

## **Supporting Informations**

### **Röschenbleck et al., – Genus-wide screening reveals four distinct types of structural plastid genome organization in *Pelargonium* (Geraniaceae)**

#### *Supplemental Figures*

**Fig. S1** Microstructural variation in selected plastome regions in *Pelargonium*.

**Fig. S2** Data set summary statistics.

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**Table S1** Specimens studied and results of the PCR- and sequencing results with GenBank accessions.

**Table S2** PCR screening and sequencing details for clades and regions.

**Table S3** PCR settings including primer primers used in PCR screening and sequencing.

**Table S4** Reconstructed gene order of 111 unique plastid genes in *Pelargonium*.

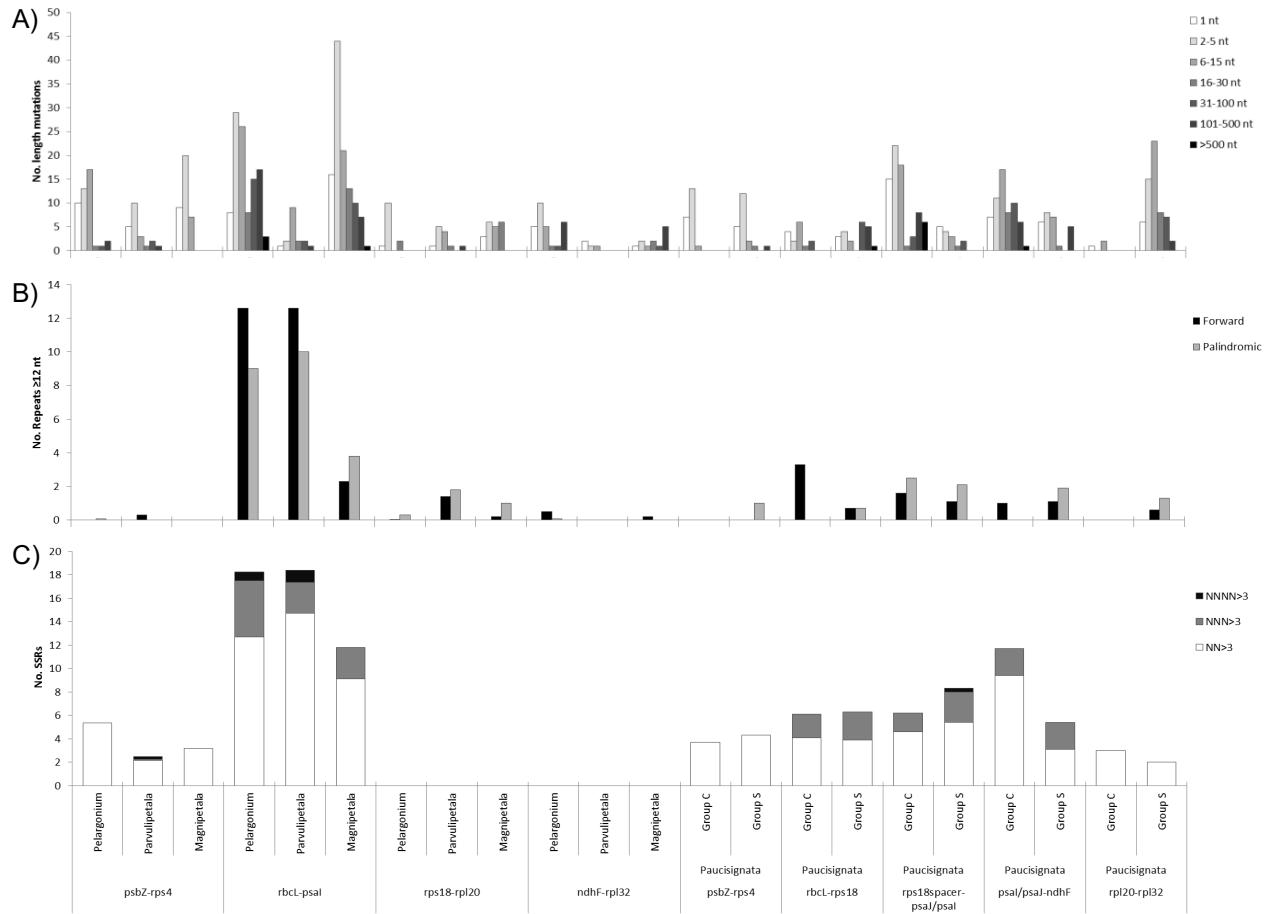
**Table S5** Length range and mean (brackets) for 10 plastome regions of *Pelargonium*.

**Table S6** Substitution rate, nucleotide divergence and GC-content in unaltered and rearranged plastome regions.

**Table S7** Average length, number, and proportion [%] of repeat-rich segments of accD-like regions.

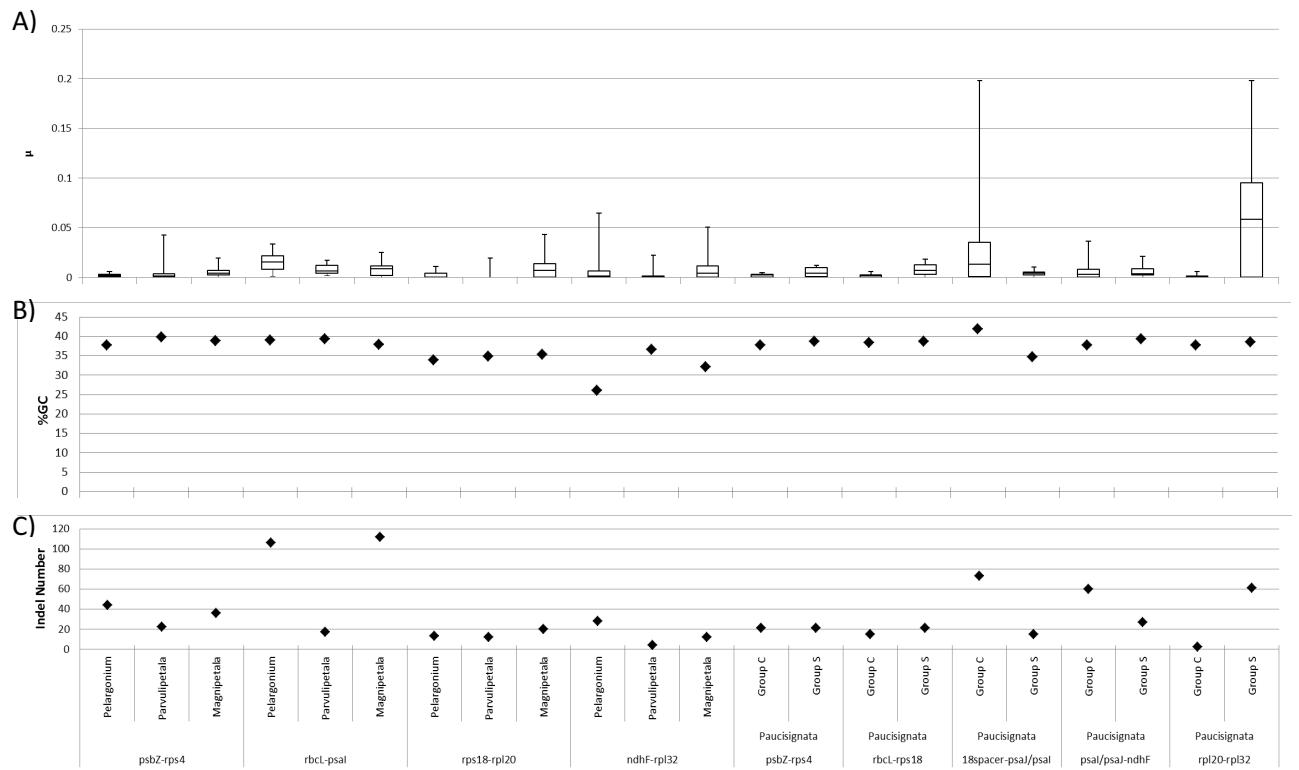
**Table S8** Summary statistics of sequence comparison for accD segments from blastN analysis.

## Supplemental Figures



**Fig. S1 Microstructural variation in selected plastome regions in *Pelargonium*. (A)**

Number of length mutations in seven different size classes. **(B)** Average number of forward and palindromic repeats of at least 12nt length. **(C)** di-, tri- and tetramer SSRs of at least three repetitions. Note that original data including more detailed metrics (e.g. standard deviations) are deposited in datadryad.org (doi: XXXXXX).



**Fig. S2 Data set summary statistics. (a)** Nucleotide substitution rates, **(b)** GC content, and **(c)** indel number are given for all regions of the subgenera *Pelargonium*, *Parvulipetala*, *Magnipetala*, and subgroups C and S of *Paucisignata*.

## Supplemental Tables

**Table S1.** Specimens studied and results of the PCR- and sequencing results with GenBank accessions (XXXXX, also see datadryad.org: doi - XXXXXX). Note that all amplicons were sequenced as far as they could be amplified; empty cells are thus not indicative of missing data.

<i>P. trifidum</i> Jacq., MSUN 3179	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	-	-	
<i>P. worcesterae</i> R. Knuth, MSUN 2746	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	-	-	
<b><i>Paucisignata</i>, Grp C</b>															
<i>P. acetosum</i> (L.) L'Hér., MSUN 526	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. barklyi</i> Scott-Elliott, MSUN 4037	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. inquinans</i> (L.) L'Hér., MSUN 530	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. multibracteatum</i> Hochstetter ex A. Rich., MSUN 2727	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. peltatum</i> (L.) L'Hér., MSUN 534	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. ranunculophyllum</i> (Eckl. & Zeyh.) Bak., MSUN 2375	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<i>P. tongaense</i> Vorster, MSUN 4031	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	GB-Nr.	-	-	GB-Nr.	GB- Nr.	GB- Nr.	-	-
<b><i>Paucisignata</i>, Grp S</b>															
<i>P. caylae</i> Humbert, MSUN 477	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	-	GB-Nr.	GB-Nr.	-	GB- Nr.	GB- Nr.	-	-
<i>P. endlicherianum</i> Fenzl, no voucher, s.loc., cult. BG MS	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	-	GB-Nr.	GB-Nr.	-	GB- Nr.	GB- Nr.	-	-
<i>P. grandicalcaratum</i> R. Knuth, STEU 758	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	-	GB-Nr.	GB-Nr.	-	GB- Nr.	GB- Nr.	-	-
<i>P. karoicum</i> Compton, MSUN 4040	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	-	GB-Nr.	GB-Nr.	-	GB- Nr.	GB- Nr.	-	-
<i>P. otaviense</i> R. Knuth, STEU 943	GB-Nr.	-	-	-	-	GB-Nr.	GB-Nr.	-	GB-Nr.	GB-Nr.	-	GB- Nr.	GB- Nr.	-	-



<i>P. alternans</i> subsp. <i>alternans</i> Wendl., MSUN 720	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. althaeoides</i> (L.) L'Hér., MSUN 4032	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. caffrum</i> (Eckl. & Zeyh.) Harv. STEU 2738	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. carnosum</i> subsp. <i>carnosum</i> (L.) L'Hér., MSUN 2737	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. coronopifolium</i> Jacq., STEU 1797	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. crassicaule</i> L'Hér., MSUN 601	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. crispum</i> (Berg.) L'Hér., MSUN 2839	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. cucullatum</i> subsp. <i>cucullatum</i> (L.) L'Hér., STEU 1043	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. desertorum</i> Vorster, MSUN 538	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. fulgidum</i> (L.) L'Hér., STEU 482	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. glutinosum</i> (Jacq.) L'Hér., STEU 1644	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. hirtum</i> (Burm.f.) Jacq., BG Muenster, s.n.	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. incrassatum</i> (Andr.) Sims, MSUN 785	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. klinghardtense</i> R. Knuth, MSUN 709	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.

<i>P. magenteum</i> J.J.A. v.d. Walt, MSUN 631	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. nanum</i> L'Hér., MSUN 345	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. oblongatum</i> E.Mey. ex. Harv., MSUN 4027	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. ovale</i> subsp. <i>ovale</i> (Burm.f.) L'Hér., BG Muenster, s.n.	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. radulifolium</i> (Eckl. & Zeyh.) Steud., MSUN 874	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. schizopetalum</i> Sweet, STEU 1873	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. sericifolium</i> J.J.A. v.d. Walt, STEU 1554	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. triandrum</i> E.M. Marais, MSUN 751	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. triste</i> (L.) L'Hér., STEU 1103	GB-Nr.	GB-Nr.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.
<i>P. xerophyton</i> Schltr. ex R. Knuth, MSUN 636	GB-Nr.	n.a.	GB-Nr.	GB-Nr.	-	-	-	-	-	-	-	-	GB- Nr.	GB- Nr.

‘-’ not detected; ‘n. a.’: positive result in PCR screening, but not sequenced; MSUN – Herbarium of the University of Muenster; STEU – Herbarium of the University of Stellenbosch; BG – Botanical Garden

**Table S2.** PCR screening and sequencing details for clades and regions.

Amplicon	No. species	Additional amplicons of flanking genes	Negative control (amplification region)
<b>Pelargonium</b>			
<i>rpoA-petB</i>	24 (24)	-	<i>rbcL</i> (IRa) rev - <i>psbA</i> for, <i>rbcL</i> (IRa) rev- <i>trnI</i> <sub>CAU</sub> rev
<i>ycf2-rpoA</i>	24 (24)	-	<i>rbcL</i> (IRa) rev - <i>psbA</i> for, <i>rbcL</i> (IRa) rev- <i>trnI</i> <sub>CAU</sub> rev
<i>ycf3</i> rev- <i>trnE</i> <sub>UUUC</sub> rev	10 (5)	<i>ycf3</i> rev- <i>trnG</i> <sub>GCC</sub> rev, <i>trnG</i> <sub>GCC</sub> for- <i>trnE</i> <sub>UUUC</sub> rev	-
<i>psbZ</i> for- <i>rps4</i> for	31 (24)	-	<i>rps4</i> for- <i>ycf3</i> rev
<i>rbcL</i> for- <i>psaI</i> rev	31 (9)	-	<i>rbcL</i> for - <i>psaJ</i> rev
<i>rps18</i> for- <i>rpl20</i> for	28 (24)	<i>psaJ</i> for- <i>rpl20</i> for, <i>psaJ</i> for- <i>rps18</i> rev	-
<i>ndhF</i> rev- <i>rpl32</i> rev	29 (24)	-	<i>ndhF</i> for- <i>rpl32</i> rev
<b>Parvulipetala</b> -			
-	-	-	<i>rbcL</i> (IRa) rev - <i>psbA</i> for, <i>rbcL</i> (IRa) rev- <i>trnI</i> <sub>CAU</sub> rev
<i>psbZ</i> for- <i>rps4</i> for	12 (12)	-	<i>rps4</i> for- <i>ycf3</i> rev
<i>rbcL</i> for- <i>psaI</i> rev	15 (3)	-	<i>rbcL</i> for- <i>rps18</i> rev, <i>rbcL</i> for- <i>psaJ</i> for
<i>rps18</i> for- <i>rpl20</i> for	16 (12)	<i>psaJ</i> for- <i>rpl20</i> for, <i>psaJ</i> for- <i>rps18</i> rev	<i>rpl20</i> for- <i>rpl32</i> for
<i>ndhF</i> for- <i>rpl32</i> rev	13 (11)	-	<i>ndhF</i> rev- <i>rpl32</i> rev
<b>Magnipetala</b>			
<i>ycf3</i> rev- <i>trnE</i> <sub>UUUC</sub> rev	9 (2)	<i>ycf3</i> rev- <i>trnG</i> <sub>GCC</sub> rev, <i>ycf3</i> rev- <i>trnY</i> <sub>GUU</sub> rev	-
<i>psbZ</i> for- <i>rps4</i> for	15 (10)	-	<i>rps4</i> for- <i>ycf3</i> rev
<i>rbcL</i> for- <i>psaI</i> rev	15 (10)	-	<i>rbcL</i> for- <i>rps18</i> rev, <i>trnN</i> <sub>GUU</sub> for- <i>psaI</i> rev
<i>rps18</i> for- <i>rpl20</i> for	16 (10)	<i>psaJ</i> for- <i>rpl20</i> for, <i>psaJ</i> for- <i>rps18</i> rev	<i>rpl20</i> for- <i>rpl32</i> for
<i>ndhF</i> rev- <i>rpl32</i> rev	16 (10)	<i>ndhF</i> for- <i>trnN</i> <sub>GUU</sub> rev	<i>ndhF</i> for- <i>trnN</i> <sub>GUU</sub> for, <i>ndhF</i> rev- <i>rpl32</i> rev
<b>Paucisignata</b>			
<i>rbcL</i> (IRa) rev- <i>psbA</i> for	14 (0)	<i>rbcL</i> (IRa) rev- <i>trnI</i> <sub>CAU</sub> rev	-
<i>ycf3</i> rev- <i>trnE</i> <sub>UUUC</sub> rev	11 (8)	<i>ycf3</i> rev- <i>trnG</i> <sub>GCC</sub> rev, <i>trnG</i> <sub>GCC</sub> for- <i>trnE</i> <sub>UUUC</sub> rev	-
<i>psbZ</i> for- <i>rps4</i> for	14 (14)	-	<i>rps4</i> for- <i>ycf3</i> rev
<i>rbcL</i> for (IRb)- <i>rps18</i> rev	17 (14)	-	-
<i>rpl20</i> rev- <i>rpl32</i> rev	15 (14)	-	<i>ndhF</i> rev- <i>rpl32</i> rev
<b>Paucisignata – Grp. C</b>			
<i>rps18</i> for- <i>psaI</i> for	9 (7)	<i>rbcL</i> for - <i>psaJ</i> for	<i>rps18</i> for- <i>psaI</i> rev
<i>ndhF</i> for- <i>psaI</i> rev	7 (7)	<i>ndhF</i> for- <i>trnN</i> <sub>GUU</sub> rev, <i>trnN</i> <sub>GUU</sub> for- <i>psaI</i> rev	<i>ndhF</i> for- <i>psaJ</i> for, <i>ndhF</i> for- <i>rps18</i> for , <i>rps18</i> rev- <i>psaJ</i> for
<b>Paucisignata – Grp. S</b>			
<i>rps18</i> for - <i>psaI</i> rev	7 (7)	<i>rbcL</i> for- <i>psaI</i> rev	<i>rps18</i> for- <i>psaJ</i> for
<i>ndhF</i> for- <i>psaJ</i> for	7 (7)	<i>ndhF</i> for- <i>trnN</i> <sub>GUU</sub> rev, <i>trnN</i> <sub>GUU</sub> for- <i>psaJ</i> for, <i>ndhF</i> for- <i>psaI</i> rev, <i>trnN</i> <sub>GUU</sub> for- <i>psaI</i> rev	<i>trnN</i> <sub>GUU</sub> for- <i>rps18</i> for, <i>rps18</i> rev- <i>psaJ</i> for

Numbers in brackets in column 2 are the number of species sequences. for – forward primer, rev – reverse primer;

**Table S3.** PCR settings including primer primers used in PCR screening and sequencing.

Region	Primer <sup>1</sup>	Primer sequence 5'→3'	Orientation	Cycles, Annealing, Elongation conditions
<i>rbcL-psbA</i>	rbcL-A	GTATCCTGGTTTCATAATCAGG	Rev	43 x, A 60°C 30sec,E 72°C 1m
	psbA	CCTTGGTATGGAAGTTATGCATG	Rev	
	rbcL-A	GTATCCTGGTTTCATAATCAGG	Rev	43 x, A 60°C 30sec,E 72°C 1m
	trnI	GTTGGGTGCTTAACCATTCAAGC	Rev	
<i>psbZ-rps4</i>	rps4	CATAGAACATTATTCTCGTCAGATTACCC	For	40x, A 54°C 0,45m, E 72°C 1,5m
	psbZ	GTACCCGTTGTATTGCTTCTC	For	45x, A 54°C 0,45m, E 72°C 1,5m
	rps4	CATAGAACATTATTCTCGTCAGATTACCC	For	40x, A 54°C 0,45m, E 72°C 1,5m
	ycf3	GGTCTTATCAATAAAATTCCATT	Rev	
<i>trnE-ycf3</i>	ycf3	GGTCTTATCAATAAAATTCCATT	Rev	45x, A 54°C 1m, E 72°C 2m
	trnE	GAGAGATGTCCTGAACCACTAGACGATG	Rev	45x, A 56°C 1m, E 72°C 2,15m
	ycf3-2	GCCTCCCTTCTCCTGAAGTTGAGG	Rev	45x, A 54°C 1m, E 72°C 2,15m
	trnG	TCTCTTGCCAAGGAGAACG	For	40x, A 54°C 0,45m, E 72°C 2,15m
	ycf3	GGTCTTATCAATAAAATTCCATT	Rev	38x, A 54°C 0,45m, E 72°C 1,15m
	trnG	CGTCTTCTCCTGGCAAAGAGA	Rev	
<i>rbcL-psaI</i>	rbcL-B	GAAGCATGTACAAGCTCGTAATG	For	38 x, A 54°C 1,5m, E 72°C 3,5m; 4m; 4,5m
	psaI	TGAAGAAATAAGAACGCCATTGC	Rev	45 x, A 54°C 1,5m, E 72°C 3,5m; 4m; 4,5m
	rbcL-B2	GTGCCGTAGCTAATCGAGTAGC	For	45x, A 54°C 1m, E 72°C 2m
	IR-1	TCAATTACTCTTTACCTGCAAATGCAAT	Rev	45x, A 56°C 1m, E 72°C 2m
	IR-2.1	GATTGAAATCGGGATCACCGCTTAC	Rev	
	IR-2.2	CTCTGAAGAGTCTCAGATTGT	Rev	
	psaI2	GCAAATGCCGAAATACTAGGC	Rev	
	RI-1.1	ACGTCCCTTTCGTTCTCGTGTGC	For	45x, A 58°C 1m, E 72°C 2m
	RI-2	CATAATCCTAGTGATTGGATTATATAC	For	45x, A 58°C 1m, E 72°C 1,5m
	RI-1.2	TGTTTCCCCTTGATTTCAGATTGA	For	
	RI-3	GTTGACAAAGGTCTCTATATTCACTATAC	For	
	RI-4	GACTTCTACTTATGAAGAACTCAATTGTG	For	
	IR-2.2	CTCTGAAGAGTCTCAGATTGT	Rev	
	RI-8	ACAAATCTGAAGACTCTTCAGAG	For	45x, A 58°C 1m, E 72°C 2m
	RI-4	GACTTCTACTTATGAAGAACTCAATTGTG	For	
<i>psaI</i>	psaI	TGAAGAAATAAGAACGCCATTGC	Rev	
	RI-1.1	ACGTCCCTTTCGTTCTCGTGTGC	For	45x, A 58°C 0,45m, E 72°C 1,5m
	RI-1.2	TGTTTCCCCTTGATTTCAGATTGA	For	
	RI-3	GTTGACAAAGGTCTCTATATTCACTATAC	For	
<i>RI-4</i>	RI-4	GACTTCTACTTATGAAGAACTCAATTGTG	For	

	RI-5	GATCCCATTGAGTGGGATTCAA GAATAGCTTCAGGCAATCCCGTG	For Rev	
	IR-3			45x, A 58°C 0,45m, E 72°C 1,5m
	RI-9	ATTGCATTGCAGGTAAAAGAGTAATTGA	For	
	RI-7	GATTGCCTGAAGCTATTCAAACAGG	For	
	psaI	TGAAGAAATAAAGAACGCCATTGC	Rev	
	rbcL-B	GAAGCATGTACAAGCTCGTAATG	For	45x, A 58°C 0,45m, E 72°C 1,5m
	RI-1	ACGTCCCTTCGTTCGTGTGC	For	
	IR-5	GATGTCATCAACGAAAAGAGGCCATTGC	Rev	
	RI-6	CTCTACTTAGCACTCCTGCATCTC	For	45x, A 58°C 0,45m, E 72°C 1,5m
	psaI	TGAAGAAATAAAGAACGCCATTGC	Rev	
	RI-5	GATCCCATTGAGTGGGATTCAA CTATCCAGATACGCAAGACAAAGAGC	For	45x, A 58°C 1m, E 72°C 2m
	IR-4		Rev	
<i>rbcL-rps18</i>	rbcL-B, rps18	GAAGCATGTACAAGCTCGTAATG GTTTAAAGTCACTCTATTCACCCGTCTAG	For Rev	45x, A 56°C 0,45m, E 72°C 1,5m 45x, A 54°C 0,45m, E 72°C 1,5m
	rbcL-B2	GTGCCGTAGCTAATCGAGTAGC	For	40x, A 54°C 0,45m, E 72°C 1,5m
	RI-1.1	ACGTCCCTTCGTTCGTGTGC	For	40x, A 54°C 1m, E 72°C 1,45m
	R18-1	GAGTCATAATCCTAGTGATTAGTCCT	For	40x, A 54°C 1m, E 72°C 1,5m
	18R-1	GTTGAATGAATATCTGCTGCCCGC	Rev	38x, A 54°C 1m, E 72°C 1,5m
<i>rpoA-ycf2</i>	rpoA-f ycf2-f	ATAGATGCCGTCTCACACCC GATGGATTTCCCGGATGAAATGAAA	Rev For	40x, A 54°C 1,5m, E 72°C 3,5m
<i>rpoA-petB</i>	petB_f	CTAGCGCTGTATTATGTTAATCC	For	40x, A 54°C 1,5m, E 72°C 3,5m
	rpoA-f	ATAGATGCCGTCTCACACCC	Rev	
<i>rps18-psaJ</i>	rbcL-B psaJ	GAAGCATGTACAAGCTCGTAATG GCAGGTCTATTGATAGAGATTAA	For For	38x, A 54°C 1,5m, E 72°C 4m
	rps18	CTAGACGGGTGAATAGAGTGACTTAAAAC	For	45x, A 56°C 1,5, E 72°C 4m 40x, A 54°C 1,5m, E 72°C 3,5m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	38x, A 54°C 1,5m, E 72°C 3,5m
	RJ-1	CTACCTACTATCCACACGAGGATAATC	For	45x, A 56°C 1m, E 72°C 2m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	45x, A 54°C 1m, E 72°C 2m
	J18-1	CGTTGTATATCTCCCCAATTGTCTAC	For	45x, A 54°C 1m, E 72°C 2,5m
	J18-2.1	TGTATTCAATTGGTTGTACAGATAGAGG	For	45x, A 54°C 1m, E 72°C 2,5m
	J18-2.2	CGGCTGTGCTATCATTCTTCTACC	For	45x, A 54°C 0,45m, E 72°C 1,5m 43x, A 54°C 0,45m, E 72°C 2,5m 40x, A 54°C 0,45m, E 72°C 2,5m
	R18-1	GAGTCATAATCCTAGTGATTAGTCCT	For	45x, A 54°C 1m, E 72°C 2,5m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	
	rps18V	CGCACTGAATTATCGCAACCAAG	For	40x, A 54°C 0,45m, E 72°C 2,5m

	rps18H	CGAGCTAGCAATTATCCGACACGCC	Rev	
	rps18V2	GGCTACGCACTGAATTATCGC	For	
<i>rps18-psaI</i>	rps18	GTTTAAAGTCACTCTATTACCCGTCTAG	For	45x, A 54°C 0,45m, E 72°C 1,5m
	psaI-2	GCAAATGCCGAAATACTAGGC	Rev	40x, A 54°C 0,45m, E 72°C 2,5m
	rps18V	CGCACTGAATTATCGAACCAAG	For	
	R18-1	GAGTCATAATCCTAGTGATTAGTCCT	For	45x, A 54°C 1m, E 72°C 2,5m
	psaI,	TGAAGAAATAAAGAACGATTGC	Rev	40x, A 54°C 0,45m, E 72°C 1,5m
	psaI-2	GCAAATGCCGAAATACTAGGC	Rev	
	rps18-1.1	CGCACTGAATTATCGAACCAAG	For	40x, A 54°C 0,45m, E 72°C 2,5m
	R0	CGAGCTAGCAATTATCCGACACGCC	Rev	
	rps18-1.2	GGCTACGCACTGAATTATCGC	For	
	rps18	GTTTAAAGTCACTCTATTACCCGTCTAG	For	45x, A 58°C 1m, E 72°C 2,5m
	psaI	TGAAGAAATAAAGAACGATTGC	Rev	45x, A 56°C 0,45m, E 72°C 2m
	rps18-1.1	CGCACTGAATTATCGAACCAAG	For	45x, A 56°C 0,45m, E 72°C 1,5m
	rps18-1.2	GGCTACGCACTGAATTATCGC	For	45x, A 54°C 0,45m, E 72°C 2,5m
	rps18-1.3	CTAGACGGGTGAATAGAGTGAC	For	45x, A 54°C 1m, E 72°C 2,5m
	I18I-1	CCG GTAGAAAGSGATTCCCTAATG	For	45x, A 54°C 1m, E 72°C 2,5m
	I18I-2	GTAGAAAGSGATTCCCTAATG	For	45x, A 54°C 0,45m, E 72°C 1,5m
	I18I-3	GTCAAGGTACCGATCCA	For	45x, A 54°C 0,45m, E 72°C 2m
	psaI-2	GCAAATGCCGAAATACTAGGC	Rev	43x, A 54°C 0,45m, E 72°C 2,5m
	I18-1	CATTCTCCGAAGGTCGCTTCTC	Rev	40x, A 54°C 0,45m, E 72°C 2m
	I18-2	AGATACGCAAGACAAAGAGCAT	Rev	
	I18-3	CTTCCAGTCTCTGCCATTATACCCAG	Rev	
	I18-4	GAAATTGAAATTACAAGACTGTCCG	Rev	
	I18-5	GACTTGCCAATCCAATTCTTG	Rev	
	I18-6	TGGTAAGGGTATTGAGGCTAA	Rev	
<i>rps18-rpl20</i>	rps18	CTAGACGGGTGAATAGAGTGACTTAAAAC	For	38x, A 54°C 0,45m, E 72°C 3m
	rpl20	CTTGCACAAATAGCTATCTCAAATAGG	For	38x, A 54°C 0,45m, E 72°C 2m
				45x, A 56°C 0,45m, E 72°C 1,5m
				45x, A 58°C 0,45m, E 72°C 1,5m
	rps18	GTTTAAAGTCACTCTATTACCCGTCTAG	Rev	38x, A 54°C 0,45m, E 72°C 3m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	45x, A 56°C 1m, E 72°C 1,5m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	40x, A 54°C 0,45m, E 72°C 1m
	rpl20	CTTGCACAAATAGCTATCTCAAATAGG	For	38x, A 54°C 0,45m, E 72°C 3m
				38x, A 54°C 0,45m, E 72°C 2m
				45x, A 56°C 0,45m, E 72°C 1,5m
<i>psaI-ndhF</i>	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	38x, A 54°C 1,5m, E 72°C 3,5m

	psaI	TGAAGAAATAAAGAACGCCATTGC	Rev	
	ndhF-2	GAGTTACGAAGGAAACTTCGAGC	For	45x, A 56°C 0,45m, E 72°C 2m
	psaI	TGAAGAAATAAAGAACGCCATTGC	Rev	45x, A 56°C 1m, E 72°C 1,5m
	trnN	GACTGGTCGTAGGTTCGAACATC	For	45x, A 54°C 1m, E 72°C 1,5m
	trnN-2	CCTCAGTAGCTCAGTGGTAGAGC	For	45x, A 54°C 0,45m, E 72°C 1,5m
	trnN-3	TTCGGCTGTTAACCGACTG	For	40x, A 54°C 0,40m, E 72°C 1m
	psaI-2	GCAAATGCCGAAATACTAGGC	Rev	40x, A 54°C 0,45m, E 72°C 1m
	IN-1	GTTGAATTGAAAGGCTCTCATCACTG	Rev	40x, A 54°C 0,45m, E 72°C 1,2m
<i>psaJ-ndhF</i>	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	45x, A 56°C 1m, E 72°C 1,5m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	45x, A 54°C 1m, E 72°C 1,5m
	ndhF-22	GAGTTACGAAGGAAACTTCGAGC	For	45x, A 54°C 0,45m, E 72°C 1,5m
	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	40x, A 54°C 0,45m, E 72°C 1,5m
	psaJ	GCAGGTCTATTGATAGAGATTAA	For	40x, A 54°C 0,45m, E 72°C 1,5m
	ndhF-2	GAGTTACGAAGGAAACTTCGAGC	For	40x, A 54°C 0,45m, E 72°C 1,5m
	trnN	GACTGGTCGTAGGTTCGAACATC	For	40x, A 54°C 0,45m, E 72°C 1,2m
	trnN-2	CCTCAGTAGCTCAGTGGTAGAGC	For	40x, A 54°C 1m, E 72°C 2,5m
	trnN-3	TTCGGCTGTTAACCGACTG	For	40x, A 54°C 0,45m, E 72°C 2,5m
	rps18	CTAGACGGGTGAATAGAGTGACTTTAAAAC	For	
<i>trnN-ndhF</i>	JN-1	CATGTCAGACTATATCTCGATCTTAAGTG		
	JN-2	CGTCACCTATGGCGTTCTCCGAACG		
	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	38x, A 54°C 0,45m, E 72°C 1,5m
	trnN	GCTCTACCACTGAGCTACTGAGG	Rev	45x, A 56°C 0,45m, E 72°C 1,5m
<i>rpl20-rpl32</i>	rpl20	CTTGCACAAATAGCTATCTCAAATAGG	For	40x, A 54°C 0,45m, E 72°C 1,5m
	rpl32	CAAAGCTTCAACGCCGCCAATG	Rev	45x, A 56°C 0,45m, E 72°C 1,5m
	rpl20-2	GATTTTCGTCGTTGTGGATCACTC	For	45x, A 60°C 0,45m, E 72°C 1,5m
	rpl32	CAAAGCTTCAACGCCGCCAATG	Rev	45x, A 54°C 0,45m, E 72°C 1,5m
<i>ndhF-rpl32</i>	ndhF	GCATAATCCATGAATATTGATATATATGTTCCAT	Rev	40x, A 54°C 0,45m, E 72°C 1,5m
	rpl32	CAAAGCTTCAACGCCGCCAATG	Rev	45x, A 56°C 0,45m, E 72°C 1,5m
	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	45x, A 54°C 0,45m, E 72°C 1,5m
	rpl32	CAAAGCTTCAACGCCGCCAATG	Rev	40x, A 54°C 0,45m, E 72°C 1,5m
	ndhF	GATGCGCGAGTTATTGATGGAATTAC	For	45x, A 56°C 0,45m, E 72°C 1,5m
	trnN-2	CCTCAGTAGCTCAGTGGTAGAGC	For	45x, A 54°C 0,45m, E 72°C 1,5m
	ndhF	GATGCGCGAGTTATTGATGGAATTAC	Rev	38x, A 54°C 0,45m, E 72°C 1,5m
	trnN-2	CCTCAGTAGCTCAGTGGTAGAGC	For	

Primers under the primary primer pair are internal primers used additionally for sequencing.

**Table S4.** Reconstructed gene order of 111 unique plastid genes in *Pelargonium*.

Subgroup	Genome arrangement
Subg. <i>Magnipetala</i> and <i>Pelargonium</i>	<b>86 -85 84 -1 -2 -3 -4 -5 -6 7 8 -9 10 11 -12 -13 -14 -15 -16 -17 -18 -19 20</b> 21 -22 -23 <b>-24 -25 -30 35 34 33 32 31 26 27 -28 29 36 -37 -38 39 40 -41 -</b> 42 -43 -44 45 -46 -47 <b>48 49 50 51 52 -53 -54 -55 -56 57 58 -59 -60 61 62</b> <b>63 -64 -65 -66 67 68 -69 70 71 72 -73 -74 -75 -76 -77 -78 -79 -80 -81 -82</b> <b>-83 -87 -88 -89 90 91 92 93 94 95 96 97 -98 -99 100 111 110 109 108</b> <b>107 106 105 104 103 -102 -101</b>
Subg. <i>Paucisignata</i>	<b>84 -1 -2 -3 -4 -5 -6 7 8 -9 10 11 -12 -13 -14 -15 -16 -17 -18 -19 20 21 -22</b> -23 -24 -25 <b>-30 35 34 33 32 62 31 26 27 -28 29 36 -37 -38 39 40 -41 -42 -</b> 43 -44 45 -46 -47 <b>48 63 -61 60 59 -58 -57 56 55 54 53 -52 -51 -50 -49 -</b> <b>98 -99 -97 -96 -95 -94 -93 -92 -91 -90 89 88 87 83 82 81 80 79 78 77 76</b> <b>75 74 73 86 85 -72 -71 -70 69 -68 -67 66 65 64 100 111 110 109 101 102</b> -103 -104 -105 -106 -107 -108
Group C	<b>84 -1 -2 -3 -4 -5 -6 7 8 -9 10 11 -12 -13 -14 -15 -16 -17 -18 -19 20 21 -22</b> -23 -24 -25 <b>-30 35 34 33 32 62 31 26 27 -28 29 36 -37 -38 39 40 -41 -42 -</b> 43 -44 45 -46 -47 <b>48 63 -61 60 59 -58 -57 55 56 54 53 -52 -51 -50 -49 -</b> <b>98 -99 -97 -96 -95 -94 -93 -92 -91 -90 89 88 87 83 82 81 80 79 78 77 76</b> <b>75 74 73 86 85 -72 -71 -70 69 -68 -67 66 65 64 100 111 110 109 101 102</b> -103 -104 -105 -106 -107 -108
Group S	<b>84 -1 -2 -3 -4 -5 -6 7 8 -9 10 11 -12 -13 -14 -15 -16 -17 -18 -19 20 21 -22</b> -23 -24 -25 <b>-30 35 34 33 32 62 31 26 27 -28 29 36 -37 -38 39 40 -41 -42 -</b> 43 -44 45 -46 -47 <b>48 63 49 50 51 52 -53 -54 -55 -56 57 58 -59 -60 61 -98</b> <b>-99 -97 -96 -95 -94 -93 -92 -91 -90 89 88 87 83 82 81 80 79 78 77 76 75</b> <b>74 73 86 85 -72 -71 -70 69 -68 -67 66 65 64 100 111 110 109 101 102 -</b> 103 -104 -105 -106 -107 -108
Subg. <i>Parvulipetala</i>	<b>86 -85 84 -1 -2 -3 -4 -5 -6 7 8 -9 10 11 -12 -13 -14 -15 -16 -17 -18 -19 20</b> 21 -22 -23 -24 -25 <b>-30 35 34 33 32 31 26 27 -28 29 36 -37 -38 39 40 -41 -</b> 42 -43 -44 45 -46 -47 <b>48 49 50 51 52 -53 -54 -55 -56 57 58 -59 -60 61 62</b> <b>63 -64 -65 -66 67 68 -69 70 71 72 -73 -74 -75 -76 -77 -78 -79 -80 -81 -82</b> <b>-83 -87 -88 -89 90 91 92 93 94 95 96 97 99 98 100 111 110 109 108 107</b> <b>106 105 104 103 -102 -101</b>

Bold numbers – genes with an altered position compared to *Melianthus*; +/- – strand orientation; underlined numbers – regions covered in PCR-screening; Gene codes: 1=*trnH<sub>GUG</sub>*; 2=*psbA*; 3=*matK*; 4=*trnK<sub>UUU</sub>*; 5=*rps16*; 6=*trnQ<sub>UUG</sub>*; 7=*psbK*; 8=*psbI*; 9=*trnS<sub>GGU</sub>*; 10=*trnG<sub>UCC</sub>*; 11=*trnR<sub>UCU</sub>*; 12=*atpA*; 13=*atpF*; 14=*atpH*; 15=*atpI*; 16=*rps2*; 17=*rpoC2*; 18=*rpoC1*; 19=*rpoB*; 20=*trnC<sub>GCA</sub>*; 21=*petN*; 22=*psbM*; 23=*trnD<sub>GUC</sub>*; 24=*trnY<sub>GUA</sub>*; 25=*trnE<sub>UUC</sub>*; 26=*psbD*; 27=*psbC*; 28=*trnS<sub>UGA</sub>*; 29=*psbZ*; 30=*trnG<sub>GCC</sub>*; 31=*trnJ<sub>CAU</sub>*; 32=*rps14*; 33=*psaB*; 34=*psaA*; 35=*ycf3*; 36=*trnS<sub>GGAA</sub>*; 37=*rps4*; 38=*trnT<sub>UGU</sub>*; 39=*trnL<sub>UAA</sub>*; 40=*trnF<sub>GAA</sub>*; 41=*ndhJ*; 42=*ndhK*; 43=*ndhC*; 44=*trnV<sub>UAC</sub>*; 45=*trnM<sub>CAU</sub>*; 46=*atpE*; 47=*atpB*; 48=*rbcL*; 49=*psaI*; 50=*ycf4*; 51=*cemA*; 52=*petA*; 53=*psbJ*; 54=*psbL*; 55=*psbF*; 56=*psbE*; 57=*petL*; 58=*petG*; 59=*trnW<sub>CCA</sub>*; 60=*trnP<sub>UGG</sub>*; 61=*psaJ*; 62=*rpl33*; 63=*rps18*; 64=*rpl20*; 65=*rps12* '5'; 66=*clpP*; 67=*psbB*; 68=*psbT*; 69=*psbN*; 70=*psbH*; 71=*petB*; 72=*petD*; 73=*rpoA*; 74=*rps11*; 75=*rpl36*; 76=*rps8*; 77=*rpl14*; 78=*rpl16*; 79=*rps3*; 80=*rpl22*; 81=*rps19*; 82=*rpl2*; 83=*rpl23*; 84=*trnI<sub>CAU</sub>*; 85=*ycf2*; 86=*trnL<sub>CAA</sub>*; 87=*ndhB*; 88=*rps7*; 89=*rps12* '3'; 90=*trnV<sub>GAC</sub>*; 91=*rrn16*; 92=*trnI<sub>GAU</sub>*; 93=*trnA<sub>UGC</sub>*; 94=*rrn23*; 95=*rrn4.5*; 96=*rrn5*; 97=*trnR<sub>ACG</sub>*; 98=*trnN<sub>GUU</sub>*; 99=*ndhF*; 100=*rpl32*; 101=*trnL<sub>UAG</sub>*; 102=*ccsA*; 103=*ndhD*; 104=*psaC*; 105=*ndhE*; 106=*ndhG*; 107=*ndhI*; 108=*ndhA*; 109=*ndhH*; 110=*rps15*; 111=*ycf1*.

**Table S5.** Length range and mean (brackets) for 10 plastome regions of *Pelargonium*.

Subgenus	<i>psbZ-rps4</i>	<i>rbcL-psaI</i>	<i>rbcL-rps18</i>	<i>18S spacer-psaJ</i>	<i>18s spacer-psaI</i>	<i>rps18-rpl20</i>	<i>psaI-ndhF</i>	<i>psaJ-ndhF</i>	<i>ndhF-rpl32</i>	<i>rpl20-rpl32</i>
<i>Pelargonium</i>	1037-1262 (1222)	4382-5258 (4780)	-	-	-	456-475 (459)	-	-	520-897 (602)	-
<i>Parvulipetala</i>	870-1029 (915)	3770-4013 (3922)	-	-	-	475-653 (505)	-	-	869-881 (876)	-
<i>Magnipetala</i>	1106-1139 (1119)	1219-3849 (3129)	-	-	-	420-475 (453)	-	-	408-869 (508)	-
<i>Paucisignata</i> , Group C	1256-1271 (1261)	-	2261-2425 (2236)	1329-3222 (2345)	-	-	2684-3477 (2911)	-	-	701-713 (703)
<i>Paucisignata</i> , Group S	668-1271 (1005)	-	1674-2163 (1937)	-	1786-2460 (2142)	-	-	1836-5111 (2441)	-	702-1312 (929)

**Table S6.** Substitution rate, nucleotide divergence, and GC-content in unaltered and rearranged plastome regions.

	Conserved regions	Rearranged regions	<i>Pelargonium</i>	<i>Parvulipetala</i>	<i>Magnipetala</i>	<i>Paucisignata</i> , Group C	<i>Paucisignata</i> , Group S
GC content [%]	34.8	38.3	34.2	37.6	36.1	38.7	38.0
Divergence [%]	2.9	3.3	2.2	1.4	4.1	2.5	5.2
Substitution rate [ $\mu$ ]	0.0078	0.0098	0.0064	0.0041	0.0086	0.0082	0.016

**Table S7.** Average length, number, and proportion [%] of repeat-rich segments of accD-like regions.

	Total Length	Sum accD	accD1 (range)	accD2 (range)	accD3 (range)	Interspersed region 1 (%length repeats)	Interspersed region 2 (% length repeats)
<i>Pelargonium</i>	3285	1167	322 (318-324)	211 (211-211)	634 (634-634)	728 (34)	1390 (53)
<i>Parvulipetala</i>	2827	887	42 (42-42)	211 (211-211)	634 (634-634)	806 (37)	1134 (43)
<i>Magnipetala</i>	2304	1089	277 (88-317)	182 (153-211)	630 (595-654)	314 (0)	901 (12)
Subclade of <i>Magnipetala</i>	234	234	-	-	234 (234-234)	-	-

**Table S8.** Summary statistics of sequence comparison for accD segments from blastN analysis.

Subgenus	accD1			accD2			accD3		
	E value	Identity [%]	Length [nt]	E value	Identity [%]	Length [nt]	E value	Identity [%]	Length [nt]
<i>Pelargonium</i>	3.E-09	69	319	0.8	67	185	5.E-135	79	599
<i>Parvulipetala</i>	-	-	-	1.4	67	199	4.E-140	78	604
<i>Magnipetala</i>	2.E-04	70	196	0.1	68	154	8.E-119	76	587