Table S1. Mitochondrial intron content in Geraniales

	Melianthus villosus	Hypseocharis bilobata	Erodium moschatum	Monsonia emarginata[1]	Geranium maderense[1]	Pelargonium citronellum
ccmFCi829	+	-	-	-	-	-
cox1i729	-					
cox2i373	-	-	-	-	-	-
cox2i691	+	-	-	-	-	-
nad1i394	trans	trans	trans	trans	trans	trans
nad1477	+	-	-	-	-	-
nad1i669	trans	-	-	-	-	-
nad1i728	+	-	-	-	-	-
nad2i156	+	-	-	-	-	-
nad2i542	trans	trans	trans	trans	trans	trans
nad2i709	+	-	-	-	-	-
nad2i1282	+	-	-	-	-	-
nad4i461	+	+	+	+	+	+
nad4i976	+	-	-	-	-	-
nad4i1399	+	+	+	+	+	+
nad5i230	+	+	+	+	+	+
nad5i1455	trans	trans	trans	trans	trans	-
nad5i1477	trans	trans	trans	trans	trans	-
nad5i1872	+	+	-	-	-	-
nad7i140	+	+	+	+	+	-
nad7i209	+	+	+	+	+	+
nad7i676	-	+	-	-	-	-
nad7i917	+	+	-	-	-	-
rpl2i917	-	-	-	-	-	-
rps3i74	+	-	-	-	-	-
rps10i235	-	-	-	-	-	-

[1] *Monsonia* and *Geranium* data from Park et al. (2015)

Table S2. Sequence and assembly data for Geraniales

	Sequence Data		Velvet Mitochondrial Genome Assembly Results				
Taxa	DNA	RNA	Kmer	Expected Coverage	# of Contigs	Min Genome Size (kb)	Kmer Coverage
Pelargonium citronellum	SRX189589	SRX910186	71	200	14	1800	28-49
Pelargonium x hortorum	SRX189591	SRX298050	71	20	25	4100	12-14
Geranium maderense	SRX189585	-	75	20	8	650	17-20
Geranium incanum	-	SRX910268					
Monsonia emarginata	SRX189588	SRX910269	71	50	15	620	13-27
Erodium moschatum	SRX189582	-	75	50	5	240	29-35
Erodium texanum	-	SRX907966					
Hypseocharis bilobata	SRX189586	SRX910270	55	20	46	2600	15-20
Melianthus villosus	SRX189587	SRX910793	71	50	6	460	34-48

Table S3. Taxa used in the phylogenetic analysis of *matR*

Group	Species	Accession Number	Reference
Geraniales	Erodium moschatum	KX824067	this study
Geraniales	Geranium maderense	KP940515	Park et al. 2015
Geraniales	Hypseocharis bilobata	KX824070	this study
Geraniales	Melianthus villosus	KX824073	this study
Geraniales	Monsonia emarginata	KX824076	this study
Geraniales	Pelargonium citronellum	KX824108-KX824109	this study
Geraniales	Viviania marifolia	KP962581	Park et al. 2015
Other Rosids	Brassica oleracea	KJ820683	Grewe et al. 2014
Other Rosids	Carica papaya	EU431224	Rice et al. unpublished
Other Rosids	Citrullus lanatus	GQ856147	Alverson et al. 2010
Other Rosids	Cucurbita pepo	GQ856148	Alverson et al. 2010
Other Rosids	Lotus japonicus	JN872551	Kazakoff et al. 2012
Other Rosids	Malus x domestica	FR714868	Goremykin et al. 2012
Other Rosids	Millettia pinnata	JN872550	Kazakoff et al. 2012
Other Rosids	Raphanus sativus	AB694744	Tanaka et al. 2012
Other Rosids	Ricinus communis	HQ874649	Rivarola et al. 2011
Other Rosids	Vigna radiata	HM367685	Alverson et al. 2011
Other Rosids	Vitis vinifera	FM179380	Goremykin et al. 2008
Asterids	Ajuga reptans	NC_023103	Zhu et al. 2014
Asterids	Boea hygrometrica	JN107812	Zhang et al. 2011
Asterids	Daucus carota	JQ248574	Iorizzo et al. 2012
Asterids	Mimulus guttatus	JN098455	Mower et al. 2011
Asterids	Nicotiana tabacum	BA000042	Sugiyama et al. 2005
Caryophyllids	Beta vulgaris	BA000009	Kubo et al. 2000
Caryophyllids	Silene conica	JF750627	Sloan et al. 2012
Caryophyllids	Silene latifolia	HM562727	Sloan et al. 2010
Caryophyllids	Silene noctiflora	JF750486	Sloan et al. 2012
Caryophyllids	Silene vulgaris	JF750429	Sloan et al. 2012
Monocots	Bambusa oldhamii	EU365401	Lin et al. unpublished
Monocots	Oryza sativa	DQ167399	Tian et al. 2006
Monocots	Phoenix dactylifera	JN375330	Fang et al. 2012
Monocots	Sorghum bicolor	DQ984518	Allen et al. unpublished
Monocots	Spirodela polyrhiza	JQ804980	Wang et al. 2012
Monocots	Tripsacum dactyloides	DQ984517	Allen et al. unpublished
Monocots	Triticum aestivum	AP008982	Ogihara et al. 2005
Monocots	Zea mays	AY506529	Clifton et al. 2004
Magnoliids	Liriodendron tulipifera	KC821969	Richardson et al. 2013
Amborellales	Amborella trichopoda	KF754803	Rice et al. 2013

Figure S1. Results of the phylogenetic analysis with the full set of angiosperm *matR* sequences.

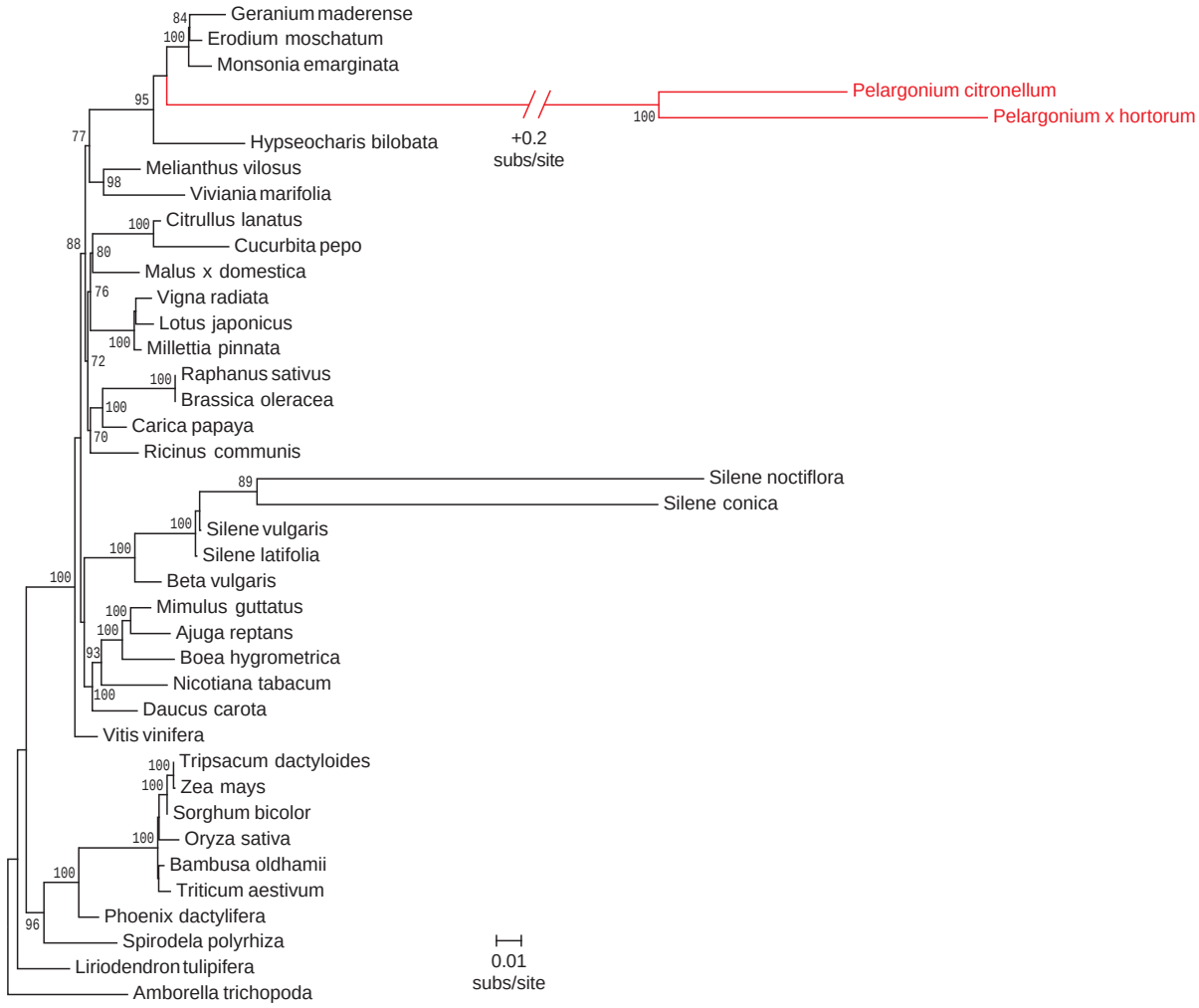

Figure S2. Schematic amino acid alignment of angiosperm mitochondrial *matR* sequences and the nuclear located *nmatRT* and *nmatRX* of *Pelargonium*. Highly conserved positions (i.e. identical amino acids in the alignment) are highlighted in black, all other positions are grey. Thin grey lines represent alignment gaps. Orange and yellow boxes show the location of maturase domains RT-2 to RT-7 and domain X, respectively.