

**Givnish et al. – American Journal of Botany – Appendix S7.** Lengths, positions, and names of coding and non-coding loci included in Zingiberales analysis.

Position in plastome	Locus/spacer name	Aligned length	Start address	Stop	Locus type	Locus ID	Spacers (0)
1	1	324	99170	99493	spacer	35	0
2	<i>psbA</i>	1062	36525	37586	gene	35	35
3	2	392	99494	99885	spacer	12	0
4	<i>matK</i>	1641	14010	15650	gene	12	12
5	<i>trnK-UUUU</i> tRNA	72	96305	96376	gene	84	84
6	3	1565	99886	10145	spacer	73	0
7	<i>rps16_w_intron</i>	1555	67743	69297	gene	73	73
8	4_5	3602	169562	17316	spacer	44	0
9	<i>psbK</i>	186	42441	42626	gene	44	44
10	6	850	101451	10230	spacer	42	0
11	<i>psbI</i>	112	42206	42317	gene	42	42
12	7_8	3228	173164	17639	spacer	86	0
13	<i>trnG-GCC_w_intron</i>	937	94043	94979	gene	86	86
14	9	281	102301	10258	spacer	84	0
15	<i>trnR-UCU</i> tRNA	72	97743	97814	gene	84	84
16	10	227	102582	10280	spacer	2	0
17	<i>atpA</i>	1524	2180	3703	gene	2	2
18	11	112	102809	10292	spacer	5	0
19	<i>atpF_w_intron</i>	1742	5626	7367	gene	5	5
20	12	891	102921	10381	spacer	6	0
21	<i>atpH</i>	246	7368	7613	gene	6	6
22	13	2031	103812	10584	spacer	7	0
23	<i>atpI</i>	759	7614	8372	gene	7	7
24	14	511	105843	10635	spacer	64	0
25	<i>rps2</i>	740	62939	63678	gene	64	64
26	15	488	106354	10684	spacer	63	0
27	<i>rpoC2</i>	4484	58455	62938	gene	63	63
28	16	260	106842	10710	spacer	62	0
29	<i>rpoC1_w_intron</i>	3165	55290	58454	gene	62	62
30	17	31	107102	10713	spacer	61	0
31	<i>rpoB</i>	3342	51948	55289	gene	61	61
32	18	2084	107133	10921	spacer	84	0
33	<i>trnC-GCA</i> tRNA	73	93675	93747	gene	84	84
34	19	1710	109217	11092	spacer	29	0

35	<i>petN</i>	90	31485	31574	gene	29	29
36	20	2088	110927	11301	spacer	46	0
37	<i>psbM</i>	105	42744	42848	gene	46	46
38	21	1612	113015	11462	spacer	84	0
39	<i>trnD-GUC</i> tRNA	74	93748	93821	gene	84	84
40	22	738	114627	11536	spacer	84	0
41	<i>trnY-GUA</i> tRNA	84	99086	99169	gene	84	84
42	23	77	115365	11544	spacer	84	0
43	<i>trnE-UUC</i> tRNA	73	93822	93894	gene	84	84
44	24	1174	115442	11661	spacer	84	0
45	<i>trnT-GGU</i> tRNA	72	97995	98066	gene	84	84
46	25	2383	116616	11899	spacer	38	0
47	<i>psbD</i>	1062	40536	41597	gene	38	38
48	<i>psbC</i>	1422	39114	40535	gene	37	37
49	26	228	118999	11922	spacer	84	0
50	<i>trnS-UGA</i> tRNA	93	97902	97994	gene	84	84
51	27	531	119227	11975	spacer	49	0
52	<i>psbZ</i>	189	43089	43277	gene	49	49
53	28	400	119758	12015	spacer	84	0
54	<i>trnG-UCC</i> tRNA	71	94980	95050	gene	84	84
55	29	357	120158	12051	spacer	84	0
56	<i>trnM-CAU</i> tRNA	75	93968	94042	gene	84	84
57	30	253	120515	12076	spacer	71	0
58	<i>rps14</i>	311	67141	67451	gene	71	71
59	31	231	120768	12099	spacer	31	0
60	<i>psaB</i>	2205	33828	36032	gene	31	31
61	32	25	120999	12102	spacer	30	0
62	<i>psaA</i>	2253	31575	33827	gene	30	30
63	33	1501	121024	12252	spacer	78	0
64	<i>ycf3_w_intron</i>	2546	85061	87606	gene	78	78
65	34	868	122525	12339	spacer	84	0
66	<i>trnS-GGA</i> tRNA	87	97815	97901	gene	84	84
67	35	549	123393	12394	spacer	66	0
68	<i>rps4</i>	648	64645	65292	gene	66	66
69	36	742	123942	12468	spacer	84	0
70	<i>trnT-UGU</i> tRNA	73	98067	98139	gene	84	84
71	37	2140	124684	12682	spacer	87	0
72	<i>trnL-UAA_w_intron</i>	896	96462	97357	gene	87	87

73	38	522	126824	12734	spacer	84	0
74	<i>trnF-GAA</i> tRNA	73	93895	93967	gene	84	84
75	39	1208	127346	12855	spacer	22	0
76	<i>ndhJ</i>	480	27675	28154	gene	22	22
77	40	146	128554	12869	spacer	23	0
78	<i>ndhK</i>	923	28155	29077	gene	23	23
79	<i>ndhC</i>	363	20959	21321	gene	15	15
80	41	3061	128700	13176	spacer	88	0
81	<i>trnV-UAC_w_intron</i>	800	98212	99011	gene	88	88
82	42	237	131761	13199	spacer	84	0
83	<i>trnM-CAU</i> tRNA	74	97444	97517	gene	84	84
84	43	301	131998	13229	spacer	4	0
85	<i>atpE</i>	413	5213	5625	gene	4	4
86	<i>atpB</i>	1509	3704	5212	gene	3	3
87	44	1847	132299	13414	spacer	50	0
88	<i>rbcL</i>	1467	43278	44744	gene	50	50
89	45	1932	134146	13607	spacer	1	0
90	<i>accD</i>	2179	1	2179	gene	1	1
91	46	1504	136078	13758	spacer	33	0
92	<i>psaI</i>	111	36279	36389	gene	33	33
93	47	507	137582	13808	spacer	79	0
94	<i>ycf4</i>	567	87607	88173	gene	79	79
95	48	1170	138089	13925	spacer	9	0
96	<i>cemA</i>	701	9456	10156	gene	9	9
97	49	356	139259	13961	spacer	24	0
98	<i>petA</i>	963	29078	30040	gene	24	24
99	50	1894	139615	14150	spacer	43	0
100	<i>psbJ</i>	123	42318	42440	gene	43	43
101	51	138	141509	14164	spacer	45	0
102	<i>psbL</i>	117	42627	42743	gene	45	45
103	52	22	141647	14166	spacer	40	0
104	<i>psbF</i>	120	41850	41969	gene	40	40
105	53	16	141669	14168	spacer	39	0
106	<i>psbE</i>	252	41598	41849	gene	39	39
107	54	2540	141685	14422	spacer	28	0
108	<i>petL</i>	101	31384	31484	gene	28	28
109	55	226	144225	14445	spacer	27	0
110	<i>petG</i>	114	31270	31383	gene	27	27

111	56	185	144451	14463	spacer	84	0
112	<i>trnW</i> -CCA tRNA	74	99012	99085	gene	84	84
113	57	257	144636	14489	spacer	84	0
114	<i>trnP</i> -UGG tRNA	74	97590	97663	gene	84	84
115	58	640	144893	14553	spacer	34	0
116	<i>psaJ</i>	135	36390	36524	gene	34	34
117	59	1025	145533	14655	spacer	58	0
118	<i>rpl33</i>	366	50391	50756	gene	58	58
119	60	382	146558	14693	spacer	74	0
120	<i>rps18</i>	659	69298	69956	gene	74	74
121	61	535	146940	14747	spacer	54	0
122	<i>rpl20</i>	463	48874	49336	gene	54	54
123	62	952	147475	14842	spacer	70	0
124	<i>rps12</i>	375	66766	67140	gene	70	70
125	62a	297	176392	17668	spacer	10	0
126	<i>clpP_w_intron</i>	3589	10157	13745	gene	10	10
127	63	717	148427	14914	spacer	36	0
128	<i>psbB</i>	1527	37587	39113	gene	36	36
129	64	249	149144	14939	spacer	48	0
130	<i>psbT</i>	108	42981	43088	gene	48	48
131	65	77	149393	14946	spacer	47	0
132	<i>psbN</i>	132	42849	42980	gene	47	47
133	66	133	149470	14960	spacer	41	0
134	<i>psbH</i>	236	41970	42205	gene	41	41
135	67	1440	149603	15104	spacer	25	0
136	<i>petB</i>	668	30041	30708	gene	25	25
137	68	1450	151043	15249	spacer	26	0
138	<i>petD</i>	561	30709	31269	gene	26	26
139	69	420	152493	15291	spacer	60	0
140	<i>rpoA</i>	1077	50871	51947	gene	60	60
141	70	109	152913	15302	spacer	69	0
142	<i>rps11</i>	456	66310	66765	gene	69	69
143	71	310	153022	15333	spacer	59	0
144	<i>rpl36</i>	114	50757	50870	gene	59	59
145	72	168	153332	15349	spacer	11	0
146	<i>infA</i>	264	13746	14009	gene	11	11
147	73	200	153500	15369	spacer	68	0
148	<i>rps8</i>	417	65893	66309	gene	68	68

149	74	467	153700	15416	spacer	52	0
150	<i>rpl14</i>	375	46301	46675	gene	52	52
151	75	186	154167	15435	spacer	53	0
152	<i>rpl16_w_intron</i>	2198	46676	48873	gene	53	53
153	76	247	154353	15459	spacer	65	0
154	<i>rps3</i>	966	63679	64644	gene	65	65
155	77	131	154600	15473	spacer	55	0
156	<i>rpl22</i>	498	49337	49834	gene	55	55
157	78	469	154731	15519	spacer	75	0
158	<i>rps19</i>	518	69957	70474	gene	75	75
159	79	350	155200	15554	spacer	84	0
160	<i>trnH-GUG</i> tRNA	76	95051	95126	gene	84	84
161	80	60	155550	15560	spacer	51	0
162	<i>rpl2_w_intron</i>	1556	44745	46300	gene	51	51
163	81	18	155610	15562	spacer	56	0
164	<i>rpl23</i>	329	49835	50163	gene	56	56
165	82	194	155628	15582	spacer	85	0
166	<i>trnI-CAU</i> tRNA	74	95127	95200	gene	85	85
167	83	505	155822	15632	spacer	77	0
168	<i>ycf2</i>	7980	77081	85060	gene	77	77
169	84	1168	156327	15749	spacer	85	0
170	<i>trnL-CAA</i> tRNA	85	96377	96461	gene	85	85
171	85	693	157495	15818	spacer	14	0
172	<i>ndhB_w_intron</i>	2265	18694	20958	gene	14	14
173	86	329	158188	15851	spacer	67	0
174	<i>rps7</i>	600	65293	65892	gene	67	67
175	87a	72	176689	17676	spacer	85	0
176	<i>trnV-GAC</i> tRNA	72	98140	98211	gene	85	85
177	87b	2785	176761	17954	spacer	82	0
178	88	482	158517	15899	spacer	82	0
179	16S rRNA	1505	88399	89903	gene	82	82
180	89	365	158999	15936	spacer	89	0
181	<i>trnI-GAU_w_intron</i>	1104	95201	96304	gene	89	89
182	90	64	159364	15942	spacer	90	0
183	<i>trnA-UGC_w_intron</i>	920	92755	93674	gene	90	90
184	91	187	159428	15961	spacer	83	0
185	23S rRNA	2851	89904	92754	gene	83	83
186	92	103	159615	15971	spacer	80	0

				7			
187	4.5S rRNA	104	88174	88277	gene	80	80
188	93	252	159718	15996	spacer	81	0
				9			
189	5S rRNA	121	88278	88398	gene	81	81
190	94	324	159970	16029	spacer	85	0
				3			
191	<i>trnR</i> -ACG tRNA	79	97664	97742	gene	85	85
192	95	750	160294	16104	spacer	85	0
				3			
193	<i>trnN</i> -GUU tRNA	72	97518	97589	gene	85	85
194	96	508	161044	16155	spacer	76	0
				1			
195	<i>ycf1</i>	6606	70475	77080	gene	76	76
196	<i>ndhF</i>	2260	23140	25399	gene	18	18
197	97	1918	161552	16346	spacer	57	0
				9			
198	<i>rpl32</i>	227	50164	50390	gene	57	57
199	98	1705	163470	16517	spacer	85	0
				4			
200	<i>trnL</i> -UAG tRNA	86	97358	97443	gene	85	85
201	99	132	165175	16530	spacer	8	0
				6			
202	<i>ccsA</i>	1083	8373	9455	gene	8	8
203	100	631	165307	16593	spacer	16	0
				7			
204	<i>ndhD</i>	1512	21322	22833	gene	16	16
205	101	174	165938	16611	spacer	32	0
				1			
206	<i>psaC</i>	246	36033	36278	gene	32	32
207	102	1306	166112	16741	spacer	17	0
				7			
208	<i>ndhE</i>	306	22834	23139	gene	17	17
209	103	409	167418	16782	spacer	19	0
				6			
210	<i>ndhG</i>	535	25400	25934	gene	19	19
211	104	676	167827	16850	spacer	21	0
				2			
212	<i>ndhI</i>	552	27123	27674	gene	21	21
213	105	142	168503	16864	spacer	13	0
				4			
214	<i>ndhA_w_intron</i>	3043	15651	18693	gene	13	13
215	<i>ndhH</i>	1188	25935	27122	gene	20	20
216	106	142	168645	16878	spacer	20	0
				6			
217	<i>rps15</i>	291	67452	67742	gene	72	72
218	107	775	168787	16956	spacer	72	0
				1			