

**Table S3.** Characteristics and distribution of 90 simple sequence repeats (SSRs) in the chloroplast genome of *Dracocephalum heterophyllum* (Lamiaceae).

| SSR type | SSR   | Size | Start (bp) | End (bp) | Location        |
|----------|---|------|------------|----------|-----------------|
| c        | (T)10c(A)10   | 21   | 7,739      | 7,759    | IGS             |
| c        | (A)14tatttaaataaattt(TAAA)3   | 41   | 7,973      | 8,013    | IGS             |
| c        | (TAT)3atataaat(ATA)3gaagatat(AAG)3  | 43   | 45,414     | 45,456   | IGS             |
| c        | (T)10attttcatagtaaataaaaaaagtgtga<br>attatttcacgttg(A)11  | 65   | 46,742     | 46,806   | intron          |
| c        | (T)11caatcgcccttttatccttcatttgtgt<br>tctttattacttaataatccaataacaataatgg<br>gttttct(TAA)3                              | 90   | 59,580     | 59,669   | IGS             |
| c        | (TGC)3agtttgagctgttctcttctegtcgcc<br>ttgaatccacaagtaccggccgaggaccaggcga<br>cttcgtacatctgtaactgtgacaatggtat(TTA)3      | 111  | 77,603     | 77,713   | <i>rps11</i>    |
| c        | (T)10gtaaaaacaagaaagaaattctatttc<br>tcgcctatttactacggcgacgaacaatcaaat<br>atcactatatttattccttttcta(CTT)3               | 107  | 82,526     | 82,632   | <i>IGS-rpl2</i> |
| c        | (TCT)3gtccgaagaaatgattcatcgaaataat<br>gagtcaccgttgatatacgacacatccgagatcgc<br>caaatgttcgggagttcctctattcaatcctttc(CTT)3 | 115  | 88,583     | 88,697   | <i>ycf2</i>     |
| c        | (AAG)3gaaaaggattgaatagaggaaactccga<br>acatttggcgatctcgatgtgtcgatatcaacg<br>gtgactcattatttcgatgaatcatttcttcggac(AGA)3  | 115  | 144,594    | 144,708  | <i>ycf2</i>     |
| c        | (GAA)3gtagaaaaaggaataaatatagtataa<br>tttgattgttcgctcgccgtagtaaataggcgaga<br>aaatagaatttcttcttctgtttttac(A)10          | 108  | 150,658    | 150,765  | <i>rp12-IGS</i> |
| p1       | (A)12   | 12   | 5,005      | 5,016    | intron          |
| p1       | (A)12   | 12   | 6,197      | 6,208    | IGS             |
| p1       | (T)10   | 10   | 8,580      | 8,589    | IGS             |
| p1       | (T)10   | 10   | 9,720      | 9,729    | IGS             |
| p1       | (T)10   | 10   | 14,014     | 14,023   | IGS             |
| p1       | (T)10   | 10   | 15,854     | 15,863   | IGS             |
| p1       | (T)11   | 11   | 18,075     | 18,085   | <i>rpoC2</i>    |
| p1       | (T)10   | 10   | 20,728     | 20,737   | <i>rpoC1</i>    |
| p1       | (A)10   | 10   | 27,212     | 27,221   | IGS             |
| p1       | (T)11   | 11   | 30,390     | 30,400   | IGS             |
| p1       | (T)12   | 12   | 34,244     | 34,255   | IGS             |
| p1       | (A)11   | 11   | 35,104     | 35,114   | IGS             |
| p1       | (T)10   | 10   | 42,286     | 42,295   | intron          |
| p1       | (T)10   | 10   | 53,436     | 53,445   | <i>atpB</i>     |
| p1       | (A)11   | 11   | 61,441     | 61,451   | <i>petA</i>     |
| p1       | (T)10   | 10   | 62,450     | 62,459   | IGS             |
| p1       | (A)11   | 11   | 64,860     | 64,870   | IGS             |

**Table S3.** (Continued)

| SSR type | SSR    | Size | Start (bp) | End (bp) | Location     |
|----------|--------|------|------------|----------|--------------|
| p1       | (T)10  | 10   | 65,226     | 65,235   | IGS          |
| p1       | (A)13  | 13   | 66,967     | 66,979   | IGS          |
| p1       | (A)18  | 18   | 69,290     | 69,307   | intron       |
| p1       | (A)12  | 12   | 72,584     | 72,595   | IGS          |
| p1       | (T)10  | 10   | 74,040     | 74,049   | intron       |
| p1       | (T)10  | 10   | 78,432     | 78,441   | IGS          |
| p1       | (A)10  | 10   | 92,424     | 92,433   | IGS          |
| p1       | (T)11  | 11   | 92,694     | 92,704   | IGS          |
| p1       | (A)11  | 11   | 117,233    | 117,243  | <i>ndhA</i>  |
| p1       | (A)10  | 10   | 122,689    | 122,698  | <i>ycf1</i>  |
| p1       | (A)11  | 11   | 140,587    | 140,597  | IGS          |
| p1       | (T)10  | 10   | 140,858    | 140,867  | IGS          |
| p2       | (AT)5  | 10   | 6,971      | 6,980    | IGS          |
| p2       | (AT)5  | 10   | 19,448     | 19,457   | <i>rpoC2</i> |
| p2       | (AT)5  | 10   | 41,036     | 41,045   | IGS          |
| p3       | (AAC)3 | 9    | 14,301     | 14,309   | <i>atPI</i>  |
| p3       | (TTA)3 | 9    | 15,123     | 15,131   | IGS          |
| p3       | (ATG)3 | 9    | 19,951     | 19,959   | <i>rpoC2</i> |
| p3       | (TTC)3 | 9    | 21,706     | 21,714   | <i>rpoC2</i> |
| p3       | (TTA)4 | 12   | 26,765     | 26,776   | IGS          |
| p3       | (TCT)3 | 9    | 36,019     | 36,027   | <i>rps14</i> |
| p3       | (ATG)3 | 9    | 37,551     | 37,559   | <i>psaB</i>  |
| p3       | (GCA)3 | 9    | 39,449     | 39,457   | <i>psaA</i>  |
| p3       | (ATG)3 | 9    | 39,775     | 39,783   | <i>psaA</i>  |
| p3       | (AAT)3 | 9    | 41,379     | 41,387   | IGS          |
| p3       | (GTA)3 | 9    | 43,613     | 43,621   | IGS          |
| p3       | (ATA)3 | 9    | 44,835     | 44,843   | <i>rps4</i>  |
| p3       | (ATT)3 | 9    | 51,242     | 51,250   | IGS          |
| p3       | (TTG)3 | 9    | 54,214     | 54,222   | IGS          |
| p3       | (GGA)3 | 9    | 57,254     | 57,262   | <i>accD</i>  |
| p3       | (TAT)3 | 9    | 57,644     | 57,652   | <i>accD</i>  |
| p3       | (TAA)3 | 9    | 58,216     | 58,224   | IGS          |
| p3       | (AAT)3 | 9    | 64,281     | 64,289   | IGS          |
| p3       | (AAC)3 | 9    | 66,727     | 66,735   | <i>rps18</i> |
| p3       | (TTA)3 | 9    | 68,469     | 68,477   | intron       |
| p3       | (TTG)3 | 9    | 71,681     | 71,689   | <i>psbB</i>  |
| p3       | (ATC)3 | 9    | 73,711     | 73,719   | intron       |
| p3       | (TGC)3 | 9    | 81,978     | 81,986   | <i>rpl22</i> |
| p3       | (TGA)3 | 9    | 89,180     | 89,188   | <i>ycf2</i>  |
| p3       | (GAA)3 | 9    | 90,428     | 90,436   | <i>ycf2</i>  |

**Table S3.** (Continued)

| SSR type | SSR      | Size | Start (bp) | End (bp) | Location      |
|----------|----------|------|------------|----------|---------------|
| p3       | (AGA)3   | 9    | 93,396     | 93,404   | <i>ndhB</i>   |
| p3       | (AGA)3   | 9    | 94,832     | 94,840   | <i>ndhB</i>   |
| p3       | (CTG)3   | 9    | 102,523    | 102,531  | <i>rrn23</i>  |
| p3       | (CAA)3   | 9    | 107,520    | 107,528  | <i>ycfI</i>   |
| p3       | (ATT)3   | 9    | 112,907    | 112,915  | <i>ndhD</i>   |
| p3       | (GCT)3   | 9    | 115,009    | 115,017  | <i>ndhE</i>   |
| p3       | (AGA)3   | 9    | 116,232    | 116,240  | <i>ndhI</i>   |
| p3       | (ATT)3   | 9    | 121,751    | 121,759  | <i>ycfI</i>   |
| p3       | (CTT)3   | 9    | 123,070    | 123,078  | <i>ycfI</i>   |
| p3       | (TTA)3   | 9    | 123,559    | 123,567  | <i>ycfI</i>   |
| p3       | (ATT)3   | 9    | 124,056    | 124,064  | <i>ycfI</i>   |
| p3       | (AAT)3   | 9    | 124,483    | 124,491  | <i>ycfI</i>   |
| p3       | (TTG)3   | 9    | 125,763    | 125,771  | <i>ycfI</i>   |
| p3       | (CAG)3   | 9    | 130,760    | 130,768  | <i>rrn23S</i> |
| p3       | (TTC)3   | 9    | 138,450    | 138,458  | <i>ndhB</i>   |
| p3       | (TCT)3   | 9    | 139,887    | 139,895  | <i>ndhB</i>   |
| p3       | (TTC)3   | 9    | 142,855    | 142,863  | <i>ycf2</i>   |
| p3       | (TCA)3   | 9    | 144,103    | 144,111  | <i>ycf2</i>   |
| p4       | (TCTA)3  | 12   | 30,938     | 30,949   | IGS           |
| p4       | (TTTC)3  | 12   | 73,365     | 73,376   | IGS           |
| p4       | (AACA)3  | 12   | 108,379    | 108,390  | <i>ndhF</i>   |
| p5       | (TAAAA)3 | 15   | 42,584     | 42,598   | intron        |
| p5       | (TATTT)3 | 15   | 44,610     | 44,624   | IGS           |