

Table S1 Genes encoded in the chloroplast genome of *Rosa chinensis* var. *spontanea*

Gene	Minimum	Maximum	Length(bp)	Direction	Exon I (bp)	Intron I (bp)	Exon II (bp)	Intron II (bp)	Exon III (bp)
<i>trnH-GUG</i>	89	162	74	reverse					
<i>psbA</i>	450	1,511	1,062	reverse					
<i>trnK-UUU</i>	1,776	4,345	2,570	reverse	35	2,498	37		
<i>matK</i>	2,069	3,580	1,512	reverse					
<i>rps16</i>	5,149	6,292	1,144	reverse	228	874	42		
<i>trnQ-UUG</i>	7,143	7,214	72	reverse					
<i>psbK</i>	7,634	7,819	186	forward					
<i>psbI</i>	8,058	8,168	111	forward					
<i>trnS-GCU</i>	8,333	8,420	88	reverse					
<i>trnG-GCC</i>	9,066	9,831	766	forward	23	695	48		
<i>trnR-UCU</i>	10,011	10,082	72	forward					
<i>atpA</i>	10,624	12,147	1,524	reverse					
<i>atpF</i>	12,200	12,754	555	reverse					
<i>atpH</i>	13,242	13,487	246	reverse					
<i>atpI</i>	14,420	15,163	744	reverse					
<i>rps2</i>	15,389	16,099	711	reverse					
<i>rpoC2</i>	16,340	20,494	4,155	reverse					
<i>rpoC1</i>	20,672	23,481	2,810	reverse	1,611	764	435		
<i>rpoB</i>	23,513	26,725	3,213	reverse					
<i>trnC-GCA</i>	27,944	28,014	71	forward					
<i>petN</i>	28,791	28,880	90	forward					
<i>psbM</i>	30,158	30,262	105	reverse					
<i>trnD-GUC</i>	30,785	30,858	74	reverse					
<i>trnY-GUA</i>	31,279	31,362	84	reverse					
<i>trnE-UUC</i>	31,422	31,494	73	reverse					
<i>trnT-GGU</i>	32,010	32,081	72	forward					
<i>psbD</i>	33,410	34,471	1,062	forward					
<i>psbC</i>	34,419	35,840	1,422	forward					
<i>trnS-UGA</i>	36,081	36,173	93	reverse					
<i>psbZ</i>	36,555	36,743	189	forward					
<i>trnG-UCC</i>	37,093	37,163	71	forward					
<i>trnM-CAU</i>	37,364	37,437	74	reverse					
<i>rps14</i>	37,600	37,902	303	reverse					
<i>psaB</i>	38,029	40,233	2,205	reverse					
<i>psaA</i>	40,259	42,511	2,253	reverse					
<i>ycf3</i>	43,222	45,235	2,014	reverse	153	766	228	741	126
<i>trnS-GGA</i>	46,113	46,199	87	forward					
<i>rps4</i>	46,492	47,097	606	reverse					
<i>trnT-UGU</i>	47,496	47,568	73	reverse					
<i>trnL-UAA</i>	48,749	49,379	631	forward	37	544	50		
<i>trnF-GAA</i>	49,785	49,857	73	forward					
<i>ndhJ</i>	50,588	51,064	477	reverse					
<i>ndhK</i>	51,187	51,867	681	reverse					
<i>ndhC</i>	51,911	52,273	363	reverse					
<i>trnV-UAC</i>	52,876	53,547	672	reverse	37	596	39		
<i>trnM-CAU</i>	53,715	53,787	73	forward					
<i>atpE</i>	53,964	54,365	402	reverse					
<i>atpB</i>	54,388	55,866	1,479	reverse					
<i>rbcL</i>	56,649	58,076	1,428	forward					
<i>accD</i>	58,740	60,203	1,464	forward					

<i>psaI</i>	60,671	60,784	114	forward					
<i>ycf4</i>	61,208	61,762	555	forward					
<i>cemA</i>	62,213	62,902	690	forward					
<i>petA</i>	63,111	64,073	963	forward					
<i>psbJ</i>	65,041	65,163	123	reverse					
<i>psbL</i>	65,300	65,416	117	reverse					
<i>psbF</i>	65,439	65,558	120	reverse					
<i>psbE</i>	65,568	65,819	252	reverse					
<i>petL</i>	67,079	67,174	96	forward					
<i>petG</i>	67,350	67,463	114	forward					
<i>trnW-CCA</i>	67,588	67,661	74	reverse					
<i>trnP-UGG</i>	67,806	67,879	74	reverse					
<i>psaJ</i>	68,317	68,451	135	forward					
<i>rpl33</i>	68,911	69,111	201	forward					
<i>rps18</i>	69,324	69,629	306	forward					
<i>rpl20</i>	69,923	70,276	354	reverse					
<i>rps12*</i>	71,057	143,071	908	mixed	114		232	536	26
<i>rps12*</i>	71,057	100,223	908	reverse	26	537	232		114
<i>clpP</i>	71,372	73,447	2,076	reverse					
<i>psbB</i>	73,899	75,425	1,527	forward					
<i>psbT</i>	75,611	75,712	102	forward					
<i>psbN</i>	75,787	75,918	132	reverse					
<i>psbH</i>	76,037	76,261	225	forward					
<i>petB</i>	76,384	77,819	1,436	forward	6	788	642		
<i>petD</i>	78,013	79,215	1,203	forward					
<i>rpoA</i>	79,416	80,411	996	reverse					
<i>rps11</i>	80,471	80,887	417	reverse					
<i>rpl36</i>	81,046	81,159	114	reverse					
<i>rps8</i>	81,640	82,044	405	reverse					
<i>rpl14</i>	82,230	82,598	369	reverse					
<i>rpl16</i>	82,737	84,120	1,384	reverse	399	976	9		
<i>rps3</i>	84,230	84,886	657	reverse					
<i>rpl22</i>	85,022	85,441	420	reverse					
<i>rps19</i>	85,534	85,812	279	reverse					
<i>rpl2</i>	85,880	87,385	1,506	reverse	434	681	391		
<i>rpl23</i>	87,404	87,685	282	reverse					
<i>trnI-CAU</i>	87,851	87,924	74	reverse					
<i>ycf2</i>	88,013	94,852	6,840	forward					
<i>trnL-CAA</i>	95,807	95,887	81	reverse					
<i>ndhB</i>	96,388	98,596	2,209	reverse	756	676	777		
<i>rps7</i>	98,910	99,377	468	reverse					
<i>trnV-GAC</i>	101,966	102,037	72	forward					
<i>rrn16</i>	102,265	103,755	1,491	forward					
<i>trnI-GAU</i>	104,053	105,078	1,026	forward	42	949	35		
<i>trnA-UGC</i>	105,143	106,027	885	forward	38	812	35		
<i>rrn23</i>	106,191	108,998	2,808	forward					
<i>rrn4.5</i>	109,097	109,199	103	forward					
<i>rrn5</i>	109,448	109,568	121	forward					
<i>trnR-ACG</i>	109,825	109,898	74	forward					
<i>trnN-GUU</i>	110,365	110,436	72	reverse					
<i>ndhF</i>	111,901	114,144	2,244	reverse					
<i>rpl32</i>	115,272	115,430	159	forward					
<i>trnL-UAG</i>	116,194	116,273	80	forward					

<i>ccsA</i>	116,368	117,333	966	forward			
<i>ndhD</i>	117,587	119,089	1,503	reverse			
<i>psaC</i>	119,214	119,459	246	reverse			
<i>ndhE</i>	119,702	120,007	306	reverse			
<i>ndhG</i>	120,247	120,777	531	reverse			
<i>ndhI</i>	121,167	121,670	504	reverse			
<i>ndhA</i>	121,754	124,062	2,309	reverse	540	1,217	552
<i>ndhH</i>	124,064	125,245	1,182	reverse			
<i>rps15</i>	125,349	125,621	273	reverse			
<i>ycf1</i>	126,011	131,737	5,727	reverse			
<i>trnN-GUU</i>	132,065	132,136	72	forward			
<i>trnR-ACG</i>	132,603	132,676	74	reverse			
<i>rrn5</i>	132,933	133,053	121	reverse			
<i>rrn4.5</i>	133,302	133,404	103	reverse			
<i>rrn23</i>	133,503	136,310	2,808	reverse			
<i>trnA-UGC</i>	136,474	137,358	885	reverse	35	812	38
<i>trnI-GAU</i>	137,423	138,448	1,026	reverse	35	949	42
<i>rrn16</i>	138,746	140,236	1,491	reverse			
<i>trnV-GAC</i>	140,464	140,535	72	reverse			
<i>rps7</i>	143,124	143,591	468	forward			
<i>ndhB</i>	143,905	146,113	2,209	forward	776	676	757
<i>trnL-CAA</i>	146,614	146,694	81	forward			
<i>ycf2</i>	147,649	154,488	6,840	reverse			
<i>trnI-CAU</i>	154,577	154,650	74	forward			
<i>rpl23</i>	154,816	155,097	282	forward			
<i>rpl2</i>	<1	>156590	1506	forward	391	681	404

* The *rps12* gene is a trans-spliced gene with the 50 end located in the LSC region and the duplicated 30 ends in the IR region.

Table S2 Size comparison of complete cp genomes of four rose species

Species	LSC	IRB	SSC	IRA	Total
<i>Rosa chinensis</i> var. <i>spontanea</i>	85910	25959	18762	25959	156590
<i>Rosa odorata</i> var. <i>gigantea</i>	85767	26053	18761	26053	156634
<i>Rosa roxburghii</i>	85852	26053	18791	26053	156749
<i>Rosa praelucens</i>	86313	26054	18765	26054	157186