



Supplementary Figure S1. Schematic of the eight *cis*-splicing genes in the *A. remotiflora* chloroplast genome. The genes are arranged from top to bottom on the *A. remotiflora* chloroplast genome, and arrows indicate the sense direction of the gene. The gene structures showed that exon regions are displayed in black color box while introns are indicated in white.

Supplementary Table S1. Characteristics of simple sequence repeats in *A. remotiflora*.

Number	Type	Structure	Size(bp)	Start	End
1	p2	(AT)6	12	15094	15105
2	p1	(G)10	10	28936	28945
3	p1	(T)12	12	31027	31038
4	p1	(T)14	14	53820	53833
5	p1	(G)10	10	56946	56955
6	p1	(T)10	10	63516	63525
7	p1	(T)10	10	73299	73308
8	p1	(T)10	10	74248	74257
9	p1	(T)11	11	79394	79404
10	p2	(TA)6	12	86102	86113
11	p1	(A)11	11	88518	88528
12	p1	(T)10	10	90736	90745
13	p1	(T)10	10	99924	99933
14	p3	(AAT)5	15	100812	100826
15	p1	(A)10	10	104232	104241
16	p1	(T)10	10	120770	120779
17	p1	(A)10	10	124219	124228
18	p1	(A)13	13	124626	124638
19	p1	(A)12	12	128260	128271
20	p1	(A)10	10	133366	133375
21	p1	(T)10	10	149504	149513
22	p1	(T)12	12	154608	154619
23	p1	(T)13	13	158241	158253
24	p1	(T)10	10	158651	158660
25	p1	(A)10	10	162100	162109

Supplementary Table S2. Characteristics of the dispersed repeats in *A. remotiflora*.

First length	First start	Repeat type ¹⁾	Second length	Second start	Interval Distance	E-value
593	30318	D	593	117558	-3	0.00E+00
593	30318	P	593	164727	-3	0.00E+00
527	98569	D	527	121135	0	0.00E+00
527	98569	P	527	161216	0	0.00E+00
511	34849	P	511	139127	-1	0.00E+00
483	30547	D	483	117787	-3	6.92E-273
483	30547	P	483	164608	-3	6.92E-273
450	115032	D	450	129865	-2	9.21E-256
450	115032	P	450	152563	-2	9.21E-256
450	129865	P	450	167396	-2	9.21E-256
450	152563	D	450	167396	-2	9.21E-256
441	152572	D	441	167405	-1	3.51E-253
374	98208	D	374	120770	-1	6.49E-213
374	98208	P	374	161734	-1	6.49E-213
343	99924	D	343	100332	-1	2.74E-194
347	98061	D	347	121063	-3	1.94E-191
347	98061	P	347	161468	-3	1.94E-191
323	98325	D	323	121772	0	2.93E-185
323	98325	P	323	160783	0	2.93E-185
310	37181	P	310	43274	-3	2.61E-169
302	37070	P	302	43393	-3	1.58E-164
292	44458	P	292	56411	-2	5.17E-161
283	44467	P	283	56411	-1	3.01E-158
281	102362	D	281	102641	-3	5.60E-152
275	98133	D	275	98569	-3	2.15E-148
257	120887	D	257	121772	-1	1.23E-142
257	120887	P	257	160849	-1	1.23E-142
257	121772	P	257	161734	-1	1.23E-142
257	160849	D	257	161734	-1	1.23E-142
254	30776	D	254	118016	-2	2.95E-138
254	30776	P	254	164608	-2	2.95E-138
256	98027	D	256	121029	-3	4.76E-137
256	98027	P	256	161593	-3	4.76E-137
245	30785	D	245	118025	-1	1.97E-135
245	30785	P	245	164608	-1	1.97E-135

242	97766	D	242	97847	-3	1.08E-128
236	23807	D	236	141531	-3	4.10E-125
231	23586	D	231	141310	-3	3.94E-122
229	98217	D	229	98653	-3	6.13E-121
229	98217	D	229	121219	-3	6.13E-121
229	98217	P	229	161430	-3	6.13E-121
229	98653	D	229	120779	-3	6.13E-121
229	98653	P	229	161870	-3	6.13E-121
229	120779	D	229	121219	-3	6.13E-121
229	120779	P	229	161430	-3	6.13E-121
229	121219	P	229	161870	-3	6.13E-121
229	161430	D	229	161870	-3	6.13E-121
225	23818	D	225	141542	-2	6.68E-121
224	23894	D	224	141618	-3	5.88E-118

* ¹⁾ Repeat type (D: direct matches; P: palindromic matches)

Supplementary Table S3. Characteristics of the tandem repeats in *A. remotiflora*.

Start	End	P ¹⁾ Size	Copy Num.	C ²⁾ Size	Match ³⁾	Indels	Score	Percent composition				Entropy (0-2)
								A	C	G	T	
5623	5654	16	2	16	93	0	55	40	18	3	37	1.67
5766	5799	17	1.9	18	94	5	61	67	0	20	11	1.21
5766	5799	9	3.9	9	92	7	61	67	0	20	11	1.21
6738	7011	114	2.4	114	87	1	368	27	22	23	26	2
8589	8635	23	2	23	100	0	94	27	12	8	51	1.69
8624	8648	13	1.9	13	100	0	50	44	0	8	48	1.32
28346	28551	70	2.9	70	91	1	333	26	20	16	36	1.93
33505	33570	24	3	22	81	12	82	28	9	28	33	1.88
35819	35858	20	2	20	90	0	62	50	2	17	30	1.59
37948	37998	21	2.3	21	83	10	57	62	5	19	11	1.49
38240	38271	17	1.9	16	93	6	55	25	25	6	43	1.77
43192	43242	19	2.7	19	72	24	54	15	17	7	58	1.6
46542	46584	22	2	21	86	13	61	30	6	11	51	1.65
46637	46684	25	1.9	25	100	0	96	35	8	14	41	1.76
49989	50014	13	2	13	100	0	52	46	0	15	38	1.46
53990	54014	12	2.1	12	100	0	50	40	0	24	36	1.55
56325	56417	20	4.7	20	100	0	186	15	35	5	44	1.69
60260	60285	13	2	13	100	0	52	30	23	0	46	1.53
60341	60445	21	5	21	100	0	210	61	19	9	9	1.53
60565	60733	84	2	84	97	0	320	27	28	15	28	1.96
60722	61207	99	4.9	100	94	1	829	29	22	8	39	1.84
62213	62257	20	2.2	20	96	0	81	46	4	31	17	1.68
69322	69399	39	2	39	92	0	129	24	14	24	37	1.92
79891	79926	17	2.1	17	89	0	54	27	19	22	30	1.98
88293	88336	21	2.1	21	100	0	88	29	9	34	27	1.87
94006	94037	16	2	16	100	0	64	43	18	6	31	1.75
97726	98121	81	4.9	81	97	0	738	24	15	12	46	1.81
98112	98161	12	3.8	12	80	15	55	6	20	0	74	1.03
98552	98597	12	3.8	12	75	18	51	6	19	0	73	1.04
100732	100817	21	3.9	21	72	14	82	34	5	9	50	1.59
101293	101467	87	2	87	100	0	350	38	18	25	18	1.93
101452	101480	15	1.9	15	100	0	58	48	20	31	0	1.5
102063	102126	33	1.9	33	100	0	128	39	3	28	29	1.72
103271	103387	39	3	39	78	2	101	26	26	22	24	2
103499	103982	51	9.5	51	81	6	383	32	16	18	33	1.93
104529	104572	12	3.7	12	87	0	61	43	0	43	13	1.44
104558	104608	9	5.3	9	80	13	57	37	9	41	11	1.75
104593	104651	24	2.5	24	97	0	109	40	5	33	20	1.74
104695	104726	12	2.7	12	100	0	64	59	15	0	25	1.36
104707	104780	33	2.2	33	95	0	130	52	13	13	20	1.73
104855	104879	12	2.1	12	100	0	50	32	44	16	8	1.76
105919	105944	12	2.2	12	100	0	52	34	0	19	46	1.5

114769	115101	26	12.8	26	88	5	487	26	23	34	15	1.94
116845	116940	46	2.1	46	100	0	192	47	22	6	22	1.73
118402	118521	18	6.7	18	95	0	213	56	1	30	10	1.43
121114	121163	12	3.8	12	80	15	55	6	20	0	74	1.03
121999	122044	12	3.8	12	75	18	51	6	19	0	73	1.04
123079	123134	26	2.2	26	83	6	69	35	8	19	35	1.83
124852	124979	30	4.3	30	100	0	256	57	20	16	6	1.61
125377	125521	72	2	72	98	0	281	48	8	26	15	1.73
125884	125937	18	3.2	18	66	15	51	48	16	18	16	1.82
125950	126003	18	3.2	18	66	15	51	48	16	18	16	1.82
125728	126112	33	11.7	33	90	0	592	45	14	22	17	1.85
126482	126706	9	25	9	74	17	166	64	0	31	3	1.15
126482	126706	69	3.1	69	77	9	193	64	0	31	3	1.15
126483	126720	27	8.5	27	78	14	214	64	0	31	3	1.17
127408	127433	9	2.9	9	100	0	52	69	11	7	11	1.37
127556	127591	18	2	18	100	0	72	55	5	22	16	1.62
129864	129934	26	2.7	27	97	2	135	25	25	33	15	1.95
130804	130916	57	2	57	98	0	217	51	11	15	22	1.75
139988	140012	13	1.9	13	100	0	50	44	0	24	32	1.54
140712	140771	30	2	30	100	0	120	40	13	30	16	1.87
151963	152075	57	2	57	98	0	217	22	15	11	51	1.75
152945	153015	26	2.7	27	95	4	135	15	33	25	25	1.95
155288	155323	18	2	18	100	0	72	16	22	5	55	1.62
155446	155471	9	2.9	9	100	0	52	11	7	11	69	1.37
156159	156395	27	8.4	27	79	14	203	3	31	0	64	1.17
156173	156397	9	25	9	74	17	166	3	31	0	64	1.15
156219	156349	69	1.9	69	85	3	183	4	31	0	63	1.2
156767	157151	33	11.7	33	90	0	592	17	22	14	45	1.85
156876	156929	18	3.2	18	64	15	51	16	18	16	48	1.82
156942	156995	18	3.2	18	64	15	51	16	18	16	48	1.82
157358	157502	72	2	72	98	0	281	15	26	8	48	1.73
157900	158027	30	4.3	30	100	0	256	6	16	20	57	1.61
160573	160605	16	2.1	16	88	5	50	21	39	12	27	1.88
160835	160880	12	3.8	12	75	18	51	73	0	19	6	1.04
161716	161765	12	3.8	12	78	17	55	74	0	20	6	1.03
164289	164348	27	2.3	27	80	11	70	0	35	3	61	1.12
164358	164477	18	6.7	18	95	0	213	10	30	1	56	1.43
165939	166034	46	2.1	46	100	0	192	22	6	22	47	1.73
167778	168110	26	12.8	26	88	5	487	15	34	23	26	1.94

* ¹⁾ P size: Period Size(bp), ²⁾ C size: Consensus Size(bp), ³⁾ Match: Percent Matches