

**Table S1 –Transcriptome reads mapping of the *Camellia sinensis* var. *assamica* chloroplast genome.**

<b>Gene name</b>	<b>Strand</b>	<b>Start position (bp)</b>	<b>End position (bp)</b>	<b>Gene size (bp)</b>	<b>Reads number</b>	<b>Coverage<sup>a</sup></b>	<b>Reads number</b>	<b>Coverage<sup>b</sup></b>
<i>trnH-GUG</i>	-	3	77	74	12	78.67%	70	100%
<i>psbA</i>	-	463	1521	1058	5984	100%	329	100%
<i>trnK-UUU</i>	-	1742	1776	34	14	100%	3	100%
<i>matK</i>	-	2048	3547	1499	426	100%	86	70%
<i>trnK-UUU</i>	-	4264	4300	36	35	100%	22	100%
<i>rps16</i>	-	5056	6178	1122	275	100%	315	100%
<i>trnQ-UUG</i>	-	7793	7864	71	4	100%	5	100%
<i>psbK</i>	+	8198	8383	185	127	100%	65	100%
<i>psbI</i>	+	8780	8890	110	32	100%	21	100%
<i>trnS-GCU</i>	-	9033	9120	87	47	100%	94	100%
<i>trnG-GCC</i>	+	9796	9818	22	13	100%	18	100%
<i>trnG-GCC</i>	+	10524	10560	36	11	100%	28	100%
<i>trnR-UCU</i>	+	10812	10883	71	15	100%	25	100%
<i>atpA</i>	-	10997	12520	1523	1625	100%	590	100%
<i>atpF</i>	-	12580	13850	1270	951	100%	1578	100%
<i>atpH</i>	-	14227	14472	245	686	100%	353	100%
<i>atpI</i>	-	15577	16320	743	674	100%	1115	100%
<i>rps2</i>	-	16530	17240	710	1808	100%	196	100%
<i>rpoC2</i>	-	17487	21611	4124	1634	100%	359	88%
<i>rpoC1</i>	-	21789	24581	2792	356	100%	65	92.62%
<i>rpoB</i>	-	24608	27820	3212	521	100%	65	63.52%
<i>trnC-GCA</i>	+	29056	29136	80	8	100%	11	100%
<i>petN</i>	+	29846	29935	89	8	100%	0	0%
<i>psbM</i>	-	31018	31122	104	58	100%	99	100%
<i>trnD-GUC</i>	-	31950	32023	73	12	100%	3	45.95%
<i>trnY-GUA</i>	-	32136	32219	83	15	100%	6	100%
<i>trnE-UUC</i>	-	32279	32351	72	4	91.78%	4	97.26%
<i>trnT-GGU</i>	+	33125	33196	71	0	0%	20	100%
<i>psbD</i>	+	34715	35776	1061	1898	100%	4040	100%
<i>psbC</i>	+	35724	37145	1421	3580	100%	3549	100%
<i>trnS-UGA</i>	-	37378	37469	91	106	100%	340	100%
<i>psbZ</i>	+	37825	38013	188	306	100%	880	100%
<i>trnG-UCC</i>	+	38285	38355	70	37	100%	69	100%
<i>trnM-CAU</i>	-	38517	38590	73	10	100%	129	100%
<i>rps14</i>	-	38744	39046	302	869	100%	2711	100%
<i>psaB</i>	-	39170	41374	2204	11265	100%	366	100%

<i>psaA</i>	-	41400	43652	2252	11377	100%	358	99.91%
<i>ycf3</i>	-	44441	46404	1963	592	100%	4028	100%
<i>trnS-GGA</i>	+	47253	47339	86	31	100%	8	96.55%
<i>rps4</i>	-	47632	48237	605	44	100%	26	78.38%
<i>trnT-UGU</i>	-	48571	48643	72	0	0%	14	100%
<i>trnL-UAA</i>	+	49624	49660	36	18	100%	382	100%
<i>trnL-UAA</i>	+	50184	50233	49	12	100%	38	100%
<i>trnF-GAA</i>	+	50606	50678	72	10	100%	3	97.26%
<i>ndhJ</i>	-	51346	51822	476	105	100%	92	100%
<i>ndhK</i>	-	51928	52776	848	222	100%	402	100%
<i>ndhC</i>	-	52656	53018	362	74	100%	204	100%
<i>trnV-UAC</i>	-	53374	54035	74	23	100.00%	88	100%
<i>trnM-CAU</i>	+	54202	54273	71	6	100%	152	100%
<i>atpE</i>	-	54477	54878	401	1991	100%	5293	100%
<i>atpB</i>	-	54875	56371	1496	14998	100%	17960	100%
<i>rbcl</i>	+	57124	58551	1427	17530	100%	773	100%
<i>accD</i>	+	59131	60621	1490	570	100%	234	100%
<i>psaI</i>	+	61363	61473	110	17	100%	7	100%
<i>ycf4</i>	+	61894	62448	554	319	100%	38	100%
<i>cemA</i>	+	63348	64043	695	129	100%	96	100%
<i>petA</i>	+	64283	65245	962	464	100%	148	95.12%
<i>psbJ</i>	-	66282	66404	122	137	100%	72	100%
<i>psbL</i>	-	66535	66651	116	175	100%	27	100%
<i>psbF</i>	-	66674	66793	119	249	100%	30	100%
<i>psbE</i>	-	66803	67054	251	488	100%	51	100%
<i>petL</i>	+	68347	68442	95	1	2.08%	1	50%
<i>petG</i>	+	68625	68738	113	39	100%	54	100%
<i>trnW-CCA</i>	-	68862	68935	73	19	100%	22	100%
<i>trnP-UGG</i>	-	69106	69179	73	56	100%	21	100%
<i>psaJ</i>	+	69570	69704	134	167	100%	469	100%
<i>rpl33</i>	+	70159	70359	200	33	100%	107	100%
<i>rps18</i>	+	70537	70842	305	73	100%	72	100%
<i>rpl20</i>	-	71105	71458	353	51	100%	137	100%
<i>ψrps12</i>	-	72239	72352	113	28	100%	40	100%
<i>clpP</i>	-	72502	74482	1980	173	100%	283	100%
<i>psbB</i>	+	74935	76461	1526	7894	100%	382	100%
<i>psbT</i>	+	76643	76750	107	65	100%	13	100%
<i>psbN</i>	-	76806	76937	131	67	100%	44	100%
<i>psbH</i>	+	77040	77261	221	184	100%	75	100%
<i>petB</i>	+	77385	78809	1424	1320	100%	345	97.33%
<i>petD</i>	+	78998	80228	1230	631	100%	162	100%
<i>rpoA</i>	-	80434	81441	1007	4706	100%	2177	100%
<i>rps11</i>	-	81507	81923	416	9897	100%	2365	100%
<i>rpl36</i>	-	82038	82151	113	1245	100%	810	100%

<i>infA</i>	-	82268	82501	233	6019	100%	1808	100%
<i>rps8</i>	-	82623	83030	407	6316	100%	5543	100%
<i>rpl14</i>	-	83220	83588	368	9435	100%	3791	100%
<i>rpl16</i>	-	83701	85130	1429	15240	100%	8782	100%
<i>rps3</i>	-	85259	85915	656	1611	100%	2349	100%
<i>rpl22</i>	-	85900	86367	467	1048	100%	1567	100%
<i>rps19</i>	-	86419	86697	278	671	100%	1605	100%
<i>rpl2</i>	-	86758	88252	1494	13889	100%	7762	100%
<i>rpl23</i>	-	88271	88552	281	1613	100%	1115	100%
<i>trnI-CAU</i>	-	88718	88791	73	44	100%	5	96.19%
<i>ycf2</i>	+	88880	95776	6896	3231	100%	462	87.77%
<i>ycf15</i>	+	95857	96105	248	84	100%	22	97.57%
<i>trnL-CAA</i>	-	96476	96556	80	9	100%	6	98.83%
<i>ndhB</i>	-	97113	99324	2211	1292	100%	5815	100%
<i>rps7</i>	-	99650	100117	467	1808	100%	9621	100%
<i>ψrps12</i>	-	100713	100964	251	2425	100%	9699	100%
<i>trnV-GAC</i>	+	102809	102880	71	12	100%	4	72.78%
<i>rrn16</i>	+	103108	104597	1489	187198	100%	10356	100%
<i>trnI-GAU</i>	+	104894	104935	75	4071	100%	188	100%
<i>trnA-UGC</i>	+	105981	106018	37	2511	100%	116	100%
<i>orf42</i>	-	106148	106276	128	5685	100%	207	100%
<i>trnA-UGC</i>	+	106831	106865	34	2203	100%	44	100%
<i>rrn23</i>	+	107018	109826	2808	438212	100%	78277	100%
<i>rrn4.5</i>	+	109925	110027	102	2653	100%	401	100%
<i>rrn5</i>	+	110248	110368	120	112	100%	50	100%
<i>trnR-ACG</i>	+	110622	110695	73	30	100%	117	100%
<i>trnN-GUU</i>	-	111291	111362	71	64	100%	142	100%
<i>ψycf1</i>	+	111675	112730	1055	672	100%	1922	100%
<i>ndhF</i>	-	112800	115046	2246	352	100%	326	79.88%
<i>rpl32</i>	+	115726	115887	161	33	100%	21	100%
<i>trnL-UAG</i>	+	116809	116888	79	404	100%	205	100%
<i>ccsA</i>	+	116978	117943	965	32	77.85%	70	83.44%
<i>ndhD</i>	-	118182	119696	1514	47	88.58%	47	66.07%
<i>psaC</i>	-	119825	120070	245	90	100%	72	100%
<i>ndhE</i>	-	120301	120606	305	18	90.52%	50	100%
<i>ndhG</i>	-	120841	121371	530	31	100%	61	100%
<i>ndhI</i>	-	121766	122269	503	108	100%	330	100%
<i>ndhA</i>	-	122364	124539	2175	307	100%	4389	100%
<i>ndhH</i>	-	124541	125722	1181	997	100%	2062	100%
<i>rps15</i>	-	125815	126087	272	210	100%	715	100%
<i>ycf1</i>	-	126470	132097	5627	4112	96.94%	22890	100%

<sup>a</sup> Transcriptome reads were from *C. sinensis* var. *assamica* and <sup>b</sup> *C. Sinensis* var.

*sinensis*.