

Table S3. Distribution of simple sequence repeats in the *Catharanthus roseus* plastome.

Repeat unit	Length (bp)	Number of SSRs	Start position (SSR-containing region) ^{a, b}
A	10	1	82,752 (<i>rpl14-rpl16</i>) ^c
	11	1	121,737 (<i>ndhA</i> intron) ^c
	12	2	4,778 (<i>trnK-UUU-rps16</i>), 115,432 (<i>rpl32-trnL-UAG</i>)
	13	2	8,345 (<i>psbI-trnS-GCU</i>), 114,150 (<i>ndhF-rpl32</i>)
	14	1	79,485 (<i>petD-rpoA</i>)
	15	1	45,392 (<i>ycf3</i> intron 1)
T	16	1	38,371 (<i>rps14-psaB</i>)
	10	8	1,714 (<i>psbA-trnK-UUU</i>), 29,386 (<i>petN-psbM</i>), 36,431 (<i>psbC-trnS-UGA</i>), 52,765 (<i>ndhC-trnV-UAC</i>), 52,934 (<i>ndhC-trnV-UAC</i>), 53,103 (<i>trnV-UAC</i> intron), 58,668 (<i>rbcL-accD</i>), 113,997 (<i>ndhF-rpl32</i>)
	11	6	7,160 (<i>rps16-trnQ-UUG</i>), 8,126 (<i>psbK-psbI</i>), 18,495 (<i>rpoC2</i>), 44,882 (<i>ycf3</i> intron 1), 61,293 (<i>psaI-ycf4</i>), 72,492 (<i>clpP</i> intron 2)
	12	6	12,282 (<i>atpF</i> intron), 54,032 (<i>trnM-CAU-atpE</i>), 72,136 (<i>clpP</i> intron 2), 84,046 (<i>rpl16</i> intron), 127,365 (<i>ycf1</i>), 127,849 (<i>ycf1</i>)
	14	2	67,144 (<i>psbE-petL</i>), 121,980 (<i>ndhA</i> intron)
	15	1	113,910 (<i>ndhF-rpl32</i>)
	16	1	81,657 (<i>infA-rps8</i>)
	AT	10	1
	12	1	119,967 (<i>ndhG-ndhI</i>)
	18	1	32,363 (<i>trnE-UUC-trnT-GGU</i>)
	TA	10	32,240 (<i>trnE-UUC-trnT-GGU</i>), 114,894 (<i>rpl32-trnL-UAG</i>)
	14	1	48,084 (<i>trnT-UGU-trnL-UAA</i>)
	AAT	12	3
AAG	12	1	2,957 (<i>matK</i>)
ATA	12	1	73,740 (<i>clpP-psbB</i>)
ATT	12	1	100,551 (<i>rps12_3'-trnV-GAC</i>)
CTT	12	1	8,655 (<i>trnS-GCU-trnG-UCC</i>)
AAAT	12	1	154,860 (<i>rpl2-Ψrps19</i>)
AAAG	12	1	111,365 (<i>Ψycf1-ndhF</i>)
ATTA	12	2	30,236 (<i>petN-psbM</i>), 32,635 (<i>trnT-GGU-psbD</i>)
ATTT	12	1	85,845 (<i>rps19-rpl2</i>)
TTTA	12	1	47,152 (<i>rps4-trnT-UGU</i>)
TCAA	12	1	4,604 (<i>trnK-UUU-rps16</i>)
TGAT	12	1	33,665 (<i>trnT-GGU-psbD</i>)
CATT	12	1	126,800 (<i>ycf1</i>)
AGATA	15	1	36,340 (<i>psbC-psbZ</i>)

^a If an SSR motif is found at the boundary between genic and intergenic regions, it is assigned to the region containing the major portion of it (e.g., (ATTA)₄, (AGATA)₃).

^b SSRs not found in *Asclepias syriaca* are in bold.

^c These two adjacent SSRs form a compound SSR, which is preceded by 33 A/T positions (TATATTTTATATTAATAAATTAATAAATAATATATATA).