

Table S1. Genes contents in the *C. monoica* and *C. sinensis* chloroplast genomes

Category	Gene groups	Gene Names
RNA genes	Transfer RNA genes (tRNA)	<i>trnA-UGC</i> ^a , <i>trnC-GCA</i> , <i>trnD-GUC</i> , <i>trnE-UUC</i> , <i>trnF-GAA</i> , <i>trnG-CAU</i> , <i>trnG-GCC</i> , <i>trnG-UCC</i> ⁺ , <i>trnH-GUG</i> , <i>trnI-CAU</i> ^{+,a} , <i>trnI-GAU</i> ^a , <i>trnK-UUU</i> ⁺ , <i>trnL-CAA</i> ^a , <i>trnL-UAA</i> ⁺ , <i>trnL-UAG</i> , <i>trnM-CAU</i> , <i>trnN-GUU</i> ^a , <i>trnP-UGG</i> , <i>trnQ-UUG</i> , <i>trnR-ACG</i> ^a , <i>trnR-UCU</i> , <i>trnS-GCU</i> , <i>trnS-GGA</i> , <i>trnS-UGA</i> , <i>trnT-GGU</i> , <i>trnT-UGU</i> , <i>trnV-GAC</i> ^a , <i>trnV-UAC</i> ⁺ , <i>trnW-CCA</i> , <i>trnY-GUA</i>
	Ribosomal RNA genes (rRNA)	<i>rrn4.5</i> ^a , <i>rrn5</i> ^a , <i>rrn16</i> ^a , <i>rrn23</i> ^a
Ribosomal proteins	Small sub-unit of ribosome	<i>rps2</i> , <i>rps3</i> , <i>rps4</i> , <i>rps7</i> ^a , <i>rps8</i> , <i>rps11</i> , <i>rps12</i> ^{+,a} , <i>rps14</i> , <i>rps15</i> , <i>rps16</i> ⁺ , <i>rps18</i> , <i>rps19</i>
Transcription Genes	Large sub-unit of ribosome	<i>rpl2</i> ^{+,a} , <i>rpl14</i> , <i>rpl16</i> ⁺ , <i>rpl20</i> , <i>rpl22</i> , <i>rpl23</i> ^a , <i>rpl32</i> , <i>rpl33</i> , <i>rpl36</i>
	DNA-dependent RNA polymerase	<i>rpoA</i> , <i>rpoB</i> , <i>rpoC1</i> ⁺ , <i>rpoC2</i>
Protein-coding genes	Photosystem I	<i>psaA</i> , <i>psaB</i> , <i>psaC</i> , <i>psaI</i> , <i>psaJ</i> , <i>ycf3</i> ⁺⁺
	Photosystem II	<i>psbA</i> , <i>psbB</i> , <i>psbC</i> , <i>psbD</i> , <i>psbE</i> , <i>psbF</i> , <i>psbH</i> , <i>psbI</i> , <i>psbJ</i> , <i>psbK</i> , <i>psbL</i> , <i>psbM</i> , <i>psbN</i> , <i>psbT</i> , <i>psbZ</i>
	Sub-unit of cytochrome	<i>petA</i> , <i>petB</i> ⁺ , <i>petD</i> ⁺ , <i>petG</i> , <i>petL</i> , <i>petN</i>
	Sub-unit of synthase	<i>atpA</i> , <i>atpB</i> , <i>atpE</i> , <i>atpF</i> ⁺ , <i>atpH</i> , <i>atpI</i>
	Large sub-unit of rubisco	<i>rbcL</i>
	NADH dehydrogenase	<i>ndhA</i> ⁺ , <i>ndhB</i> ^{+,a} , <i>ndhC</i> , <i>ndhD</i> , <i>ndhE</i> , <i>ndhF</i> , <i>ndhG</i> , <i>ndhH</i> , <i>ndhI</i> , <i>ndhJ</i> , <i>ndhK</i>
	ATP-dependent protease subunit P	<i>clpP</i> ⁺
Other genes	Cp envelope membrane protein	<i>cemA</i>
	C-type cytochrome synthesis	<i>ccsA</i>
	Translation initiation factor,	<i>infA</i>
	Maturase	<i>matK</i>
	Sub-unit acetyl-coA carboxylase	<i>accD</i>
	Hypothetical proteins	<i>ycf2</i> ^a , <i>ycf4</i> , <i>ycf15</i> ^a
	Component of TIC complex	<i>ycf1</i> ^a

^a Gene with multiple copies; ⁺Gene with one intron and ⁺⁺Gene with two introns

Table S2. Exons and introns lengths in *C. monoica* and *C. sinensis* chloroplast genomes

Gene	Location	Exon I (bp)		Intron I (bp)		Exon II (bp)		Intron II (bp)		Exon III (bp)	
		<i>C. m</i>	<i>C. s</i>	<i>C. m</i>	<i>C. s</i>	<i>C. m</i>	<i>C. s</i>	<i>C. m</i>	<i>C. s</i>	<i>C. m</i>	<i>C. s</i>
<i>atpF</i>	LSC	410	410	696	693	143	143				
<i>clpP1</i>	LSC	287	287	291	291	70	70				
<i>ndhA</i>	SSC	541	541	1037	1039	552	552				
<i>ndhB</i>	IR	757	757	678	678	774	774				
<i>petB</i>	LSC	5	5	805	801	641	641				
<i>petD</i>	LSC	7	7	742	741	474	474				
<i>rpl16</i>	LSC	398	398	1030	1030	8	8				
<i>rpl2</i>	IR	433	433	661	661	390	390				
<i>rpoC1</i>	LSC	1610	1610	736	743	431	431				
<i>rps12</i>	IR	25	25	539	539	231	231				
<i>rps16</i>	LSC	208	208	870	870	39	39				
<i>trnA-UGC</i>	IR	37	37	798	798	34	34				
<i>trnG-UCC</i>	LSC	22	22	684	685	47	47				
<i>trnI-GAU</i>	IR	36	36	946	946	34	34				
<i>trnK-UUU</i>	LSC	34	34	2460	2463	36	36				
<i>trnL-UAA</i>	LSC	34	34	490	490	49	49				
<i>trnV-UAC</i>	LSC	36	36	585	585	35	35				
<i>ycf3</i>	LSC	154	154	750	745	227	227	727	736	123	123

Table S3. Codon-anticodon recognition patterns and codon usage of the *C. monoica* chloroplast genome

Codon	Amino Acid	RSCU	tRNA	Codon	Amino Acid	RSCU	tRNA
UUU	Phe	1.24	trnF-GAA	UAU	Tyr	1.29	trnY-GUA
UUC	Phe	0.76		UAC	Tyr	0.71	
UUA	Leu	1.3	trnL-UAA	UAA	Stop	1.01	
UUG	Leu	1.37	trnL-CAA	UAG	Stop	0.85	
CUU	Leu	1.28	trnL-UAG	CAU	His	1.31	trnH-GUG
CUC	Leu	0.65		CAC	His	0.69	
CUA	Leu	0.82		CAA	Gln	1.32	trnQ-UUG
CUG	Leu	0.59		CAG	Gln	0.68	
AUU	Ile	1.41	trnI-GAU	AAU	Asn	1.3	trnN-GUU
AUC	Ile	0.83		AAC	Asn	0.7	
AUA	Ile	0.75	trnI-CAU	AAA	Lys	1.27	trnK-UUU
AUG	Met	1	trnM-CAU	AAG	Lys	0.73	
GUU	Val	1.4	trnV-GAC	GAU	Asp	1.37	trnD-GUC
GUC	Val	0.83		GAC	Asp	0.63	
GUA	Val	1.1		GAA	Glu	1.33	trnE-UUC
GUG	Val	0.67	trnV-UAC	GAG	Glu	0.67	
UCU	Ser	1.34	trnS-GGA	UGU	Cys	1.11	trnC-GCA
UCC	Ser	0.9		UGC	Cys	0.89	
UCA	Ser	1.42		UGA	Stop	1.14	
UCG	Ser	0.79	trnS-UGA	UGG	Trp	1	trnW-CCA
CCU	Pro	1.06	trnP-UGG	CGU	Arg	0.62	trnR-ACG
CCC	Pro	0.91		CGC	Arg	0.35	trnR-UCU
CCA	Pro	1.2		CGA	Arg	0.99	
CCG	Pro	0.82		CGG	Arg	0.76	
ACU	Thr	1		AGA	Arg	1.99	
ACC	Thr	0.98		AGG	Arg	1.29	
ACA	Thr	1.26	trnT-GGU	AGU	Ser	0.76	trnS-GCU
ACG	Thr	0.75	trnT-UGU	AGC	Ser	0.78	
GCU	Ala	1.16	trnA-UGC	GGU	Gly	0.88	trnG-GCC
GCC	Ala	0.87		GGC	Gly	0.66	
GCA	Ala	1.19		GGA	Gly	1.32	
GCG	Ala	0.78		GGG	Gly	1.13	trnG-UCC

Table S4. Codon-anticodon recognition patterns and codon usage of the *C. sinensis* chloroplast genome

Codon	Amino Acid	RSCU	tRNA	Codon	Amino Acid	RSCU	tRNA
UUU	Phe	1.21	trnF-GAA	UAU	Tyr	1.33	trnY-GUA
UUC	Phe	0.79		UAC	Tyr	0.67	
UUA	Leu	1.17	trnL-UAA	UAA	Stop	0.97	
UUG	Leu	1.38	trnL-CAA	UAG	Stop	0.98	
CUU	Leu	1.25	trnL-UAG	CAU	His	1.29	trnH-GUG
CUC	Leu	0.71		CAC	His	0.71	
CUA	Leu	0.87		CAA	Gln	1.3	trnQ-UUG
CUG	Leu	0.63		CAG	Gln	0.7	
AUU	Ile	1.33	trnI-GAU	AAU	Asn	1.29	trnN-GUU
AUC	Ile	0.77		AAC	Asn	0.71	
AUA	Ile	0.9	trnI-CAU	AAA	Lys	1.27	trnK-UUU
AUG	Met	1	trnM-CAU	AAG	Lys	0.73	
GUU	Val	1.26	trnV-GAC	GAU	Asp	1.44	trnD-GUC
GUC	Val	0.83		GAC	Asp	0.56	
GUA	Val	1.17		GAA	Glu	1.33	trnE-UUC
GUG	Val	0.73	trnV-UAC	GAG	Glu	0.67	
UCU	Ser	1.52	trnS-GGA	UGU	Cys	1.25	trnC-GCA
UCC	Ser	0.91		UGC	Cys	0.75	
UCA	Ser	1.3		UGA	Stop	1.06	
UCG	Ser	0.75	trnS-UGA	UGG	Trp	1	trnW-CCA
CCU	Pro	1.11	trnP-UGG	CGU	Arg	0.79	trnR-ACG
CCC	Pro	0.89		CGC	Arg	0.37	trnR-UCU
CCA	Pro	1.17		CGA	Arg	1.06	
CCG	Pro	0.83		CGG	Arg	0.79	
ACU	Thr	1.2		AGA	Arg	1.85	
ACC	Thr	0.97		AGG	Arg	1.14	
ACA	Thr	1.18	trnT-GGU	AGU	Ser	0.83	trnS-GCU
ACG	Thr	0.65	trnT-UGU	AGC	Ser	0.68	
GCU	Ala	1.44	trnA-UGC	GGU	Gly	1.03	trnG-GCC
GCC	Ala	0.75		GGC	Gly	0.56	
GCA	Ala	1.08		GGA	Gly	1.3	
GCG	Ala	0.73		GGG	Gly	1.11	trnG-UCC

Table S5. Predicted RNA editing site in the *C. monoica* and *C. sinensis* chloroplast genome.

Gene	Nucleotide position	Amino acid position	Triplet position within codon	Base conversion	Codon change	Amino acid conversion
<i>atpA</i>	791	264	2	C→U	CCC→CUC	P→L
<i>atpF</i>	92	31	2	C→U	CCA→CUA	P→L
<i>rps2</i>	248	83	2	C→U	UCA→UUA	S→L
<i>rpoC2</i>	3731	1244	2	C→U	UCA→UUA	S→L
<i>rpoB</i>	338	113	2	C→U	UCU→UUU	S→F
	551	184	2	C→U	UCA→UUA	S→L
	2426	809	2	C→U	UCA→UUA	S→L
<i>rps14</i>	80	27	2	C→U	UCA→UUA	S→L
	149	50	2	C→U	CCA→CUA	P→L
<i>psbL</i>	2	1	2	C→U	ACG→AUG	T→M
<i>petB</i>	611	204	2	C→U	CCA→CUA	P→L
<i>rpoA</i>	200	67	2	C→U	UCU→UUU	S→F
	830	277	2	C→U	UCA→UUA	S→L
<i>rpl23</i>	71	24	2	C→U	UCU→UUU	S→F
	89	30	2	C→U	UCA→UUA	S→L
<i>ndhB</i>	467	156	2	C→U	CCA→CUA	P→L
	586	196	1	C→U	CAU→UAU	H→Y
	611	204	2	C→U	UCA→UUA	S→L
	737	246	2	C→U	CCA→CUA	P→L
	746	249	2	C→U	UCU→UUU	S→F
	830	277	2	C→U	UCA→UUA	S→L
	836	279	2	C→U	UCA→UUA	S→L
	1481	494	2	C→U	CCA→CUA	P→L
<i>ndhF</i>	290	97	2	C→U	UCA→UUA	S→L
<i>ndhD</i>	2	1	2	C→U	ACG→AUG	T→M
	383*	128	2	C→U	UCG→UUG	S→L
	599	200	2	C→U	UCA→UUA	S→L
	674	225	2	C→U	UCG→UUG	S→L
	878	293	2	C→U	UCA→UUA	S→L
	1298	433	2	C→U	UCA→UUA	S→L
<i>ndhA</i>	41	114	2	C→U	UCA→UUA	S→L
	961	321	1	C→U	CCU→UCU	P→S
	1073	358	2	C→U	UCC→UUC	S→F

*The Prediction of RNA editing site in *ndhD* (383) were found only in *C. monoica*.

Table S6. Repeat sequences present in the *C. monoica* chloroplast genome.

SN	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	131	53132	P	IGS	57844	IGS	0 8.75e-70
2	109	91875	F	ycf2	91893	ycf2	0 1.54e-56
3	109	91875	P	ycf2	143623	ycf2	0 1.54e-56
4	109	91893	P	ycf2	143641	ycf2	0 1.54e-56
5	109	143623	F	ycf2	143641	ycf2	0 1.54e-56
6	91	91875	F	ycf2	91911	ycf2	0 1.06e-45
7	91	91875	P	ycf2	143623	ycf2	0 1.06e-45
8	91	91911	P	ycf2	143659	ycf2	0 1.06e-45
9	91	143623	F	ycf2	143659	ycf2	0 1.06e-45
19	73	91875	F	ycf2	91929	ycf2	0 7.27e-35
11	73	91875	P	ycf2	143623	ycf2	0 7.27e-35
12	73	91929	P	ycf2	143677	ycf2	0 7.27e-35
13	73	143623	F	ycf2	143677	ycf2	0 7.27e-35
14	55	91875	F	ycf2	91947	ycf2	0 4.99e-24
15	55	91875	P	ycf2	143623	ycf2	0 4.99e-24
16	55	91947	P	ycf2	143695	ycf2	0 4.99e-24
17	55	143623	F	ycf2	143695	ycf2	0 4.99e-24
18	52	90299	F	ycf2	90431	ycf2	0 3.20e-22
19	52	90299	P	ycf2	145142	ycf2	0 3.20e-22
20	52	90431	P	ycf2	145274	ycf2	0 3.20e-22
21	52	145142	F	ycf2	145274	ycf2	0 3.20e-22
22	44	73850	P	IGS	73850	IGS	0 2.09e-17
23	39	44505	F	ycf3 - intron	81274	rpl16 - intron	0 2.14e-14
24	39	85766	F	IGS	85802	IGS	0 2.14e-14
25	39	85766	P	IGS	149784	IGS	0 2.14e-14
26	39	85802	P	IGS	149820	IGS	0 2.14e-14
27	39	149784	F	IGS	149820	IGS	0 2.14e-14
28	38	58729	F	accD	58768	accD	0 8.58e-14
29	37	91875	F	ycf2	91965	ycf2	0 3.43e-13
30	37	91875	P	ycf2	143623	ycf2	0 3.43e-13
31	37	91965	P	ycf2	143713	ycf2	0 3.43e-13
32	37	143623	F	ycf2	143713	ycf2	0 3.43e-13
33	35	90394	F	ycf2	90412	ycf2	0 5.49e-12
34	35	90394	P	ycf2	145178	ycf2	0 5.49e-12
35	35	90412	P	ycf2	145196	ycf2	0 5.49e-12
36	35	145178	F	ycf2	145196	ycf2	0 5.49e-12
37	34	68896	F	rps18	68917	rps18	0 2.20e-11
38	33	88040	F	ycf2	88115	ycf2	0 8.78e-11
39	33	88040	P	ycf2	147477	ycf2	0 8.78e-11
40	33	88115	P	ycf2	147552	ycf2	0 8.78e-11
41	33	147477	F	ycf2	147552	ycf2	0 8.78e-11
42	31	58717	F	accD	58795	accD	0 1.41e-09
43	29	8210	P	IGS	46026	trnS-GGA	0 2.25e-08
44	29	39587	F	psaB	41811	psaA	0 2.25e-08
45	28	91816	F	ycf2	91879	ycf2	0 9.00e-08
46	28	91816	F	ycf2	91897	ycf2	0 9.00e-08
47	28	91816	F	ycf2	91915	ycf2	0 9.00e-08
48	28	91816	F	ycf2	91933	ycf2	0 9.00e-08
49	28	91816	F	ycf2	91951	ycf2	0 9.00e-08

Table S7. Repeat sequences present in the *C. sinensis* chloroplast genome.

SN	Repeat Size	Repeat Position 1	Repeat Type	Repeat Location 1	Repeat Position 2	Repeat Location 2	E-Value
1	109	92151	F	ycf2	92169	ycf2	0 1.54e-56
2	109	92151	P	ycf2	143896	ycf2	0 1.54e-56
3	109	92169	P	ycf2	143914	ycf2	0 1.54e-56
4	109	143896	F	ycf2	143914	ycf2	0 1.54e-56
5	91	92151	F	ycf2	92187	ycf2	0 1.06e-45
6	91	92151	P	ycf2	143896	ycf2	0 1.06e-45
7	91	92187	P	ycf2	143932	ycf2	0 1.06e-45
8	91	143896	F	ycf2	143932	ycf2	0 1.06e-45
9	73	58690	F	accD	58729	accD	0 7.29e-35
19	73	92151	F	ycf2	92205	ycf2	0 7.29e-35
11	73	92151	P	ycf2	143896	ycf2	0 7.29e-35
12	73	92205	P	ycf2	143950	ycf2	0 7.29e-35
13	73	143896	F	ycf2	143950	ycf2	0 7.29e-35
14	65	53085	P	IGS	57871	IGS	0 4.78e-30
15	55	92151	F	ycf2	92223	ycf2	0 5.01e-24
16	55	92151	P	ycf2	143896	ycf2	0 5.01e-24
17	55	92223	P	ycf2	143968	ycf2	0 5.01e-24
18	55	143896	F	ycf2	143968	ycf2	0 5.01e-24
19	52	90575	F	ycf2	90707	ycf2	0 3.21e-22
20	52	90575	P	ycf2	145415	ycf2	0 3.21e-22
21	52	90707	P	ycf2	145547	ycf2	0 3.21e-22
22	52	145415	F	ycf2	145547	ycf2	0 3.21e-22
23	45	58788	F	accD	58827	accD	0 5.25e-18
24	44	74149	P	IGS	74149	IGS	0 2.10e-17
25	39	44469	F	ycf3	81585	rp116 - intron	0 2.15e-14
26	37	53151	P	IGS	57833	IGS	0 3.44e-13
27	37	92151	F	ycf2	92241	ycf2	0 3.44e-13
28	37	92151	P	ycf2	143896	ycf2	0 3.44e-13
29	37	92241	P	ycf2	143986	ycf2	0 3.44e-13
30	37	143896	F	ycf2	143986	ycf2	0 3.44e-13
31	35	53202	F	IGS	57805	IGS	0 5.51e-12
32	34	58690	F	accD	58768	accD	0 2.20e-11
33	34	69200	F	rps18	69221	rps18	0 2.20e-11
34	33	88316	F	ycf2	88391	ycf2	0 8.81e-11
35	33	88316	P	ycf2	147750	ycf2	0 8.81e-11
36	33	88391	P	ycf2	147825	ycf2	0 8.81e-11
37	33	147750	F	ycf2	147825	ycf2	0 8.81e-11
38	29	8223	P	IGS	45984	trnS-GGA	0 2.26e-08
39	29	39556	F	psaB	41780	psaA	0 2.26e-08
40	28	92092	F	ycf2	92155	ycf2	0 9.02e-08
41	28	92092	F	ycf2	92173	ycf2	0 9.02e-08
42	28	92092	F	ycf2	92191	ycf2	0 9.02e-08
43	28	92092	F	ycf2	92209	ycf2	0 9.02e-08
44	28	92092	F	ycf2	92227	ycf2	0 9.02e-08
45	28	92092	F	ycf2	92245	ycf2	0 9.02e-08
46	28	92092	P	ycf2	143901	ycf2	0 9.02e-08
47	28	92092	P	ycf2	143919	ycf2	0 9.02e-08
48	28	92092	P	ycf2	143937	ycf2	0 9.02e-08
49	28	92092	P	ycf2	143955	ycf2	0 9.02e-08

Table S8. Simple sequence repeats in the chloroplast genome of *C. monoica*

Repeat	Length (bp)	Number	Start position
A	8	24	99; 9205; 18832; 21290; 22497; 28979; 29893; 37168; 37340; 47697; 63589; 63596; 65185; 66160; 82245; 89723; 92659; 96064; 108910; 109603; 113220; 133807; 137550; 151728
	9	18	1581; 4197; 13679; 37168; 37478; 38204; 46172; 47125; 57606; 64394; 64451; 64642; 70009; 88737; 111654; 114148; 138852; 151728
	10	8	4606; 55177; 55590; 68800; 80746; 82092; 112592; 115721
	11	4	43114; 60721; 69327; 151728
	12	4	8181; 66398; 74939; 8181
	13	1	31826
	14	1	33329
	17	1	45632
C	8	3	146864; 19301; 22627
	9	1	37478
	10	1	142763
G	8	4	4606; 35094; 76550; 88737
	10	1	92854
T	8	32	4468; 4606; 7574; 7781; 13096; 16801; 27284; 43114; 43701; 44197; 49527; 50923; 51434; 52566; 60958; 61693; 66977; 70009; 73617; 79608; 82092; 83821; 98069; 101812; 114734; 124265; 124393; 124839; 124993; 139555; 142960; 145896
	9	21	4606; 28762; 30526; 32426; 33076; 36302; 45104; 61693; 71970; 74420; 83127; 83514; 83821; 96766; 114035; 121722; 124265; 124561; 124640; 125414; 146864
	10	7	8691; 12305; 16511; 77769; 81489; 121563; 126617
	11	2	9634; 83821
	12	2	60009; 119235
	13	4	18689; 65928; 80207; 112592
	14	1	111488
	18	1	51766
AT	5	1	20062
TA	5	1	43114
AAAC	3	1	68800
AATA	3	1	108910
ACAA	3	1	112006
CTTT	3	1	43840
GAAA	2	1	119235
TAAA	3	1	149501
TATT	3	1	55590
TTAA	3	1	30392
TTGA	3	1	14550
TTTA	3	2	9851; 86114
TATTT	3	1	47572

Table S9. Simple sequence repeats in the chloroplast genome of *C. sinensis*

Repeat	Length (bp)	Number	Start position
A	8	25	9209; 18819; 21277; 22484; 28994; 29908; 37138; 37310; 57561; 60762; 63631; 65487; 66463; 75238; 82556; 89999; 92935; 96338; 109188; 109881; 113497; 117591; 134082; 137825; 151965
	9	13	4623; 37138; 38173; 45417; 47084; 69105; 70315; 81058; 82403; 89013; 114312; 139127; 151965
	10	7	13672; 37447; 43084; 46130; 55504; 64943; 115990
	11	7	100; 4177; 8195; 31804; 64691; 64752; 73917
	12	3	55130; 66702; 151965
	13	2	1589; 69631
	14	3	4177; 33306; 45601
	15	1	112864
C	8	5	19288; 22614; 37447; 143038; 147137
G	8	3	35065; 89013; 93130
T	8	36	4485; 4623; 7588; 7795; 12310; 13098; 16788; 27272; 28778; 36273; 43084; 43667; 44161; 49120; 49484; 50877; 52519; 55504; 60999; 67281; 68758; 69631; 70315; 73917; 79921; 84132; 98343; 102086; 115003; 124536; 124664; 125110; 125264; 139830; 143233; 146169
	9	19	8696; 32402; 51729; 66584; 72270; 74719; 82403; 83438; 83825; 84132; 97040; 114312; 121835; 121993; 124536; 124832; 124911; 125685; 147137
	10	9	16498; 30546; 60436; 61734; 78082; 81800; 111766; 119505; 126888
	11	2	9638; 51388
	12	4	45074; 60048; 80520; 84132
	13	2	18676; 112864
	14	1	66230
AT	5	1	20049
TA	5	1	43084
AAAC	3	1	69105
AATA	3	1	109188
ACAA	3	1	112278
CTTT	3	1	43806
GAAA	3	1	119505
GGCA	3	1	6529
TAAA	3	1	149774
TATT	3	1	55504
TTAA	3	1	30412
TTTA	3	2	9856; 86390