Supplement to: T. H. Samigullin, M. D. Logacheva, E. I. Terenteva, G. V. Degtjareva, and C. M. Vallejo-Roman, Plastid Genome of *Seseli montanum*: Complete Sequence and Comparison with Plastomes of Other Members of the Apiaceae Family (ISSN 0006-2979, Biochemistry (Moscow), 2016, Vol. 81, No. 9, pp. 981-985)

Table S1. List of primers used for gap closure and junction verification

Primer names	Sequence	Position in plastome	Used for
Ses1:1909U21	F: TTTGATCCAATAGCGTTCCGT	146,635-146,655	PCR
Ses1:2179L20	R: TGTTCTATCAAGAGGGCGGT	893-912	PCR
SePa2:65750U20	F: ACAGCAACGCACTTTCAATC	66,190-66,209	PCR
SePa2:65965L20	R: CTCGTTCTTGTAGTTAGGTC	66,420-66,439	PCR
Ses3:18710U22	F: TGAGTTCTAGTATCATAAGTGT	84,989-85,010	PCR
Ses3:19323L21	R: GTGATTGAGTTCAGTAGTTCC	86,464-86,484	PCR
Ses4:12733U21	F: CTTCGAGAATCAGAAAGATCC	99,077-99,097	PCR
Ses4:12933L20	R: TATTTCGTACCCTTCGCTCA	99,262-99,281	PCR
Ses5:1887U18	F: GGGCGCAGCTCATGAAGG	128,998-129,015	PCR
Ses5:2042L22	R: GCTTGTGATAAAGAGGATAAGT	127,348-127,369	PCR
Ses1:12539U20	AAATGCCCTACCTTTGAGTG	86,621-86,640	sequencing
Ses1:13201L21	AGGCCGTGTAATTAATACTTG	1081-1101	sequencing

Table S2. Genes encoded in the *Seseli montanum* plastome

Functional category	Group of genes	Gene name
Self-replication	rRNA genes	*rrn16*[c], *rrn23*[c], *rrn4.5*[c], *rrn5*[c]
	tRNA genes	*trnA-UGC*[a,c], *trnC-GCA*, *trnD-GUC*, *trnE-UUC*, *trnF-GAA*, *trnG-GCC*, *trnG-UCC*[a], *trnH-GUG*, *trnI-CAU*[c], *trnI-GAU*[a,c], *trnK-UUU*[a], *trnL-CAA*[c], *trnL-UAA*[a], *trnL-UAG*, *trnfM-CAU*, *trnM-CAU*, *trnN-GUU*[c], *trnP-UGG*, *trnQ-UUG*, *trnR-ACG*[c], *trnR-UCU*, *trnS-GCU*, *trnS-GGA*, *trnS-UGA*, *trnT-GGU*, *trnT-UGU*, *trnV-GAC*[c], *trnV-UAC*[a], *trnW-CCA*, *trnY-GUA*
	ribosomal small subunit	*rps2*, *rps3*, *rps4*, *rps7 c*, *rps8*, *rps11*, *rps12_5'-end*, *rps12_3'-end*[a,c], *rps14*, *rps15*, *rps16*[a], *rps18*, *rps19*
	ribosomal large subunit	*rpl2*[a,c], *rpl14*, *rpl16*[a], *rpl20*, *rpl22*, *rpl23*[c], *rpl32*, *rpl33*, *rpl36*
	DNA-dependent RNA polymerase	*rpoA*, *rpoB*, *rpoC1*[a], *rpoC2*
Photosynthesis	large subunit of RUBISCO	*rbcL*
	photosystem I	*psaA*, *psaB*, *psaC*, *psaI*, *psaJ*, *ycf3*[b]
	photosystem II	*psbA*, *psbB*, *psbC*, *psbD*, *psbE*, *psbF*, *psbH*, *psbI*, *psbJ*, *psbK*, *psbL*, *psbM*, *psbN*, *psbT*, *psbZ*
	NADH dehydrogenase	*ndhA*[a], *ndhB*[a,c], *ndhC*, *ndhD*, *ndhE*, *ndhF*, *ndhG*, *ndhH*, *ndhI*, *ndhJ*, *ndhK*
	cytochrome *b/f* complex	*petA*, *petB*[a], *petD*[a], *petG*, *petL*, *petN*
	ATP synthase	*atpA*, *atpB*, *atpE*, *atpF*, *atpH*, *atpI*
Other	maturase	*matK*
	subunit of acetyl-CoA carboxylase	*accD*
	envelope membrane protein	*cemA*
	protease	*clpP*[b]
	translational initiation factor	*infA*
	c-type cytochrome synthesis	*ccsA*
	conserved open reading frames (ycf)	*ycf1*, *ycf2*

[a] Containing one intron.

[b] Containing two introns.

[c] Genes in the IR regions (i.e. have two copies in the plastome).