0.0162;DP=123;FR=R;LCR=
441	cp	140612	.	C	A	.	.	AF=0.0155;DP=129;FR=R;LCR=
442	cp	141795	.	G	T	.	.	AF=0.0137;DP=146;FR=R;LCR=
443	cp	141797	.	G	T	.	.	AF=0.0134;DP=148;FR=R;LCR=
444	cp	141938	.	G	T	.	.	AF=0.0173;DP=115;FR=R;LCR=
445	cp	142220	.	G	T	.	.	AF=0.0159;DP=125;FR=R;LCR=
446	cp	142596	.	G	T	.	.	AF=0.0173;DP=115;FR=R;LCR=
447	cp	142656	.	C	A	.	.	AF=0.0159;DP=125;FR=R;LCR=
448	cp	142825	.	G	T	.	.	AF=0.0164;DP=121;FR=R;LCR=
449	cp	142896	.	C	A	.	.	AF=0.0179;DP=111;FR=R;LCR=
450	cp	142958	.	C	A	.	.	AF=0.017;DP=117;FR=R;LCR=

451	cp	143331	.	G	T	.	.	AF=0.0133;DP=150;FR=R;LCR=
452	cp	143399	.	C	A	.	.	AF=0.0179;DP=111;FR=R;LCR=
453	cp	143970	.	A	G,T	.	.	AF=0.977;DP=131;FR=R;LCR=
454	cp	144378	.	G	T,C	.	.	AF=0.0179;DP=111;FR=R;LCR=
455	cp	145210	.	A	G	.	.	AF=0.0171;DP=116;FR=R;LCR=
456	cp	145633	.	G	T	.	.	AF=0.0161;DP=124;FR=R;LCR=
457	cp	146971	.	C	T	.	.	AF=0.986;DP=142;FR=R;LCR=SNR
458	cp	146994	.	T	TNAA.	.	.	AF=0;DP=256;FR=R;LCR=
459	cp	146994	.	T	TNAA.	.	.	AF=0;DP=256;FR=R;LCR=
460	cp	147040	.	G	T	.	.	AF=0.0167;DP=119;FR=R;LCR=
461	cp	147080	.	AGATTATAAGAT	A	.	.	AF=0.984;DP=258;FR=R;LCR=
462	cp	147548	.	G	T,C	.	.	AF=0.017;DP=117;FR=R;LCR=
463	cp	147650	.	G	T	.	.	AF=0.016;DP=125;FR=R;LCR=
464	cp	147685	.	C	A	.	.	AF=0.0154;DP=129;FR=R;LCR=
465	cp	148071	.	G	T	.	.	AF=0.0152;DP=131;FR=R;LCR=
466	cp	148215	.	G	T	.	.	AF=0.983;DP=119;FR=R;LCR=
467	cp	148334	.	G	T	.	.	AF=0.013;DP=307;FR=R;LCR=
468	cp	148385	.	C	A	.	.	AF=0.0179;DP=111;FR=R;LCR=
469	cp	148535	.	C	A	.	.	AF=0.0168;DP=118;FR=R;LCR=
470	cp	148652	.	G	T	.	.	AF=0.0153;DP=130;FR=R;LCR=
471	cp	148936	.	C	A	.	.	AF=0.0174;DP=114;FR=R;LCR=
472	cp	148954	.	C	A	.	.	AF=0.017;DP=117;FR=R;LCR=
473	cp	149262	.	G	T	.	.	AF=0.0132;DP=151;FR=R;LCR=
474	cp	149298	.					
475		G,A	.					AF=0.976;DP=123;FR=R;LCR=
476	cp	149486	.	TTCAGAAT	T	.	.	AF=0.0121;DP=248;FR=R;LCR=
477	cp	149499	.	A	T	.	.	AF=0.0163;DP=123;FR=R;LCR=
478	cp	149893	.	T	G	.	.	AF=0.0186;DP=107;FR=R;LCR=
479	cp	150167	.	G	T	.	.	AF=0.0149;DP=134;FR=R;LCR=
480	cp	150347	.	G	T	.	.	AF=0.0207;DP=144;FR=R;LCR=
481	cp	150356	.	T	C	.	.	AF=0.0155;DP=128;FR=R;LCR=
482	cp	150415	.	T	C,A	.	.	AF=0.983;DP=114;FR=R;LCR=
483	cp	150946	.	C	A	.	.	AF=0.0149;DP=134;FR=R;LCR=
484	cp	151122	.	C	A	.	.	AF=0.0139;DP=144;FR=R;LCR=
485	cp	151182	.	C	A	.	.	AF=0.016;DP=124;FR=R;LCR=
486	cp	151517	.	C	A	.	.	AF=0.0181;DP=110;FR=R;LCR=
487	cp	152058	.	C	A	.	.	AF=0.0151;DP=330;FR=R;LCR=SNR
488	cp	152228	.	G	A	.	.	AF=0.0156;DP=128;FR=R;LCR=
489	cp	152233	.	C	T	.	.	AF=0.0163;DP=122;FR=R;LCR=
490	cp	152239	.	G	A,T	.	.	AF=0.0166;DP=120;FR=R;LCR=
491	cp	152370	.	G	A	.	.	AF=0.0181;DP=110;FR=R;LCR=
492	cp	152685	.	C	A	.	.	AF=0.0148;DP=135;FR=R;LCR=
493	cp	152798	.	A	G	.	.	AF=0.0134;DP=149;FR=R;LCR=
494	cp	152823	.	C	A	.	.	AF=0.015;DP=133;FR=R;LCR=
495	cp	153092	.	C	A	.	.	AF=0.0138;DP=145;FR=R;LCR=
496	cp	153149	.	G	T	.	.	AF=0.0129;DP=154;FR=R;LCR=
497	cp	153202	.	A	G,T	.	.	AF=0.987;DP=149;FR=R;LCR=
498	cp	153326	.	T	C	.	.	AF=0.0161;DP=123;FR=R;LCR=
499	cp	153737	.	C	A	.	.	AF=0.0131;DP=153;FR=R;LCR=
500	cp	154239	.	G	T	.	.	AF=0.0161;DP=124;FR=R;LCR=
501	cp	154388	.	G	T	.	.	AF=0.0139;DP=144;FR=R;LCR=
502	cp	154429	.	G	A	.	.	AF=0.0138;DP=145;FR=R;LCR=
503	cp	154989	.	G	T	.	.	AF=0.0165;DP=120;FR=R;LCR=
504	cp	155386	.	C	A	.	.	AF=0.0149;DP=134;FR=R;LCR=
505	cp	155387	.	G	T	.	.	AF=0.0151;DP=132;FR=R;LCR=
506	cp	155395	.	G	T	.	.	AF=0.0161;DP=123;FR=R;LCR=
507	cp	155736	.	C	A	.	.	AF=0.0179;DP=111;FR=R;LCR=
508	cp	155808	.	C	A	.	.	AF=0.0139;DP=143;FR=R;LCR=
509	cp	155858	.	G	A	.	.	AF=0.0132;DP=151;FR=R;LCR=
510	cp	155883	.	G	A	.	.	AF=0.013;DP=153;FR=R;LCR=

511	cp	156055	.	C	A,T	.	.	AF=0.0174,;DP=115;FR=R;LCR=
512	cp	156280	.	C	A	.	.	AF=0.0174;DP=114;FR=R;LCR=SNR
513	cp	156893	.	A	G,T	.	.	AF=0.983,;DP=118;FR=R;LCR=
514	cp	156952	.	C	A	.	.	AF=0.015;DP=133;FR=R;LCR=
515	cp	157141	.	G	T	.	.	AF=0.0177;DP=112;FR=R;LCR=
516	cp	157706	.	T	G,C	.	.	AF=0.974,;DP=116;FR=R;LCR=
517	cp	157904	.	T	C,A	.	.	AF=0.986,;DP=294;FR=R;LCR=SNR
518	cp	157943	.	A	T	.	.	AF=0.0168;DP=119;FR=R;LCR=
519	cp	157954	.	C	A	.	.	AF=0.0244;DP=122;FR=R;LCR=
520	cp	157981	.	G	T	.	.	AF=0.015;DP=133;FR=R;LCR=
521	cp	158455	.	A	G,T	.	.	AF=0.98,;DP=148;FR=R;LCR=
522	cp	158772	.	C	A	.	.	AF=0.0149;DP=133;FR=R;LCR=
523	cp	159533	.	G	T	.	.	AF=0.0137;DP=418;FR=F;LCR=
524	cp	159762	.	G	T	.	.	AF=0.0168;DP=119;FR=R;LCR=
525	cp	160254	.	C	T	.	.	AF=0.0155;DP=193;FR=F;LCR=
526	cp	160594	.	G	A	.	.	AF=0.0157;DP=254;FR=F;LCR=
527	cp	160684	.	C	A	.	.	AF=0.0188;DP=106;FR=R;LCR=
528	cp	160713	.	C	A	.	.	AF=0.0188;DP=106;FR=R;LCR=
529	cp	161320	.	G	T	.	.	AF=0.0109;DP=274;FR=F;LCR=
530	cp	161523	.	A	T	.	.	AF=0.0145;DP=207;FR=F;LCR=
531	cp	161561	.	C	A	.	.	AF=0.0104;DP=192;FR=F;LCR=
532	cp	161741	.	G	A	.	.	AF=0.0117;DP=256;FR=F;LCR=
533	cp	162276	.	CC	C	.	.	AF=0.0109;DP=274;FR=R;LCR=SNR
534	cp	162276	.	CC	C	.	.	AF=0.0109;DP=274;FR=R;LCR=SNR
535	cp	162278	.	C	.	.	.	AF=,;DP=3;FR=R;LCR=SNR
536	cp	162278	.	C	.	.	.	AF=,;DP=3;FR=R;LCR=SNR
537	cp	162307	.	T	C	.	.	AF=0.0107;DP=186;FR=F;LCR=SNR
538	cp	162361	.	G	T	.	.	AF=0.0112;DP=179;FR=F;LCR=
539	cp	162365	.	A	T,C	.	.	AF=0.99,;DP=199;FR=F;LCR=
540	cp	162387	.	G	T	.	.	AF=0.0132;DP=151;FR=F;LCR=SNR
541	cp	162426	.	T	A	.	.	AF=0.0208;DP=144;FR=F;LCR=SNR
542	cp	162481	.	A	G	.	.	AF=0.0103;DP=193;FR=F;LCR=

543 **Figure S12. The original and full-length gel electrophoresis results of the**
544 **amplification of DNA barcodes using designed primers.**

545 This is the original and uncropped gel electrophoresis plot for the cropped image shown in Figure 7.
546 Lane M was the marker of DL1000. The upper lanes from left to right corresponded to products
547 amplified from the individual 1 and individual 2 of *A. galanga* (Alga), *A. hainanensis* (Alha), *A. nigra*
548 (*Alni*), *A. officinarum* (Alof), and *A. oxyphylla* (Alox) by primer Alpp, respectively. The lower lanes
549 from left to right corresponded to products amplified from the individual 2 and individual 1 of Alga,
550 Alha, Alni, Alof, and Alox by primer Alpr, respectively.



551

552 **Figure S13. The alignment of amplicons produced by designed Alpp primers.**

553 The ID of each sequence is shown on the left side of each panel. The ID is the concatenation of
 554 species name, plant individual id, and primer name. The rightmost number in each column represents
 555 the position of the base at that position in the amplicon. The SNPs and Indel are shown in red
 556 squares. The nucleotides identical across all plastomes are shaded in black, whereas those
 557 conserved in 60% of the sequences are shaded in gray. *Alpinia galanga*: Alga; *A. hainanensis*: Alha;
 558 *A. nigra*: Alni; *A. officinarum*: Aloh; *A. oxyphylla*: Alox. Arabic numerals represent different individuals.

560	Alga1_Alpp	-----aaaagtca-acga--tcacacaggt-aaatgtag	: 29
561	Alga2_Alpp	-----t-caaaacat-cgaa--tcacacaggt-aaatgtag	: 31
562	Alga3_Alpp	-----gcaaagaacga-tcga--atcacacaggt-aaatgtag	: 32
563	Alga4_Alpp	-----a--cagactaatcgca--tcacacaggt-aaatgtag	: 32
564	Alga6_Alpp	-----gcgaca-atga--atcacacaggt-aaatgtag	: 27
565	Alga7_Alpp	-----a--cacaggga-acga--atcacacaggt-aaatgtag	: 31
566	Alga8_Alpp	-----gaaaaggcaaa--cga--atcacacaggt-aaatgtag	: 32
567	Alga0_Alpp	agaacagttggccttcgattatTTTggatcgatcg-aaat--acacacaggt-aaatgtag	: 57
568	Alha1_Alpp	a-----aaagcga-acga--tacacacaggt-aaatgtag	: 30
569	Alha2_Alpp	c-----aagacta-acga--atcacacaggt-aaatgtag	: 30
570	Alha3_Alpp	caaaacatgcat-----cga--tcacacaggt-aaatgtag	: 32
571	Alha6_Alpp	a-----cagaca-acga--taaacacaggt-aaatgtag	: 28
572	Alha7_Alpp	ccaaaaggccaa-----cgaa--tacacacaggt-aaatgtag	: 34
573	Alha8_Alpp	acaagcatcga-----tcacacaggt-aaatgtag	: 27
574	Alha0_Alpp	agaacagttggccttcgattatTTTggatcgatcg-aaat--acacacaggt-aaatgtag	: 57
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578	Alni4_Alpp	-----g--aaagacat-cgaa--tacacacaggt-aaatgtag	: 30
579	Alni6_Alpp	-----a--aaagacca-tcga--tcacacaggt-aaatgtag	: 30
580	Alni7_Alpp	-----g--cagaacca-acga--tcacacaggt-aaatgtag	: 31
581	Alni8_Alpp	-----ccaatgaaggc-atcg--atcacacaggt-aaatgtag	: 32
582	Alni0_Alpp	agaacagttggccttcgattatTTTggatcgatcg-aaat--acacacaggt-aaatgtag	: 57
583	Alof1_Alpp	-----cagaacaa-tcga--tcacacaggt-aaatgtag	: 30
584	Alof2_Alpp	-----aaaggca-acga--tacacacaggt-aaatgtag	: 28
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587	Alof6_Alpp	-----gaagacca-tcg--atcacacaggt-aaatgtag	: 28
588	Alof7_Alpp	-----acagacca-acgaatacacacaggt-aaatgtag	: 31
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592	Alox2_Alpp	g-----aaaggcaaa-cgaa--tcacacaggt-aaatgtag	: 32
593	Alox3_Alpp	-----gaagaacaa-tcga--tcacacaggt-aaatgtag	: 30
594	Alox6_Alpp	g-----aaggccca-acga--atcacacaggt-aaatgtag	: 31
595	Alox7_Alpp	-----aaagggcaa-tcga--tcacacaggt-aaatgtag	: 31
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612	Alha0_Alpp	ccaaaaaaaaagaattgggctgctatTTTgatgtaactatTTtagatataatctaatc atg	: 117
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833 Alga0_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgttagatgataagtaaaaaagcag : 450
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835 Alha2_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgttagatgataagtaaaaaagcag : 437
836 Alha3_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgttagatgataagtaaaaaagcag : 439
837 Alha6_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgttagatgataagtaaaaaagcag : 435

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838 Alha7_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 441
839 Alha8_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 434
840 Alha0_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 464
841 Alni1_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 421
842 Alni2_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 422
843 Alni3_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 422
844 Alni4_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 422
845 Alni6_Alpp : ttcaatcgaclgactgattttgactgactgatttttaaaatgataaggaaCaaagcag : 421
846 Alni7_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 422
847 Alni8_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 424
848 Alni0_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 449
849 Alof1_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 408
850 Alof2_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 406
851 Alof3_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 407
852 Alof4_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 407
853 Alof6_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 406
854 Alof7_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 409
855 Alof8_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 408
856 Alof0_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 435
857 Alox1_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 407
858 Alox2_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 410
859 Alox3_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 408
860 Alox6_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 409
861 Alox7_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 409
862 Alox0_Alpp : ttcaatcaaattagtcattttgactgactggtttttacgtagatgataagtaaaaaagcag : 435
863
864 Alga1_Alpp : ----- : -
865 Alga2_Alpp : taggaactagaatgaa-cagtgcagta-- : 450
866 Alga3_Alpp : taggaactagaatgaa-cagtgcagta-- : 451
867 Alga4_Alpp : taggaactagaatgaa-cagtgcagta-- : 452
868 Alga6_Alpp : ----- : -
869 Alga7_Alpp : ----- : -
870 Alga8_Alpp : taggaactagaatgaa-cagtgcagta-- : 451
871 Alga0_Alpp : taggaactagaatgaa-cagtgcagta-- : 475
872 Alha1_Alpp : taggaactagaatgaa-cagtgcagta-- : 463
873 Alha2_Alpp : taggaactagaatgaa-cagtgcagta-- : 463
874 Alha3_Alpp : taggaactagaatgaa-cagtgcagta-- : 465
875 Alha6_Alpp : taggaactagaatgaa-cagtgcagta-- : 460
876 Alha7_Alpp : taggaactagaatgaa-cagtgcagta-- : 467
877 Alha8_Alpp : taggaactagaatgaa-cagtgcagta-- : 460
878 Alha0_Alpp : taggaactagaatgaa-cagtgcagta-- : 489
879 Alni1_Alpp : taggaactagaatgaa-cagtgcagta-- : 447
880 Alni2_Alpp : taggaactagaatgaa-cagtgcagtaaa : 450
881 Alni3_Alpp : taggaactagaatgaa-cagtgcagta-- : 448
882 Alni4_Alpp : taggaactagaatgaa-cagtgcagta-- : 448
883 Alni6_Alpp : aacgaactagaatgaa-cagtgcagta-- : 447
884 Alni7_Alpp : taggaactagaatgaa-cagtgcagta-- : 448
885 Alni8_Alpp : taggaactagaatgaa-cagtgcagta-- : 450
886 Alni0_Alpp : taggaactagaatgaa-cagtgcagta-- : 474
887 Alof1_Alpp : taggaactagaatgaa-cagtgcagta-- : 434
888 Alof2_Alpp : taggaactagaatgaa-cagtgcagta-- : 431
889 Alof3_Alpp : taggaactagaatgaa-cagtgcagta-- : 433
890 Alof4_Alpp : taggaactagaatgaa-cagtgcagta-- : 432
891 Alof6_Alpp : taggaactagaatgaa-cagtgcagta-- : 432
892 Alof7_Alpp : taggaactagaatgaa-cagtgcagta-- : 435
893 Alof8_Alpp : taggaactagaatgaa-cagtgcagta-- : 435
894 Alof0_Alpp : taggaactagaatgaa-cagtgcagta-- : 460
895 Alox1_Alpp : taggaactagaatgaa-cagtgcagta-- : 433
896 Alox2_Alpp : taggaactagaatgaa-cagtgcagta-- : 436
897 Alox3_Alpp : taggaactagaatgaa-cagtgcagta-- : 433
898 Alox6_Alpp : taggaactagaatgaa-cagtgcagta-- : 435
899 Alox7_Alpp : taggaactagaatgaa-cagtgcagta-- : 435
900 Alox0_Alpp : taggaactagaatgaa-cagtgcagta-- : 460

901

902 **Figure S14. The alignment of amplicons produced by designed Alpr primers.**

903 The ID of each sequence is shown on the left side of each panel. The ID is the concatenation of
904 species name, plant individual id, and primer name. The rightmost number in each column represents
905 the position of the base at that position in the amplicon. The SNPs and Indel are shown in red
906 squares. The nucleotides identical across all plastomes are shaded in black, whereas those
907 conserved in 60% of the sequences are shaded in gray. *Alpinia galanga*: Alga; *A. hainanensis*: Alha;
908 *A. nigra*: Alni; *A. officinarum*: Alof; *A. oxyphylla*: Alox. Arabic numerals represent different individuals.

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910 Alga1_Alpr : ggggg-----tgagagagataactt-aa : 21
911 Alga2_Alpr : c-ggg-----atagagagataactt-a : 19
912 Alga3_Alpr : g-ggg-----gaagagagataactt-a : 19
913 Alga4_Alpr : t-gac-----gcaagagataactt-a : 19
914 Alga6_Alpr : cgggg-----cgagagagataactt-a : 20
915 Alga7_Alpr : aggaa-----taaggaggaagataactt-aa : 24
916 Alga8_Alpr : g-gga-----gagaagagataactt-a : 19
917 Alga0_Alpr : tagggagggttccgctaataatcatagcatagaaaagaagaagataactt-aa : 50
918 Alha1_Alpr : gggg-----tgagagagataactt-a : 17
919 Alha2_Alpr : gggg-----tcggagataactt-a : 17
920 Alha3_Alpr : gggg-----atgagagaaactt-a : 17
921 Alha6_Alpr : agg-----agagagtctt-a : 14
922 Alha7_Alpr : aggg-----atgagagtctt-a : 17
923 Alha8_Alpr : cgga-----ggagagtctt-a : 15
924 Alha0_Alpr : tagggagggttccgctaataatcatagcataga----aagaagataactt-aa : 45
925 Alni1_Alpr : gcggt-----gagaagagataactt-a : 20
926 Alni3_Alpr : -agga-----gagaagagataactt-a : 19
927 Alni3_Alpr : ggggc-----taggagagataactt-a : 20
928 Alni4_Alpr : --ggg-----cgagagagataactt-a : 18
929 Alni6_Alpr : --ggg-----ctagagagataactt-a : 18
930 Alni7_Alpr : tgggc-----gaagaagagataactt-aa : 22
931 Alni8_Alpr : cgggg-----ctgagagagataactt-a : 21
932 Alni0_Alpr : tagggagggttccgctaataatcatagcatagaaaagaagaagataactt-aa : 50
933 Alof1_Alpr : ggacg-----aagagaactt-a : 16
934 Alof2_Alpr : agatt-----aaagaggaactt-a : 18
935 Alof3_Alpr : aggat-----aagaggtctt-a : 16
936 Alof4_Alpr : gggac-----tgaggagaactt-aa : 19
937 Alof5_Alpr : ggggc-----taggagaactt-a : 17
938 Alof6_Alpr : aggac-----gaggagaactt-a : 17
939 Alof7_Alpr : cgggg-----tagagaactt-aa : 17
940 Alof8_Alpr : gtgga-----cgagagaactt-a : 17
941 Alof0_Alpr : tagggagggttccgctaataatcatagcataga----aagaagataactt-aa : 45
942 Alox1_Alpr : ggggc-----gagaagaactt-a : 17
943 Alox2_Alpr : ggggc-----gaggagaactt-a : 17
944 Alox6_Alpr : gtgga-----tagagatctt-a : 16
945 Alox7_Alpr : gggaa-----taaggaggaactt-a : 19
946 Alox0_Alpr : tagggagggttccgctaataatcatagcataga----aagaagataactt-aa : 45
947
948 Alga1_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 71
949 Alga2_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 69
950 Alga3_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 69
951 Alga4_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 69
952 Alga6_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 70
953 Alga7_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 74
954 Alga8_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 69
955 Alga0_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 100
956 Alha1_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 66
957 Alha2_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 66
958 Alha3_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 66
959 Alha6_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 63
960 Alha7_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 66
961 Alha8_Alpr : a-ttaataaaaataataaatttagtggatttaggataggaacaattgatag : 64
962 Alha0_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 95
963 Alni1_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 70
964 Alni3_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 69
965 Alni3_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 70
966 Alni4_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 68
967 Alni6_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 68
968 Alni7_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 72
969 Alni8_Alpr : attaaataaaaataataaatttagtggatttaggataggaacaattgatag : 71

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970 Alni0_Alpr : attaaataaaataataaatttagtggatttaggataggaacaattgatag : 100
971 Alof1_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 55
972 Alof2_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 57
973 Alof3_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 55
974 Alof4_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 58
975 Alof5_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 56
976 Alof6_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 56
977 Alof7_Alpr : attaaataaaa-----tagtggatttaggataggaacaattgatag : 57
978 Alof8_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 56
979 Alof0_Alpr : attaaataaaa-----tagtggatttaggataggaacaattgatag : 85
980 Alox1_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 56
981 Alox2_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 56
982 Alox6_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 55
983 Alox7_Alpr : a-ttaataaaa-----tagtggatttaggataggaacaattgatag : 58
984 Alox0_Alpr : attaaataaaa-----tagtggatttaggataggaacaattgatag : 85
985
986 Alga1_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 121
987 Alga2_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 119
988 Alga3_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 119
989 Alga4_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 119
990 Alga6_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 120
991 Alga7_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 124
992 Alga8_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 119
993 Alga0_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 150
994 Alha1_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 116
995 Alha2_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 116
996 Alha3_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 116
997 Alha6_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 113
998 Alha7_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 116
999 Alha8_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 114
1000 Alha0_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 145
1001 Alni1_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 120
1002 Alni3_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 119
1003 Alni3_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 120
1004 Alni4_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 118
1005 Alni6_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 118
1006 Alni7_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 122
1007 Alni8_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 121
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1009 Alof1_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 105
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1011 Alof3_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 105
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1013 Alof5_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 106
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1015 Alof7_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 107
1016 Alof8_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 106
1017 Alof0_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 135
1018 Alox1_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 106
1019 Alox2_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 106
1020 Alox6_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 105
1021 Alox7_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 108
1022 Alox0_Alpr : ttagaaggaatttgatttcttaattattacttcataaaattattat : 135
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1028 Alga6_Alpr : attactctatatctatat----- : 138
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1041 Alni3_Alpr : attactctatatctatat----- : 138

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1045 Alni8_Alpr : attactctatatctatat----- : 139
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1058 Alox6_Alpr : attactctatatctatat----- : 123
1059 Alox7_Alpr : attactctatatctatat----- : 126
1060 Alox0_Alpr : attactctatatctatat----- : 153
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1062 Alga1_Alpr : -----atctataaaatataaaaggtaaaatttttacttaa : 173
1063 Alga2_Alpr : -----atctataaaatataaaaggtaaaatttttacttaa : 171
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1081 Alni6_Alpr : -----atctataaaatataaaaggtaaaatttttacttaa : 170
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1083 Alni8_Alpr : -----atctataaaatataaaaggtaaaatttttacttaa : 173
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1097 Alox7_Alpr : -----atctataaaatataaaaggtaaaatttttacttaa : 160
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1100 Alga1_Alpr : tctta----attacattaat-----attaatt : 196
1101 Alga2_Alpr : tctta----attacattaat-----attaatt : 194
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1103 Alga4_Alpr : tctta----attacattaat-----attaatt : 194
1104 Alga6_Alpr : tctta----attacattaat-----attaatt : 195
1105 Alga7_Alpr : tctta----attacattaat-----attaatt : 199
1106 Alga8_Alpr : tctta----attacattaat-----attaatt : 194
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1108 Alha1_Alpr : tctta----attacattaa-----t : 184
1109 Alha2_Alpr : tctta----attacattaa-----t : 184
1110 Alha3_Alpr : tctta----attacattaa-----t : 184
1111 Alha6_Alpr : tctta----attacattaa-----t : 181
1112 Alha7_Alpr : tctta----attacattaa-----t : 184
1113 Alha8_Alpr : tctta----attacattaa-----t : 182

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1114 Alha0_Alpr : -tctta-----attacattaa-----t : 213
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1147 Alha2_Alpr : attaattattaattt---aat-----aaataagaatt---tcatg : 218
1148 Alha3_Alpr : attaattattaattt---aat-----aaataagaatt---tcatg : 218
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1150 Alha7_Alpr : attaattattaattt---aat-----aaataagaatt---tcatg : 218
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1289
1290 Alga1_Alpr : ga----- : 385
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1322 Alox1_Alpr : ga----- : 375
1323 Alox2_Alpr : ga----- : 375
1324 Alox6_Alpr : gatttagcgggaaccctccctaa----- : 394
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1328 Alga1_Alpr : ----- : -
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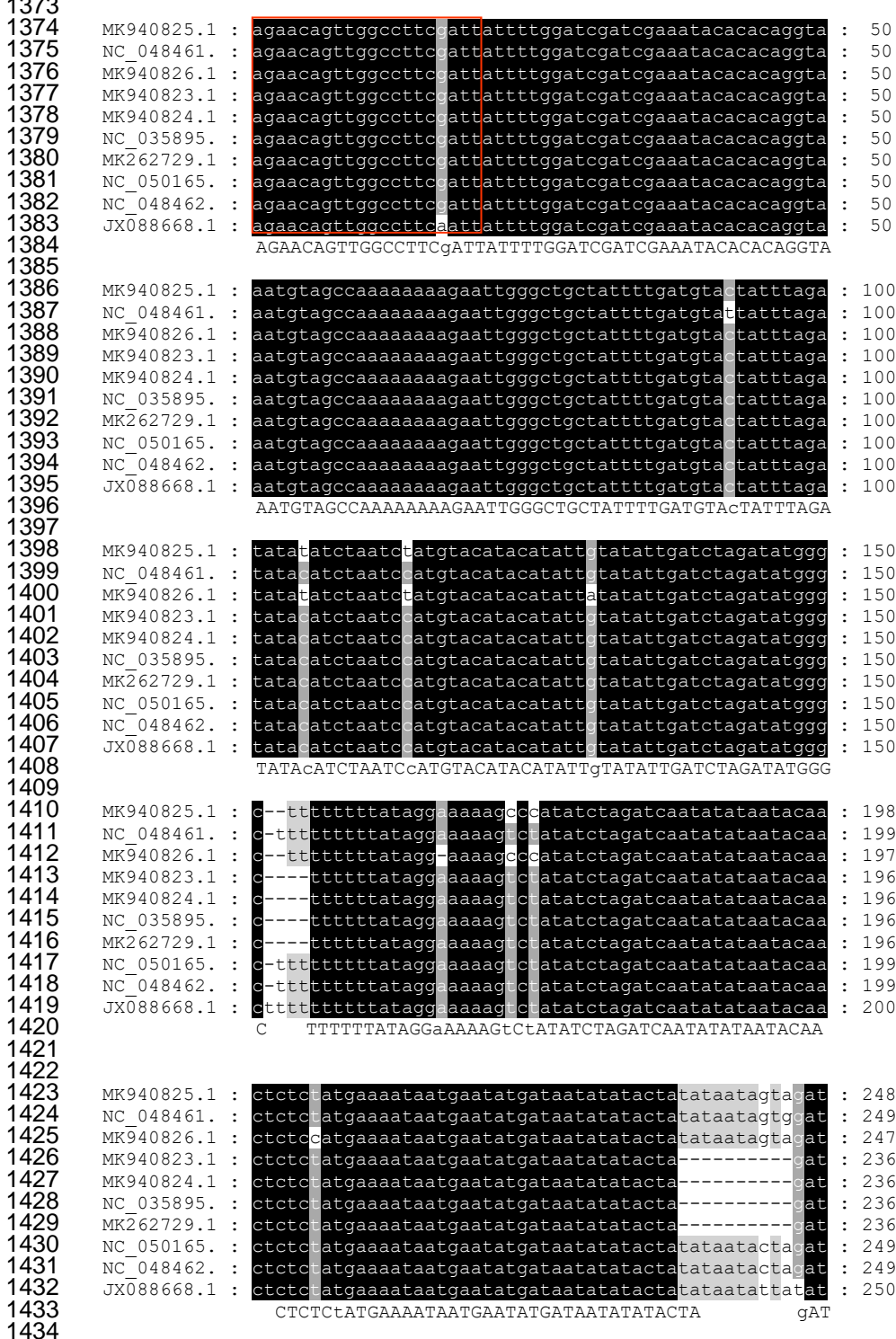
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1335 Alga0_Alpr : ----- : -
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1337 Alha2_Alpr : ----- : -
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1343 Alni1_Alpr : ----- : -
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1347 Alni6_Alpr : ----- : -
1348 Alni7_Alpr : ----- : -
1349 Alni8_Alpr : ----- : -
1350 Alni0_Alpr : ----- : -
1351 Aloh1_Alpr : ----- : -
1352 Aloh2_Alpr : ----- : -
1353 Aloh3_Alpr : ----- : -
1354 Aloh4_Alpr : ----- : -
1355 Aloh5_Alpr : ----- : -
1356 Aloh6_Alpr : ----- : -
1357 Aloh7_Alpr : ----- : -
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1361 Alox2_Alpr : ----- : -
1362 Alox6_Alpr : ----- : -
1363 Alox7_Alpr : ----- : -
1364 Alox0_Alpr : ----- : -
1365

```

1366 **Figure S15. The alignment of amplicons in 10 *Alpinia* plastomes produced by**
 1367 **designed Alpp primers in silico.**

1368 The ID of each sequence is shown on the left side of each panel. The ID is the accession numbers of
 1369 species in GenBank (Table S24). The rightmost number in each column represents the position of the
 1370 base at that position in the amplicon. The SNPs and Indel are shown in red squares. The nucleotides
 1371 identical across all plastomes are shaded in black, whereas those conserved in 60% of the
 1372 sequences are shaded in gray.

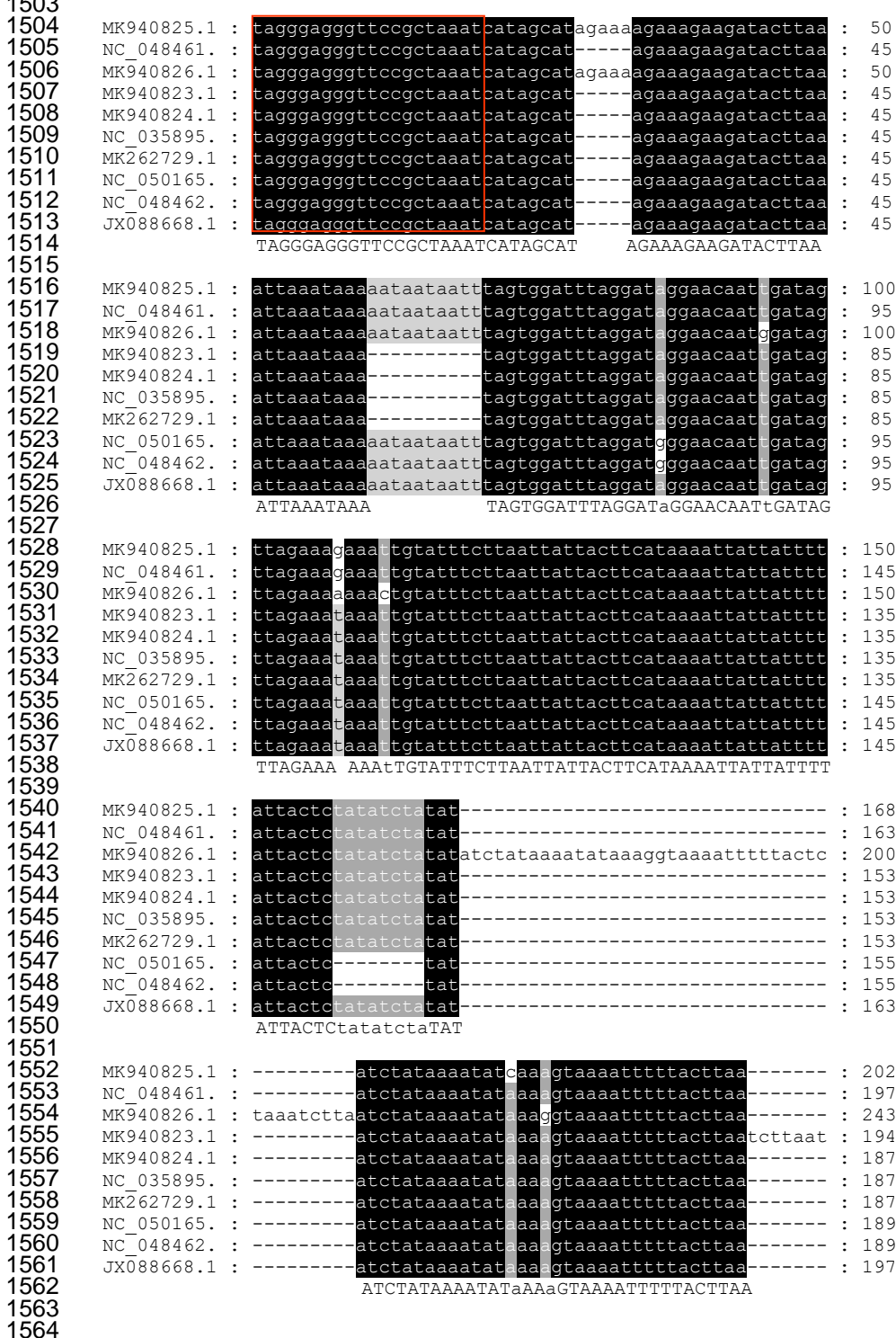


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1442 MK262729.1 : aactataccatactatcaggccttagatagtagtactatctcagatac----- : 281
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1446 AACTATACCATACTATCTAGGCTTAGATAGTACTATCTCAGATAC
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1448 MK940825.1 : atctcagataccttatgattccagccgatcatttctttcgtttaagactt : 348
1449 NC_048461.1 : atctcagataccttatgattccagccgatcatttctttcgtttaagactt : 349
1450 MK940826.1 : atctcagataccttatgattccagccgatcatttctttcgtttaagactt : 347
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1454 MK262729.1 : -----ttatgattccagccgatcatttctttcgtttaagactt : 320
1455 NC_050165.1 : -----ttatgattccagccgatcatttctttcgtttaagactt : 333
1456 NC_048462.1 : -----ttatgattccagccgatcatttctttcgtttaagactt : 333
1457 JX088668.1 : atctcagataccttatgattccagccgatcatttctttcgtttaagactt : 350
1458 TTATgATTCCAGCCaGATCATTTCTTTTCGTTTAAGACTT
1459
1460 MK940825.1 : aaagtttga-----cttcaatcattgataagaactaataatt : 385
1461 NC_048461.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 399
1462 MK940826.1 : gaagtttga-----cttcaatcattgataagaactaataatt : 384
1463 MK940823.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 370
1464 MK940824.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 370
1465 NC_035895.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 370
1466 MK262729.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 370
1467 NC_050165.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 383
1468 NC_048462.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 383
1469 JX088668.1 : gaagtttgaatccctttcctttcttcaatcattgataagaactaataatt : 400
1470 gAAGTTTgAatccctttcctttCTTCAATCATTTGATAAGAACTAATAATT
1471
1472 MK940825.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 435
1473 NC_048461.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 449
1474 MK940826.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 434
1475 MK940823.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 420
1476 MK940824.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 420
1477 NC_035895.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 420
1478 MK262729.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 420
1479 NC_050165.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 433
1480 NC_048462.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 433
1481 JX088668.1 : caagtttcaatcaaattagtcattttgactgactggtttttacgtagatga : 450
1482 CAAGTTTCAATCAAATTAGTCATTTTGACTGACTGTTTTTACGTAGATGA
1483
1484 MK940825.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 475
1485 NC_048461.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 489
1486 MK940826.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 474
1487 MK940823.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 460
1488 MK940824.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 460
1489 NC_035895.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 460
1490 MK262729.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 460
1491 NC_050165.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 473
1492 NC_048462.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 473
1493 JX088668.1 : taagtaaaaaagcagtaggaactagaatgaacagtgagcagt : 490
1494 TAAGTAAAAAAGCAGTAGGAAC TAGAATGAACAGTGACAGT

1495

1496 **Figure S16. The alignment of amplicons in 10 *Alpinia* plastomes produced by**
 1497 **designed Alpr primers in silico.**

1498 The ID of each sequence is shown on the left side of each panel. The ID is the accession numbers of
 1499 species in NCBI (Table S24). The rightmost number in each column represents the position of the
 1500 base at that position in the amplicon. The SNPs and Indel are shown in red squares. The nucleotides
 1501 identical across all plastomes are shaded in black, whereas those conserved in 60% of the
 1502 sequences are shaded in gray.



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1565 MK940825.1 : -tcttaattacattaattttattatcttaattacattaa--ttaattatt : 249
1566 NC_048461.1 : -tctta-----attacattaa-----tatt : 216
1567 MK940826.1 : -tcttaattac-----attacattaaatattaattatt : 274
1568 MK940823.1 : tcttaattac-----attacattaa-----tatt : 219
1569 MK940824.1 : -tcttaattac-----attacattaaatattaattatt : 218
1570 NC_035895.1 : -tcttaattac-----attacattaaatattaattatt : 218
1571 MK262729.1 : -tcttaattac-----attacattaaatattaattatt : 218
1572 NC_050165.1 : -tcttaattac-----attacattaa-----tatt : 213
1573 NC_048462.1 : -tcttaattac-----attacattaa-----tatt : 213
1574 JX088668.1 : -tctta-----attacattaa-----tatt : 216
1575          TCTTAattac          ATTACATTAA          TATT
1576
1577
1578 MK940825.1 : aattagaatttaataaa--aaataagaatttaatgataatgataattg : 297
1579 NC_048461.1 : aattagaatttaataaa--aaataagaatt-----tcatgataattg : 254
1580 MK940826.1 : aattagaatttaataaa--aaataagaatt-----taatgataattg : 312
1581 MK940823.1 : aattaataatttaataaataaaataagaatt-----tcatgataattg : 263
1582 MK940824.1 : aattaataatttaataaataaaataagaatt-----tcatgataattg : 262
1583 NC_035895.1 : aattaataatttaataaataaaataagaatt-----tcatgataattg : 262
1584 MK262729.1 : aattaataatttaataaataaaataagaatt-----tcatgataattg : 262
1585 NC_050165.1 : aattaataatttaataaaataagaatt-----tcatgataattg : 251
1586 NC_048462.1 : aattaataatttaataaaataagaatt-----tcatgataattg : 251
1587 JX088668.1 : aattaataatttaataaaataagaatt-----tcatgataattg : 254
1588          AATTAaTAAATTAAT          AAATAAGAATT          TcATGATAATTG
1589
1590
1591 MK940825.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbaat : 347
1592 NC_048461.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 304
1593 MK940826.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbaat : 362
1594 MK940823.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 313
1595 MK940824.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 312
1596 NC_035895.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 312
1597 MK262729.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 312
1598 NC_050165.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 301
1599 NC_048462.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 301
1600 JX088668.1 : caacgaatttttagaaaatttatttctagttagtcacttttatttbat : 304
1601          CAACGAATTTTAgAAAATTCATTTCTAGTTAGTCACITTTTATTTcAT
1602
1603
1604 MK940825.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 397
1605 NC_048461.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 354
1606 MK940826.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 412
1607 MK940823.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 363
1608 MK940824.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 362
1609 NC_035895.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 362
1610 MK262729.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 362
1611 NC_050165.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 351
1612 NC_048462.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 351
1613 JX088668.1 : ttatttttgtttcttcttctttagctcagatcgaaaatataagagttaa : 354
1614          TTATTTTGTGTTTCTTCTTCTTcAGCTCAGATCGAAAATATAAGAGTTAA
1615
1616
1617 MK940825.1 : gccgatacaaaaat--gaaagggggtttatggctaagggttaag : 438
1618 NC_048461.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 395
1619 MK940826.1 : gccgatacaaaaataaaagggggtttatggctaagggttaag : 455
1620 MK940823.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 404
1621 MK940824.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 403
1622 NC_035895.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 403
1623 MK262729.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 403
1624 NC_050165.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 392
1625 NC_048462.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 392
1626 JX088668.1 : gccgatacaaaaat--taaagggggtttatggctaagggttaag : 395
1627          GCCGATACAAAAT t AAAGGGGGTTTATGGCTAAGGGTAAG

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