Table S3. Distribution of nucleotide SSR sequences in the chloroplast genome of *Campsis grandiflora*. aintergenic spacers, bnon-coding region, ccoding sequences. p1: base number in repeat unit is 1. p2: base number in repeat unit is 2. c: complex repeat unit

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| **SSR nr.** | **SSR type** | **SSR sequence** | **Size** | **Start** | **End** | **Location** |
| 1 | p1\* | (A)11 | 11 | 4417 | 4427 | IGSa (*trn*K-UUU-*rps*16) |
| 2 | c\* | (G)12......(T)11 | 90 | 4729 | 4818 | IGS (*trn*K-UUU-*rps*16) |
| 3 | c | (T)10......(A)10 | 33 | 5227 | 5259 | NCRb (*rps*16) |
| 4 | p1 | (T)10 | 10 | 6514 | 6523 | IGS (*rps*16-*trn*Q-UUG) |
| 5 | p2\* | (AT)6 | 12 | 7300 | 7311 | IGS (*trn*Q-UUG-*psb*K) |
| 6 | p1 | (T)11 | 11 | 8096 | 8106 | IGS (*psb*K- *psb*I) |
| 7 | p1 | (T)12 | 12 | 8699 | 8710 | IGS (*trn*S-GCU-*trn*S-CGA) |
| 8 | p1 | (A)10 | 10 | 9088 | 9097 | NCR (*trn*S-CGA) |
| 9 | p1 | (A)12 | 12 | 9288 | 9299 | NCR (*trn*S-CGA) |
| 10 | p1 | (T)13 | 13 | 12360 | 12372 | NCR (*atp*F) |
| 11 | p1 | (T)10 | 10 | 13055 | 13064 | IGS (*atp*F-*atp*H) |
| 12 | p1 | (T)13 | 13 | 16316 | 16328 | IGS (*rps*2-*rpo*C2) |
| 13 | p1 | (T)11 | 11 | 18523 | 18533 | CDSc (*rpo*C2) |
| 14 | p1 | (A)13 | 13 | 30556 | 30568 | IGS (*psb*M-*trn*D-GUC) |
| 15 | p1 | (T)15 | 15 | 35278 | 35292 | IGS (*psb*C-*trn*S-UGA) |
| 16 | p1 | (A)10 | 10 | 35665 | 35674 | IGS (*trn*S-UGA-*psb*Z) |
| 17 | c | (C)11(A)12......(A)10 | 126 | 36063 | 36188 | IGS (*psb*Z- *trn*G-GCC) |
| 18 | p1 | (A)10 | 10 | 42253 | 42262 | IGS (*psa*A-*ycf*3) |
| 19 | p1 | (T)12 | 12 | 43351 | 43362 | NCR (*ycf*3) |
| 20 | p1 | (A)15 | 15 | 45133 | 45147 | IGS (*ycf*3-*trn*S-GGA) |
| 21 | p1 | (T)13 | 13 | 46348 | 46360 | IGS (*rps*4-*trn*T-UGU) |
| 22 | p2 | (TA)7 | 14 | 46521 | 46534 | IGS (*rps*4-*trn*T-UGU) |
| 23 | p1 | (T)12 | 12 | 46997 | 47008 | IGS (*trn*T-UGU-*trn*L-UAA) |
| 24 | p1 | (A)14 | 14 | 47200 | 47213 | IGS (*trn*T-UGU-*trn*L-UAA) |
| 25 | p1 | (T)10 | 10 | 47394 | 47403 | IGS (*trn*T-UGU-*trn*L-UAA) |
| 26 | p1 | (A)11 | 11 | 47672 | 47682 | NCR (*trn*L-UAA) |
| 27 | p1 | (A)13 | 13 | 50719 | 50731 | IGS (*rps*12-*rpl*20) |
| 28 | p1 | (T)10 | 10 | 51740 | 51749 | IGS (*rpl*20-*rps*18) |
| 29 | p1 | (A)11 | 11 | 54064 | 54074 | IGS (*pet*G-*pet*L) |
| 30 | p1 | (A)11 | 11 | 56505 | 56515 | IGS (*psb*J-*pet*A) |
| 31 | p1 | (A)11 | 11 | 59480 | 59490 | IGS(*cem*A-*ycf*4) |
| 32 | p1 | (A)13 | 13 | 59698 | 59710 | IGS(*cem*A-*ycf*4) |
| 33 | p1 | (A)10 | 10 | 66643 | 66652 | CDS(*atp*B) |
| 34 | c | (A)11……(A)10 | 72 | 70320 | 70391 | IGS(*trn*V-UAC-*ndh*C) |
| 35 | p1 | (A)12 | 12 | 72924 | 72935 | IGS(*ndh*J-*psb*B) |
| 36 | c | (C)10t……(A)13 | 24 | 75071 | 75094 | IGS(*psb*B-*psb*T) |
| 37 | p1 | (A)12 | 12 | 76115 | 76126 | IGS(*psb*H*-pet*B) |
| 38 | p1 | (T)14 | 14 | 79098 | 79111 | CDS(*rpo*A) |
| 39 | p1 | (T)11 | 11 | 81011 | 81021 | IGS(*inf*A-*rps*8) |
| 40 | p1 | (T)13 | 13 | 81524 | 81536 | IGS(*rps*8-*rpl*14) |
| 41 | c | (T)16……(A)13 | 91 | 82696 | 82786 | NCR(*rpl*16) |
| 42 | p1 | (T)10 | 10 | 85084 | 85093 | IGS(*rps*19-*rpl*2) |
| 43 | p1 | (A)10 | 10 | 112523 | 112532 | CDS(*ndh*F) |
| 44 | p1 | (A)12 | 12 | 113079 | 113090 | IGS(*ndh*F- *trn*L-UAG) |
| 45 | c | (T)12……(A)10 | 69 | 118216 | 118284 | CDS(*ndh*E) |
| 46 | p1 | (T)10 | 10 | 118434 | 118443 | IGS(*ndh*E-*ndh*G) |
| 47 | p1 | (T)14 | 14 | 121791 | 121804 | CDS(*ndh*A) |
| 48 | p1 | (T)10 | 10 | 125467 | 125476 | CDS(*ycf*1) |
| 49 | p1 | (A)13 | 13 | 125891 | 125903 | CDS(*ycf*1) |
| 50 | p1 | (A)10 | 10 | 128627 | 128636 | CDS(*ycf*1) |
| 51 | p1 | (A)10 | 10 | 154255 | 154264 | IGS(*rpl*2-*trn*H-GUG) |