

**Appendix 1. Description of the JLA+ sequence characters varying among the cpDNA haplotypes of *Eucalyptus perriniana* and the GENBANK accession number where the sequence can be consulted**

BP <sup>A</sup> Mutation <sup>B</sup>	GENBANK no.	Haplotype																			
		CC41	CC56	CC58	CC59	CC60	CC61	CC63	CC64	CC65	CG31	CG32	S78	S81	S102	DQ915436	S103	DQ915437	DQ915434	ET18	ET19
52 A/C/T	DQ915426	A	A	A	A	C	A	A	A	A	A	A	A	A	T	A	A	A	A	A	A
65 AATTATT	AY620896	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	1	1	1	1
74 POLY A	DQ915427	2	2	2	2	C	C	2	2	C	2	2	6	6	6	5	2	2	2	2	2
96 TTATTATTCA <sub>5</sub> TA - GAGTAATTAATCA <sub>5</sub>	DQ915428	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	0	0
144 C	DQ915429	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
163 AAAAATAGG - AGTAATTAAT	DQ915430	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
187 C/G/?	DQ915431	G	G	G	G	G	G	G	G	C	C	?	?	?	?	?	?	?	?	?	?
187 SGAAT	DQ915432	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0
199 C/G	DQ915433	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G	G
291 TA	DQ915424	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0
293 TA	DQ915425	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
297 POLY T	AY620899	2	2	4	A	2	3	4	A	A	4	3	J	J	J	J	N	N	I		
315 A	DQ915436	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0
319 GG/CC = 1/2	DQ915437	2	2	2	2	2	2	2	2	2	2	2	2	2	2	2	1	1	2		
324 T	DQ915438	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	1	0	1
325 POLY A	S81	2	2	0	7	9	6	3	0	7	3	3	A	J	H	I	K	K	C		
379 C	S102	0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0
380 POLY A	DQ915439	6	5	4	4	3	5	7	4	4	7	7	1	1	1	1	5	5	6		
485 G/T	ET18	T	T	G	T	T	T	G	T	T	T	T	T	T	T	T	T	T	T	T	
486 A/C	ET19	A	A	A	A	C	C	A	A	A	A	A	A	A	A	A	A	A	A	A	
512 TAACATTTCTA - TCTTAATTATGAG	I22	1	1	1	1	1	1	1	1	1	1	1	0	0	0	0	0	0	0	0	0
630 A	DQ915435	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
648 POLY A	DQ915436	3	4	4	3	4	6	3	4	3	3	3	4	4	4	4	5	5	4		
AAAGGGTTGAAAA																					
741 GAATGTATATAAA		0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0
TTC																					
AAAGGGTTGAAAA																					
886 GAATGTAGATAAA		0	0	0	0	0	0	0	0	0	0	0	1	1	1	1	0	0	0	0	0
TTC																					
1051 CTTCTTaTGTTGA - AGTAAgAAAAAA		1	0	0	0	0	1	0	1	0	0	1	1	0	0	0	0	0	0	0	0

<sup>A</sup>Base pair number in a larger sequence alignment available from the authors on request.

<sup>B</sup>Poly A/T tracts were coded as multistate characters. Codes for all known states are available from the authors on request.