

Table S1. 33 regions of the four *Ilex* cp genome sequence alignment (window of 600 sites) with significantly high (above 0.006) nucleotide diversity and different sequence identity (%) based on nucleotide sequence of *I. integra*.

Window	<i>Ilex</i> cp genome location	Locus	Region	Sequence length (bp)	π	<i>I. rotunda</i>		<i>I. cornuta</i>		<i>I. x wandoensis</i>	
						Sequence Identity (%)	E value	Sequence Identity (%)	E value	Sequence Identity (%)	E value
315-914	251-850	<i>trnH^{GUG}-psbA</i>	LSC	600-664	0.011	99.06	0.0	99.67	0.0	99.67	0.0
1815-2423	1751-2359	<i>trnK^{UUU}-matK</i>	LSC	600-609	0.012	97.37	0.0	99.84	0.0	100	0.0
4325-5044	4261-4979	<i>matK-rps16</i>	LSC	600-720	0.015	98.23	5e-169	99.86	0.0	100	0.0
7206-7805	7193-7792	<i>rps16-trnQ^{UUG}</i>	LSC	600	0.026	97.50	0.0	100	0.0	100	0.0
10217-10816	10140-10739	<i>trnG^{UCC}</i>	LSC	600	0.014	98.67	0.0	99.83	0.0	100	0.0
10467-11071	10449-11049	<i>trnG^{GCC}-trnR^{UCU}</i>	LSC	601-604	0.021	98.01	0.0	99.83	0.0	99.83	0.0
12222-12823	12141-12740	<i>atpA-atpF</i>	LSC	600-602	0.008	98.84	0.0	99.83	0.0	99.83	0.0
14476-15080	14393-14993	<i>atpH-atpI</i>	LSC	601-605	0.012	98.67	0.0	99.17	0.0	99.17	0.0
18737-19336	18648-19247	<i>rpoC2</i>	LSC	600	0.008	99.17	0.0	99.83	0.0	99.83	0.0
25241-25840	25152-25751	<i>rpoB</i>	LSC	600	0.008	99.17	0.0	99.83	0.0	99.83	0.0
27991-28593	27902-28502	<i>rpoB-trnC^{GCA}</i>	LSC	600-603	0.017	98.17	0.0	99.67	0.0	99.67	0.0
30246-30851	30154-30753	<i>petN-psbM</i>	LSC	600-606	0.008	98.18	0.0	99.83	0.0	99.83	0.0
33524-34124	33407-34007	<i>trnT^{GGU}-psbD</i>	LSC	600-601	0.008	99.00	0.0	99.83	0.0	99.83	0.0
37527-38137	37408-38010	<i>trnS^{UGA}-psbZ</i>	LSC	602-609	0.008	98.35	0.0	98.36	0.0	98.52	0.0
38289-38896	38162-38765	<i>trnG^{CCC}-trnM^{CAU}</i>	LSC	604	0.012	97.86	0.0	99.67	0.0	99.67	0.0
43547-44146	43416-44015	<i>psaA-ycf3</i>	LSC	600	0.008	99.17	0.0	100	0.0	100	0.0
46552-47155	46416-47017	<i>ycf3-trnS^{GGA}</i>	LSC	600-604	0.008	98.84	0.0	99.67	0.0	100	0.0
48337-49297	48168-49125	<i>trnT^{UGU}</i>	LSC	360-716	0.014	97.36	0.0	99.13	2e-114	99.13	2e-114
48587-49547	48418-49375	<i>trnL^{UAA}</i>	LSC	602-958	0.012	97.81	0.0	99.63	0.0	99.63	0.0
52950-53553	52776-53375	<i>ndhC-trnV^{UAC}</i>	LSC	600-604	0.014	98.01	0.0	99.67	0.0	99.67	0.0
56961-57570	56778-57379	<i>atpB-rbcL</i>	LSC	602-610	0.010	98.35	0.0	98.52	0.0	100	0.0
68579-69187	68013-68612	<i>psbE-petL</i>	LSC	600-609	0.014	98.79	0.0	100	0.0	100	0.0
74372-74981	73771-74374	<i>clpP</i>	LSC	600-609	0.010	98.84	0.0	99.18	0.0	100	0.0
77132-77731	76525-77124	<i>psbB-psbN</i>	LSC	600	0.010	99.00	0.0	99.67	0.0	99.67	0.0
77382-77981	76775-77374	<i>psbT-psbH</i>	LSC	600	0.008	99.17	0.0	99.83	0.0	99.83	0.0
79633-80232	79026-79625	<i>petB-petD</i>	LSC	600	0.008	99.17	0.0	100	0.0	99.50	0.0
82885-83490	82277-82876	<i>rpl36-rps8</i>	LSC	600-606	0.008	99.17	0.0	99.01	0.0	99.01	0.0
85911-86516	85290-85889	<i>rpl16-rpl22</i>	LSC	600-606	0.008	98.18	0.0	99.83	0.0	99.83	0.0
116224-116825	115553-116152	<i>ndhF-rpl32</i>	SSC	600-602	0.010	98.50	0.0	99.83	0.0	99.83	0.0
117984-118583	117305-117904	<i>trnL^{UAG}-ccsA</i>	SSC	600	0.012	98.83	0.0	99.83	0.0	100	0.0
121240-121839	120557-121156	<i>ndhE</i>	SSC	600	0.010	99.16	0.0	99.83	0.0	99.83	0.0
123990-124589	123307-123906	<i>ndhA</i>	SSC	600	0.008	99.17	0.0	99.83	0.0	99.83	0.0
127494-128093	126807-127406	<i>ycf1</i>	SSC	600	0.014	98.67	0.0	100	0.0	100	0.0

Note: Locus = *I. integra* cp genome used as reference sequences to identity between *I. rotunda*, *I. cornuta*, and *I. x wandoensis*.