

Supporting information for

Comparative Chloroplast Genomics of *Calligonum leucocladum* from Kazakhstan: Genetic Basis for Arid Adaptation and Agroforestry Applications

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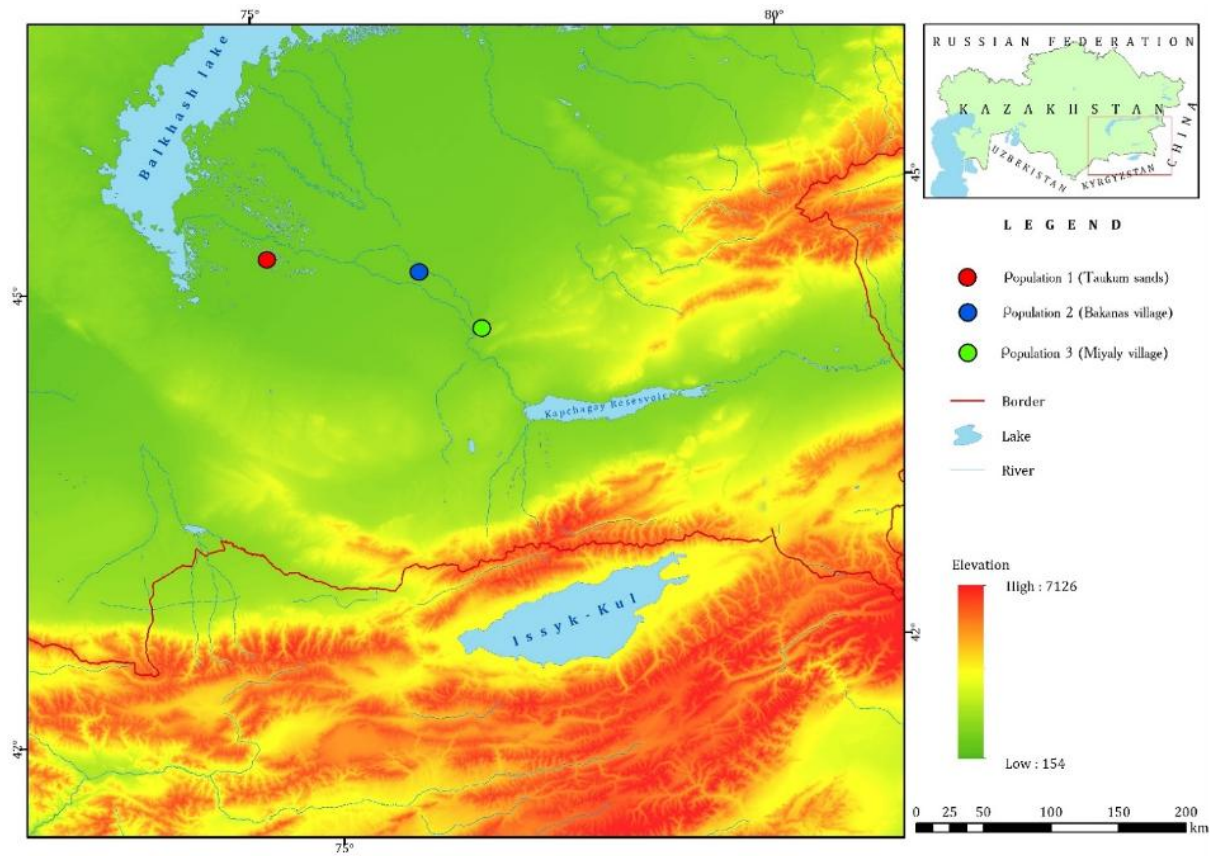


Fig. S1: Study region map.

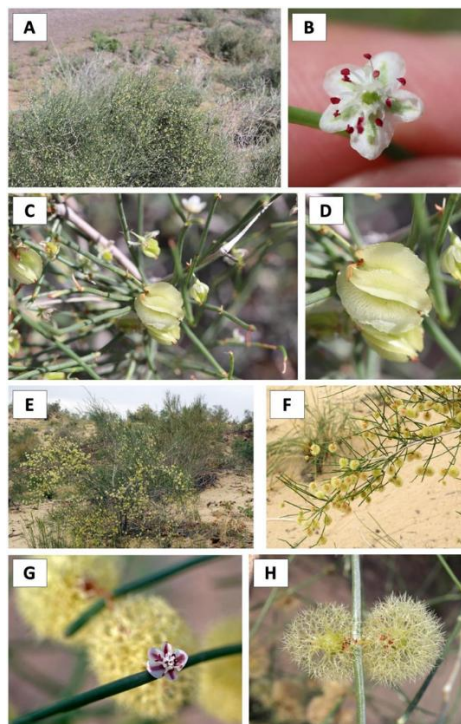


Fig. S2: Illustration of the morphological differences between *C. leucocladum* and *C. caput-medusae*. A–D: our expedition photographs (deposited on the iNaturalist platform with Research Grade status); E–G: photographs by Pavel Gorbunov; H: photograph by Alexander Fateryga, all published on the platform Plantarium.ru.

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>ndhB</i> exon 1	exon	149528	150304	777	1	forward
<i>ndhB</i> CDS	CDS	149528	151739	1533	2	forward
<i>ndhB</i> gene	gene	149528	151739	2212	1	forward
<i>rps7</i> CDS	CDS	148724	149191	468	1	forward
<i>rps7</i> gene	gene	148724	149191	468	1	forward
<i>trnV</i> -GAC tRNA	tRNA	146314	146385	72	1	reverse
<i>trnV</i> -GAC gene	gene	146314	146385	72	1	reverse
<i>rrn16</i> rRNA	rRNA	144597	146087	1491	1	reverse
<i>rrn16</i> gene	gene	144597	146087	1491	1	reverse
<i>trnI</i> -GAU exon 1	exon	144261	144302	42	1	reverse
<i>trnI</i> -GAU tRNA	tRNA	143287	144302	77	2	reverse
<i>trnI</i> -GAU exon 2	exon	143287	143321	35	1	reverse
<i>trnI</i> -GAU gene	gene	143287	144302	1016	1	reverse
<i>trnA</i> -UGC exon 1	exon	143183	143220	38	1	reverse
<i>trnA</i> -UGC exon 2	exon	142345	142381	37	1	reverse
<i>trnA</i> -UGC	tRNA	142344	143220	74	2	reverse
<i>trnA</i> -UGC gene	gene	142344	143220	877	1	reverse
<i>rrn23</i> rRNA	rRNA	139379	142188	2810	1	reverse
<i>rrn23</i> gene	gene	139379	142188	2810	1	reverse
<i>rrn4.5</i> rRNA	rRNA	139176	139278	103	1	reverse
<i>rrn4.5</i> gene	gene	139176	139278	103	1	reverse
<i>rrn5</i> rRNA	rRNA	138802	138924	123	1	reverse
<i>rrn5</i> gene	gene	138802	138924	123	1	reverse
<i>trnR</i> -ACG tRNA	tRNA	138473	138546	74	1	reverse
<i>trnR</i> -ACG gene	gene	138473	138546	74	1	reverse
<i>trnN</i> -GUU tRNA	tRNA	137790	137861	72	1	forward
<i>trnN</i> -GUU gene	gene	137790	137861	72	1	forward

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>ycf1</i> CDS	CDS	131814	137261	5448	1	reverse
<i>ycf1</i> gene	gene	131814	137261	5448	1	reverse
repeat A (IRa) repeat region	repeat_region	131559	162085	30527	1	reverse
<i>rps15</i> CDS	CDS	131264	131527	264	1	reverse
<i>rps15</i> gene	gene	131264	131527	264	1	reverse
<i>ndhH</i> CDS	CDS	129984	131165	1182	1	reverse
<i>ndhH</i> gene	gene	129984	131165	1182	1	reverse
<i>ndhA</i> exon 1	exon	129424	129982	559	1	reverse
<i>ndhA</i> exon 2	exon	127722	128260	539	1	reverse
<i>ndhA</i> CDS	CDS	127722	129982	1098	2	reverse
<i>ndhA</i> gene	gene	127722	129982	2261	1	reverse
<i>ndhI</i> CDS	CDS	127106	127618	513	1	reverse
<i>ndhI</i> gene	gene	127106	127618	513	1	reverse
<i>ndhG</i> CDS	CDS	126235	126765	531	1	reverse
<i>ndhG</i> gene	gene	126235	126765	531	1	reverse
<i>ndhE</i> CDS	CDS	125707	126009	303	1	reverse
<i>ndhE</i> gene	gene	125707	126009	303	1	reverse
<i>psaC</i> CDS	CDS	125207	125452	246	1	reverse
<i>psaC</i> gene	gene	125207	125452	246	1	reverse
<i>ndhD</i> CDS	CDS	123574	125094	1521	1	reverse
<i>ndhD</i> gene	gene	123574	125094	1521	1	reverse
<i>ccsA</i> CDS	CDS	122383	123348	966	1	forward
<i>ccsA</i> gene	gene	122383	123348	966	1	forward
<i>trnL</i> -UAG tRNA	tRNA	122168	122247	80	1	forward
<i>trnL</i> -UAG gene	gene	122168	122247	80	1	forward
<i>rpl32</i> CDS	CDS	121375	121548	174	1	forward
<i>rpl32</i> gene	gene	121375	121548	174	1	forward

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
small single copy region (SSC)	misc_feature	118214	131558	13345	1	forward
<i>ndhF</i> CDS	CDS	118148	120391	2244	1	reverse
<i>ndhF</i> gene	gene	118148	120391	2244	1	reverse
<i>ycf1</i> CDS	CDS	112511	117958	5448	1	forward
<i>ycf1</i> gene	gene	112511	117958	5448	1	forward
<i>trnN</i> -GUU tRNA	tRNA	111911	111982	72	1	reverse
<i>trnN</i> -GUU gene	gene	111911	111982	72	1	reverse
<i>trnR</i> -ACG tRNA	tRNA	111226	111299	74	1	forward
<i>trnR</i> -ACG gene	gene	111226	111299	74	1	forward
<i>rrn5</i> rRNA	rRNA	110848	110970	123	1	forward
<i>rrn5</i> gene	gene	110848	110970	123	1	forward
<i>rrn4.5</i> rRNA	rRNA	110494	110596	103	1	forward
<i>rrn4.5</i> gene	gene	110494	110596	103	1	forward
<i>rrn23</i> rRNA	rRNA	107584	110393	2810	1	forward
<i>rrn23</i> gene	gene	107584	110393	2810	1	forward
<i>trnA</i> -UGC exon 2	exon	107391	107427	37	1	forward
<i>trnA</i> -UGC	tRNA	106552	107428	74	2	forward
<i>trnA</i> -UGC exon 1	exon	106552	106589	38	1	forward
<i>trnA</i> -UGC gene	gene	106552	107428	877	1	forward
<i>trnI</i> -GAU exon 2	exon	106451	106485	35	1	forward
<i>trnI</i> -GAU tRNA	tRNA	105470	106485	77	2	forward
<i>trnI</i> -GAU exon 1	exon	105470	105511	42	1	forward
<i>trnI</i> -GAU gene	gene	105470	106485	1016	1	forward
<i>rrn16</i> rRNA	rRNA	103685	105175	1491	1	forward
<i>rrn16</i> gene	gene	103685	105175	1491	1	forward
<i>trnV</i> -GAC tRNA	tRNA	103387	103458	72	1	forward
<i>trnV</i> -GAC gene	gene	103387	103458	72	1	forward

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>rps7</i> CDS	CDS	100581	101048	468	1	reverse
<i>rps7</i> gene	gene	100581	101048	468	1	reverse
<i>ndhB</i> exon 1	exon	99468	100244	777	1	reverse
<i>ndhB</i> exon 2	exon	98033	98788	756	1	reverse
<i>ndhB</i> CDS	CDS	98033	100244	1533	2	reverse
<i>ndhB</i> gene	gene	98033	100244	2212	1	reverse
<i>trnL</i> -CAA tRNA	tRNA	97387	97467	81	1	reverse
<i>trnL</i> -CAA gene	gene	97387	97467	81	1	reverse
<i>ycf2</i> CDS	CDS	90249	96494	6246	1	forward
<i>ycf2</i> gene	gene	90249	96494	6246	1	forward
<i>trnI</i> -CAU tRNA	tRNA	89841	89914	74	1	reverse
<i>trnI</i> -CAU gene	gene	89841	89914	74	1	reverse
<i>rpl23</i> CDS	CDS	89364	89624	261	1	reverse
<i>rpl23</i> gene	gene	89364	89624	261	1	reverse
<i>rpl2</i> exon 1	exon	88953	89345	393	1	reverse
<i>rpl2</i> exon 2	exon	87856	88290	435	1	reverse
<i>rpl2</i> CDS	CDS	87856	89345	828	2	reverse
<i>rpl2</i> gene	gene	87856	89345	1490	1	reverse
repeat A (IRa) repeat region	repeat_region	87687	118213	30527	1	forward
<i>rps19</i> CDS	CDS	87513	87794	282	1	reverse
<i>rps19</i> gene	gene	87513	87794	282	1	reverse
<i>rpl22</i> CDS	CDS	87017	87469	453	1	reverse
<i>rpl22</i> gene	gene	87017	87469	453	1	reverse
<i>rps3</i> CDS	CDS	86376	87032	657	1	reverse
<i>rps3</i> gene	gene	86376	87032	657	1	reverse
<i>rpl16</i> exon 2	exon	84862	85260	399	1	reverse
<i>rpl16</i> gene	gene	84862	86249	1388	1	reverse

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>rpl14</i> CDS	CDS	84372	84740	369	1	reverse
<i>rpl14</i> gene	gene	84372	84740	369	1	reverse
<i>rps8</i> CDS	CDS	83803	84207	405	1	reverse
<i>rps8</i> gene	gene	83803	84207	405	1	reverse
<i>infA</i> CDS	CDS	83451	83684	234	1	reverse
<i>infA</i> gene	gene	83451	83684	234	1	reverse
<i>rpl36</i> CDS	CDS	83234	83347	114	1	reverse
<i>rpl36</i> gene	gene	83234	83347	114	1	reverse
<i>rps11</i> CDS	CDS	82688	83104	417	1	reverse
<i>rps11</i> gene	gene	82688	83104	417	1	reverse
<i>rpoA</i> CDS	CDS	81593	82606	1014	1	reverse
<i>rpoA</i> gene	gene	81593	82606	1014	1	reverse
<i>petD</i> exon 2	exon	80933	81407	475	1	forward
<i>petD</i> gene	gene	80239	81407	1169	1	forward
<i>petB</i> exon 2	exon	79387	80028	642	1	forward
<i>petB</i> gene	gene	78621	80028	1408	1	forward
<i>psbH</i> CDS	CDS	78286	78507	222	1	forward
<i>psbH</i> gene	gene	78286	78507	222	1	forward
<i>psbN</i> CDS	CDS	78052	78183	132	1	reverse
<i>psbN</i> gene	gene	78052	78183	132	1	reverse
<i>psbT</i> CDS	CDS	77879	77980	102	1	forward
<i>psbT</i> gene	gene	77879	77980	102	1	forward
<i>psbB</i> CDS	CDS	76192	77718	1527	1	forward
<i>psbB</i> gene	gene	76192	77718	1527	1	forward
<i>clpP</i> exon 1	exon	75658	75726	69	1	reverse
<i>clpP</i> exon 2	exon	74226	74516	291	1	reverse
<i>clpP</i> exon 3	exon	73322	73591	270	1	reverse

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>clpP</i> CDS	CDS	73322	75726	630	3	reverse
<i>clpP</i> gene	gene	73322	75726	2405	1	reverse
<i>rps12</i> exon 1	exon	73084	73197	114	1	reverse
<i>rpl20</i> CDS	CDS	71925	72317	393	1	reverse
<i>rpl20</i> gene	gene	71925	72317	393	1	reverse
<i>rps18</i> CDS	CDS	71533	71847	315	1	forward
<i>rps18</i> gene	gene	71533	71847	315	1	forward
<i>rpl33</i> CDS	CDS	70874	71074	201	1	forward
<i>rpl33</i> gene	gene	70874	71074	201	1	forward
<i>psaJ</i> CDS	CDS	70192	70326	135	1	forward
<i>psaJ</i> gene	gene	70192	70326	135	1	forward
<i>trnP</i> -UGG tRNA	tRNA	69728	69801	74	1	reverse
<i>trnP</i> -UGG gene	gene	69728	69801	74	1	reverse
<i>trnW</i> -CCA tRNA	tRNA	69348	69421	74	1	reverse
<i>trnW</i> -CCA gene	gene	69348	69421	74	1	reverse
<i>petG</i> CDS	CDS	69121	69234	114	1	forward
<i>petG</i> gene	gene	69121	69234	114	1	forward
<i>petL</i> CDS	CDS	68820	68915	96	1	forward
<i>petL</i> gene	gene	68820	68915	96	1	forward
<i>psbE</i> CDS	CDS	67403	67654	252	1	reverse
<i>psbE</i> gene	gene	67403	67654	252	1	reverse
<i>psbF</i> CDS	CDS	67275	67394	120	1	reverse
<i>psbF</i> gene	gene	67275	67394	120	1	reverse
<i>psbL</i> CDS	CDS	67131	67247	117	1	reverse
<i>psbL</i> gene	gene	67131	67247	117	1	reverse
<i>psbJ</i> CDS	CDS	66874	66996	123	1	reverse
<i>psbJ</i> gene	gene	66874	66996	123	1	reverse

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>petA</i> CDS	CDS	65017	65979	963	1	forward
<i>petA</i> gene	gene	65017	65979	963	1	forward
<i>cemA</i> CDS	CDS	64114	64809	696	1	forward
<i>cemA</i> gene	gene	64114	64809	696	1	forward
<i>paqII</i> CDS	CDS	62728	63282	555	1	forward
<i>paqII</i> gene	gene	62728	63282	555	1	forward
<i>psaI</i> CDS	CDS	62176	62286	111	1	forward
<i>psaI</i> gene	gene	62176	62286	111	1	forward
<i>accD</i> CDS	CDS	60084	61508	1425	1	forward
<i>accD</i> gene	gene	60084	61508	1425	1	forward
<i>rbcL</i> CDS	CDS	58136	59563	1428	1	forward
<i>rbcL</i> gene	gene	58136	59563	1428	1	forward
<i>atpB</i> CDS	CDS	55863	57359	1497	1	reverse
<i>atpB</i> gene	gene	55863	57359	1497	1	reverse
<i>atpE</i> CDS	CDS	55465	55866	402	1	reverse
<i>atpE</i> gene	gene	55465	55866	402	1	reverse
<i>trnM</i> -CAU tRNA	tRNA	55225	55297	73	1	forward
<i>trnM</i> -CAU gene	gene	55225	55297	73	1	forward
<i>trnV</i> -UAC exon 1	exon	55016	55053	38	1	reverse
<i>trnV</i> -UAC tRNA	tRNA	54388	55053	75	2	reverse
<i>trnV</i> -UAC exon 2	exon	54388	54424	37	1	reverse
<i>trnV</i> -UAC gene	gene	54388	55053	666	1	reverse
<i>ndhC</i> CDS	CDS	53575	53937	363	1	reverse
<i>ndhC</i> gene	gene	53575	53937	363	1	reverse
<i>ndhK</i> CDS	CDS	52844	53695	852	1	reverse
<i>ndhK</i> gene	gene	52844	53695	852	1	reverse
<i>ndhJ</i> CDS	CDS	52252	52728	477	1	reverse

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>ndhJ</i> gene	gene	52252	52728	477	1	reverse
<i>trnF</i> -GAA tRNA	tRNA	51431	51503	73	1	forward
<i>trnF</i> -GAA gene	gene	51431	51503	73	1	forward
<i>trnL</i> -UAA exon 2	exon	51014	51063	50	1	forward
<i>trnL</i> -UAA tRNA	tRNA	50459	51063	87	2	forward
<i>trnL</i> -UAA exon 1	exon	50459	50495	37	1	forward
<i>trnL</i> -UAA gene	gene	50459	51063	605	1	forward
<i>trnT</i> -UGU tRNA	tRNA	49414	49486	73	1	reverse
<i>trnT</i> -UGU gene	gene	49414	49486	73	1	reverse
<i>rps4</i> CDS	CDS	47982	48578	597	1	reverse
<i>rps4</i> gene	gene	47982	48578	597	1	reverse
<i>trnS</i> -GGA tRNA	tRNA	47575	47661	87	1	forward
<i>trnS</i> -GGA gene	gene	47575	47661	87	1	forward
<i>pafI</i> exon 1	exon	46526	46654	129	1	reverse
<i>pafI</i> exon 2	exon	45575	45802	228	1	reverse
<i>pafI</i> exon 3	exon	44685	44837	153	1	reverse
<i>pafI</i> CDS	CDS	44685	46654	510	3	reverse
<i>pafI</i> gene	gene	44685	46654	1970	1	reverse
<i>psaA</i> CDS	CDS	41698	43950	2253	1	reverse
<i>psaA</i> gene	gene	41698	43950	2253	1	reverse
<i>psaB</i> CDS	CDS	39468	41672	2205	1	reverse
<i>psaB</i> gene	gene	39468	41672	2205	1	reverse
<i>rps14</i> CDS	CDS	39042	39344	303	1	reverse
<i>rps14</i> gene	gene	39042	39344	303	1	reverse
<i>trnfM</i> -CAU tRNA	tRNA	38819	38891	73	1	reverse
<i>trnfM</i> -CAU gene	gene	38819	38891	73	1	reverse
<i>trnG</i> -GCC tRNA	tRNA	38591	38660	70	1	forward

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>trnG</i> -GCC gene	gene	38591	38660	70	1	forward
<i>psbZ</i> CDS	CDS	38086	38274	189	1	forward
<i>psbZ</i> gene	gene	38086	38274	189	1	forward
<i>trnS</i> -UGA tRNA	tRNA	37652	37739	88	1	reverse
<i>trnS</i> -UGA gene	gene	37652	37739	88	1	reverse
<i>psbC</i> CDS	CDS	35957	37378	1422	1	forward
<i>psbC</i> gene	gene	35957	37378	1422	1	forward
<i>psbD</i> CDS	CDS	34948	36009	1062	1	forward
<i>psbD</i> gene	gene	34948	36009	1062	1	forward
<i>trnT</i> -GGU tRNA	tRNA	33505	33576	72	1	forward
<i>trnT</i> -GGU gene	gene	33505	33576	72	1	forward
<i>trnE</i> -UUC tRNA	tRNA	32470	32542	73	1	reverse
<i>trnE</i> -UUC gene	gene	32470	32542	73	1	reverse
<i>trnY</i> -GUA tRNA	tRNA	32329	32412	84	1	reverse
<i>trnY</i> -GUA gene	gene	32329	32412	84	1	reverse
<i>trnD</i> -GUC tRNA	tRNA	31845	31918	74	1	reverse
<i>trnD</i> -GUC gene	gene	31845	31918	74	1	reverse
<i>psbM</i> CDS	CDS	30833	30937	105	1	reverse
<i>psbM</i> gene	gene	30833	30937	105	1	reverse
<i>petN</i> CDS	CDS	30002	30091	90	1	forward
<i>petN</i> gene	gene	30002	30091	90	1	forward
<i>trnC</i> -GCA tRNA	tRNA	29046	29117	72	1	forward
<i>trnC</i> -GCA gene	gene	29046	29117	72	1	forward
<i>rpoB</i> CDS	CDS	24556	27768	3213	1	reverse
<i>rpoB</i> gene	gene	24556	27768	3213	1	reverse
<i>rpoC1</i> exon 1	exon	24098	24529	432	1	reverse
<i>rpoC1</i> exon 2	exon	21717	23330	1614	1	reverse

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>rpoC1</i> CDS	CDS	21717	24529	2046	2	reverse
<i>rpoC1</i> gene	gene	21717	24529	2813	1	reverse
<i>rpoC2</i> CDS	CDS	17455	21549	4095	1	reverse
<i>rpoC2</i> gene	gene	17455	21549	4095	1	reverse
<i>rps2</i> CDS	CDS	16493	17203	711	1	reverse
<i>rps2</i> gene	gene	16493	17203	711	1	reverse
<i>atpI</i> CDS	CDS	15523	16266	744	1	reverse
<i>atpI</i> gene	gene	15523	16266	744	1	reverse
<i>atpH</i> CDS	CDS	14590	14835	246	1	reverse
<i>atpH</i> gene	gene	14590	14835	246	1	reverse
<i>atpF</i> exon 1	exon	14015	14158	144	1	reverse
<i>atpF</i> exon 2	exon	12846	13256	411	1	reverse
<i>atpF</i> CDS	CDS	12846	14158	555	2	reverse
<i>atpF</i> gene	gene	12846	14158	1313	1	reverse
<i>atpA</i> CDS	CDS	11256	12773	1518	1	reverse
<i>atpA</i> gene	gene	11256	12773	1518	1	reverse
<i>trnR</i> -UCU tRNA	tRNA	10972	11043	72	1	forward
<i>trnR</i> -UCU gene	gene	10972	11043	72	1	forward
<i>trnG</i> -UCC exon 2	exon	10814	10862	49	1	forward
<i>trnG</i> -UCC tRNA	tRNA	10092	10862	72	2	forward
<i>trnG</i> -UCC exon 1	exon	10092	10114	23	1	forward
<i>trnG</i> -UCC gene	gene	10092	10862	771	1	forward
<i>trnS</i> -GCU tRNA	tRNA	8925	9012	88	1	reverse
<i>trnS</i> -GCU gene	gene	8925	9012	88	1	reverse
<i>psbI</i> CDS	CDS	8711	8821	111	1	forward
<i>psbI</i> gene	gene	8711	8821	111	1	forward
<i>psbK</i> CDS	CDS	8308	8493	186	1	forward

Name	Type	Minimum	Maximum	Length	# Intervals	Direction
<i>psbK</i> gene	gene	8308	8493	186	1	forward
<i>trnQ</i> -UUG tRNA	tRNA	7904	7975	72	1	reverse
<i>trnQ</i> -UUG gene	gene	7904	7975	72	1	reverse
<i>rps16</i> exon 1	exon	6393	6432	40	1	reverse
<i>rps16</i> exon 2	exon	5309	5535	227	1	reverse
<i>rps16</i> CDS	CDS	5309	6432	267	2	reverse
<i>rps16</i> gene	gene	5309	6432	1124	1	reverse
<i>trnK</i> -UUU exon 1	exon	4296	4332	37	1	reverse
<i>matK</i> CDS	CDS	2052	3578	1527	1	reverse
<i>matK</i> gene	gene	2052	3578	1527	1	reverse
<i>trnK</i> -UUU tRNA	tRNA	1750	4332	72	2	reverse
<i>trnK</i> -UUU exon 2	exon	1750	1784	35	1	reverse
<i>trnK</i> -UUU gene	gene	1750	4332	2583	1	reverse
<i>psbA</i> CDS	CDS	446	1507	1062	1	reverse
<i>psbA</i> gene	gene	446	1507	1062	1	reverse
<i>trnH</i> -GUG tRNA	tRNA	3	77	75	1	reverse
<i>trnH</i> -GUG gene	gene	3	77	75	1	reverse
large single copy region (LSC)	misc_feature	1	87686	87686	1	forward

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