

Table S3. Repeated sequences of the *F. longipetiolata* chloroplast genome.

| ID | Length I | Repeat I Start | Type | Length II | Repeat II Start | Hamming distance | E-value  | Gene              | Region  |
|----|----------|----------------|------|-----------|-----------------|------------------|----------|-------------------|---------|
| 1  | 46       | 33060          | P    | 46        | 33060           | 0                | 1.42E-18 | IGS               | LSC;LSC |
| 2  | 44       | 77633          | P    | 44        | 77633           | -2               | 1.94E-13 | IGS               | LSC;LSC |
| 3  | 43       | 49726          | F    | 43        | 49769           | 0                | 9.11E-17 | IGS               | LSC;LSC |
| 4  | 42       | 46568          | F    | 42        | 101950          | -3               | 1.13E-10 | ycf3;IGS          | LSC;IRb |
| 5  | 42       | 46568          | P    | 42        | 144031          | -3               | 1.13E-10 | ycf3;IGS          | LSC;IRa |
| 6  | 40       | 101948         | F    | 40        | 124264          | -1               | 7.00E-13 | IGS;ndhA          | IRb;SSC |
| 7  | 40       | 124264         | P    | 40        | 144035          | -1               | 7.00E-13 | ndhA;IGS          | SSC;IRa |
| 8  | 38       | 13406          | P    | 38        | 13406           | 0                | 9.33E-14 | IGS               | LSC;LSC |
| 9  | 38       | 46568          | F    | 38        | 124266          | -1               | 1.06E-11 | ycf3;ndhA         | LSC;SSC |
| 10 | 36       | 7917           | P    | 36        | 48217           | -3               | 2.88E-07 | trnS-GCU;trnS-GGA | LSC;LSC |
| 11 | 35       | 78991          | P    | 35        | 124267          | -3               | 1.06E-06 | petB;ndhA         | LSC;SSC |
| 12 | 34       | 13377          | P    | 34        | 13377           | -2               | 1.21E-07 | IGS               | LSC;LSC |
| 13 | 34       | 131681         | P    | 34        | 131681          | -2               | 1.21E-07 | ycf1;ycf1         | SSC;SSC |
| 14 | 33       | 41548          | F    | 33        | 43772           | -3               | 1.41E-05 | psaB;psaA         | LSC;LSC |
| 15 | 33       | 84962          | F    | 33        | 124255          | -3               | 1.41E-05 | rpl16;ndhA        | LSC;SSC |
| 16 | 33       | 73951          | R    | 33        | 73955           | -3               | 1.41E-05 | clpP;clpP         | LSC;LSC |
| 17 | 32       | 92485          | F    | 32        | 92506           | -3               | 5.12E-05 | ycf2;ycf2         | IRb;IRb |
| 18 | 32       | 92485          | P    | 32        | 153485          | -3               | 5.12E-05 | ycf2;ycf2         | IRb;IRa |
| 19 | 32       | 92506          | P    | 32        | 153506          | -3               | 5.12E-05 | ycf2;ycf2         | IRb;IRa |
| 20 | 32       | 153485         | F    | 32        | 153506          | -3               | 5.12E-05 | ycf2;ycf2         | IRa;IRa |
| 21 | 32       | 51860          | C    | 32        | 68575           | -3               | 5.12E-05 | IGS               | LSC;LSC |
| 22 | 31       | 7912           | F    | 31        | 38127           | -3               | 1.86E-04 | trnS-GCU;trnS-UGA | LSC;LSC |
| 23 | 31       | 68387          | P    | 31        | 68387           | -3               | 1.86E-04 | IGS               | LSC;LSC |
| 24 | 31       | 84971          | F    | 31        | 124264          | -3               | 1.86E-04 | rpl16;ndhA        | LSC;SSC |
| 25 | 30       | 110882         | F    | 30        | 110913          | -1               | 5.51E-07 | IGS               | IRb;IRb |
| 26 | 30       | 110882         | P    | 30        | 135080          | -1               | 5.51E-07 | IGS               | IRb;IRa |
| 27 | 30       | 110913         | P    | 30        | 135111          | -1               | 5.51E-07 | IGS               | IRb;IRa |
| 28 | 30       | 135080         | F    | 30        | 135111          | -1               | 5.51E-07 | IGS               | IRa;IRa |
| 29 | 30       | 46580          | F    | 30        | 101962          | -2               | 2.39E-05 | ycf3;IGS          | LSC;IRb |
| 30 | 30       | 46580          | P    | 30        | 144031          | -2               | 2.39E-05 | ycf3;IGS          | LSC;IRa |
| 31 | 30       | 38131          | P    | 30        | 48224           | -3               | 6.71E-04 | trnS-UGA;trnS-GGA | LSC;LSC |
| 32 | 30       | 73955          | P    | 30        | 102162          | -3               | 6.71E-04 | clpP;IGS          | LSC;IRb |
| 33 | 30       | 73955          | F    | 30        | 143831          | -3               | 6.71E-04 | clpP;IGS          | LSC;IRa |
| 34 | 30       | 73953          | R    | 30        | 73958           | -2               | 2.39E-05 | clpP;clpP         | LSC;LSC |
| 35 | 30       | 49911          | R    | 30        | 49917           | -3               | 6.71E-04 | IGS               | LSC;LSC |
| 36 | 30       | 49911          | R    | 30        | 49913           | -3               | 6.71E-04 | IGS               | LSC;LSC |
| 37 | 30       | 74592          | R    | 30        | 74595           | -3               | 6.71E-04 | clpP;clpP         | LSC;LSC |

Note: Type represents the type of repeat sequence, F stands for forward repetition, P for palindromic repetition, R for reverse repetition, and C for complement repetition; IGS represents the intergenic space.