

Table S6. Tandem repeats in the *D. Chrysotoxum* mitogenome

Indices	Period Size	Copy Number	Consensus Size	Percent Matches	Percent Indels	Score	A	C	G	T	Entropy (0-2)
81039--81066	13	2.2	13	100	0	56	25	7	14	53	1.66
133196--133220	12	2.1	12	100	0	50	20	24	8	48	1.76
170971--171010	17	2.4	16	91	4	62	67	15	5	12	1.38
230640--230678	21	1.9	19	90	10	60	12	25	7	53	1.65
304272--304300	15	1.9	15	100	0	58	62	0	20	17	1.33
315553--315631	31	2.6	31	96	4	144	59	2	12	25	1.46
317917--317953	19	1.9	19	94	0	65	27	10	5	56	1.55
319814--319845	11	2.9	11	90	0	55	78	0	18	3	0.89
391383--391412	15	2.0	15	100	0	60	46	0	20	33	1.51
396962--396999	18	2.1	18	95	0	67	36	44	13	5	1.66
401285--401314	15	2.0	15	93	0	51	6	16	13	63	1.50
401894--401923	15	2.0	15	100	0	60	20	33	0	46	1.51
429412--429441	15	2.0	15	100	0	60	46	0	20	33	1.51
434991--435028	18	2.1	18	95	0	67	36	44	13	5	1.66
439314--439343	15	2.0	15	93	0	51	6	16	13	63	1.50
439923--439952	15	2.0	15	100	0	60	20	33	0	46	1.51
507027--507056	6	4.8	6	92	8	51	30	33	20	16	1.94
547863--547888	13	2.0	13	100	0	52	30	7	15	46	1.74
567076--567105	15	2.0	15	100	0	60	46	0	33	20	1.51

Parameters: Total length (Period size * Copy number) >= 30 and Percent Matches >= 90%