

Mitochondrial genome - *Chromera velia* CCAP 1602/1 (KC899110)

	370	380	390	400	410	420	430	440	450
Consensus	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
CoxI_PCR	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
Illumina_1	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTT--	-----	-----	-----	-----	-----
Illumina_2	-----	-----TTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
Illumina_3	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_4	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_5	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_1 (5')	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
iPCR_2 (5')	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
iPCR_3 (5')	TTAGTTGTTG	TAATATTATA	ACCACAAATA	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
iPCR_4 (5')	TTAGTTGTTG	TAATATTATA	ACCACAAATG	CCAAATTTGG	CGGCCGTGAT	TATTCGGTTG	AACTCCCAA	CTGCTTGTAT	AAGCGGGCAA
iPCR_2 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_3 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_4 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----

											
	460	470	480	490	500	510	520	530	540											
Deduced AA					M	F	T	Q	S	E	L	L	A	M	L	M	G	K	P	F
Consensus	TTGGTGTGT	CCAGGGAAAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
CoxI_PCR	TTGGTGTGT	CCAGGGAAAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
Illumina_1	-----	-----	-----	-----	-----	-----	-----	-----	-----											
Illumina_2	TTGGTGTGT	CCAGGGAAAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
Illumina_3	-----	-----	-----	-----	-----	-----	-----	-----	-----											
Illumina_4	-----	-----	-----	-----	-----	-----	-----	-----	-----											
Illumina_5	-----	-----	-----	-----	-----	-----	-----	-----	-----											
iPCR_1 (5')	TTGGTGTGT	CCAGGGAGAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
iPCR_2 (5')	TTGGTGTGT	CCAGGGAGAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
iPCR_3 (5')	TTGGTGTGT	CCAGGGAGAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
iPCR_4 (5')	TTGGTGTGT	CCAGGGAAAT	AATAATCTGA	CTCATCATAG	TATGTTTACA	CAGAGTGAGC	TGCTAGCTAT	GTTAATGGGA	AAACCCTTTG											
iPCR_2 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----											
iPCR_3 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----											
iPCR_4 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----											

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      1090      1100      1110      1120      1130      1140      1150      1160      1170
Deduced AA  L  G  W  T  L  Y  P  P  L  S  T  I  I  Y  L  L  S  I  N  I  I  I  I  G  L  L  V  S  G  I
Consensus   TAGGTTGGAC CCTATACCT CCATTATCCA CTATTATATA TCTTTTATCG ATCAATATAA TAATTATTGG TTTATTGGTT TCTGGAATTT
CoxI_PCR    TAGGTTGGAC CCTATACCT CCATTATCCA CTATTATATA TCTTTTATCG ATCAATATAA TAATTATTGG TTTATTGGTT TCTGGAATTT
Illumina_1  -----
Illumina_2  -----
Illumina_3  -----
Illumina_4  TAGGTTGGAC CCTATACCT CCATTATCCA CTATTATATA TCTTTTATCG ATCAATATAA TAATTATTGG TTTATTGGTT TCTGGAATTT
Illumina_5  -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') -----
iPCR_3 (3') -----
iPCR_4 (3') -----

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      1180      1190      1200      1210      1220      1230      1240      1250      1260
Deduced AA  S  S  I  L  S  S  I  N  F  I  Y  T  I  I  I  I  Y  T  G  L  N  N  S  D  I  N  M  Y  S  T
Consensus   CCAGTATATT ATCTAGTATT AATTTTATTT ATACTATTAT TATTATTTAT ACAGGATTAA ATAATTCCGA TATTAATATG TATTCAACGT
CoxI_PCR    CCAGTATATT ATCTAGTATT AATTTTATTT ATACTATTAT TATTATTTAT ACAGGATTAA ATAATTCCGA TATTAATATG TATTCAACGT
Illumina_1  -----
Illumina_2  -----
Illumina_3  -----
Illumina_4  CCAGTATATT ATCTAGTATT AATTTTATTT ATACTATTAT TATTATTTAT ACAGGATTAA ATAATTCCGA TATTAATATG TATTCAACGT
Illumina_5  -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') -----
iPCR_3 (3') -----
iPCR_4 (3') -----

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	1630	1640	1650	1660	1670	1680	1690	1700	1710																							
Deduced AA	T	F	I	T	I	L	I	S	I	P	T	G	T	K	L	F	N	W	Y	S	T	L	L	H	S	F	I	I	N	N		
Consensus	CTTTTATTAC	TATTCTTATT	AGTATACCAA	CCGGAACCAA	ATTATTCAAT	TGGTACTCCA	CATTATTACA	TTCATTTATT	ATTAATAAAT																							
CoxI_PCR	CTTTTATTAC	TATTCTTATT	AGTATACCAA	CCGGAACCAA	ATTATTCAAT	TGGTACTCCA	CATTATTACA	TTCATTTATT	ATTAATAAAT																							
Illumina_1	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
Illumina_2	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
Illumina_3	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
Illumina_4	CTTTTATTAC	TATTCTTATT	AGTATACCAA	CCGGAACCAA	ATTATTCAAT	TGGTACTCCA	CATTATTACA	TTCATTTATT	ATTAATAAAT																							
Illumina_5	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_1 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_2 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_3 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_4 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_2 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_3 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							
iPCR_4 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																							

	1720	1730	1740	1750	1760	1770	1780	1790	1800																						
Deduced AA	Y	L	N	I	Y	C	L	F	F	L	L	S	F	L	L	G	G	V	T	G	V	I	L	G	N	S	L	V	D	L	
Consensus	ATCTTAATAT	TTATTGTTTA	TTCTTTTAT	TATCATTCTT	ATTAGGTGGA	GTTACCGGGG	TTATACTTGG	GAATTCATTA	GTAGATTTGG																						
CoxI_PCR	ATCTTAATAT	TTATTGTTTA	TTCTTTTAT	TATCATTCTT	ATTAGGTGGA	GTTACCGGGG	TTATACTTGG	GAATTCATTA	GTAGATTTGG																						
Illumina_1	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
Illumina_2	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
Illumina_3	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
Illumina_4	ATCTTAATAT	TTATTGTTTA	TTCTTTTAT	TATCATTCTT	ATTAGGTGGA	GTTACCGGGG	TTATACTTGG	GAATTCATTA	GTAGATTTGG																						
Illumina_5	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_1 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_2 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_3 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_4 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_2 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_3 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						
iPCR_4 (3')	-----	-----	-----	-----	-----	-----	-----	-----	-----																						

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      1990      2000      2010      2020      2030      2040      2050      2060      2070
Deduced AA  L  C  G  L  F  I  P  M  H  Y  S  G  L  F  T  L  P  R  R  I  P  D  L  I  D  G  L  N  C  W
Consensus   TATGCGGTCT GTTTATTCCT ATGCATTACT CAGGATTATT CACTTTACCC CGAAGAATTC CTGATTTAAT CGATGGTTTG AATTGTTGGA
CoxI_PCR    TATGCGGTCT GTTTATTCCT ATGCATTACT CAGGATTATT CACTTTACCC CGAAGAATTC CTGATTTAAT CGATGGTTTG AATTGTTGGA
Illumina_1  -----
Illumina_2  -----
Illumina_3  -----
Illumina_4  TATGCGGTCT GTTTATTCCT ATGCATTACT CAGGATTATT CACTTTACCC CGAAGAATTC CTGATTTA-- -----
Illumina_5  -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') -----
iPCR_3 (3') TATGCGGTCT GTTTATTCCT ATGCATTACT CAGGATTATT CACTTTACCC CGAAGAATTC CTGATTTAAT CGATGGTTTG AATTGTTGGA
iPCR_4 (3') TATGCGGTCT GTTTATTCCT ATGCATTACT CAGGATTATT CACTTTACCC CGAGAATTC CTGATTTAAT CGATGGTTTG AATTGTTGGA

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      2080      2090      2100      2110      2120      2130      2140      2150      2160
Deduced AA  N  S  L  S  S  L  T  S  G  I  V  F  C  S  F  S  V  L  T  P  Y  N  P  I  I  N  I  D  E  *
Consensus   ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT
CoxI_PCR    ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT
Illumina_1  -----
Illumina_2  -----
Illumina_3  -----
Illumina_4  -----
Illumina_5  ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT
iPCR_3 (3') ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT
iPCR_4 (3') ACAGTTTATC GTCTCTAACA TCAGGTATAG TTTTCTGTTC ATTCTCTGTG TTGACCCCGT ATAATCCAAT AATTAACATC GATGAATAGT

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      2170      2180      2190      2200      2210      2220      2230      2240      2250
Consensus  TGCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGTTATAA C-----
CoxI_PCR   ATCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGT-----
Illumina_1 -----
Illumina_2 -----
Illumina_3 -----
Illumina_4 -----
Illumina_5 TGCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGTTATAA C-----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') TGCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGTTATAA CAGACCAACA ACACCTTCTG
iPCR_3 (3') TGCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGTTATAA CAGACCAACA ACACCTTCTG
iPCR_4 (3') TGCTGGGTTA GCTAGTGATT TGGTATGTAA GAGGAATGCC TGTATGGGAC AGTCGTATGC CGGGTTATAA CAGACCAACA GCACCTTCTG

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      2260      2270      2280      2290      2300      2310      2320      2330      2340
Consensus  -----
CoxI_PCR   -----
Illumina_1 -----
Illumina_2 -----
Illumina_3 -----
Illumina_4 -----
Illumina_5 -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') TTCATCCCTC TATAGCTATA TGTACTGTGT GTGTGGGATT ATTGGTAGAA CACGGTTATT CATTATCTAT GCCACATGC CTGTGGGAGT
iPCR_3 (3') TTCATCCCTC TATAGCTATA TGTACTGTGT GTGTGGGATT ATTGGTAGAA CACGGTTATT CATTATCTAT GCCACATGC CTGTGGGAGT
iPCR_4 (3') TTCATCCCTC TATAGCTATA TGTACTGTGT GTGTGGGTTAA GGTGGACAA GGACTCCTGC ATTATATTGT GTGCCTCATC GCTAGTTCAG

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      2350      2360      2370      2380      2390      2400      2410      2420      2430
Consensus -----
CoxI_PCR -----
Illumina_1 -----
Illumina_2 -----
Illumina_3 -----
Illumina_4 -----
Illumina_5 -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') GTTGGATAAA TATTAGAGTT GAACACACAC AGATAACACA CACAGATAAT ATTAATAGAA CGGTTATACG TGGGTTGGTA GTTCAGATAT
iPCR_3 (3') GTTGGATAAA TATTAGAGTT GAACACACAC AGATAACACA CACAGATAAT ATTAATAGAA CGGTTATACG TGGGTTGGTA GTTCAGATAT
iPCR_4 (3') ATATCTACCT TTCCTAGTAG TTATACCTGT GTGGACAACA CCTCCTGGGA CACACGAATT CTCTCTGAGC AATCTCTGTT CAATATCTTT

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      2440      2450      2460      2470      2480      2490      2500      2510      2520
Consensus -----
CoxI_PCR -----
Illumina_1 -----
Illumina_2 -----
Illumina_3 -----
Illumina_4 -----
Illumina_5 -----
iPCR_1 (5') -----
iPCR_2 (5') -----
iPCR_3 (5') -----
iPCR_4 (5') -----
iPCR_2 (3') CTACCTTCC TAGTAGTTAT ACCTGTGTGG ACAACACCTC CTGGGACACA CGAATTCTCT CTGAGCAATC TCTGTTCAAT ATCTTTTATT
iPCR_3 (3') CTACCTTCC TAGTAGTTAT ACCTGTGTGG ACAACACCTC CTGGGACACA CGAATTCTCT CTGAGCAATC TCTGTTCAAT ATCTTTTATT
iPCR_4 (3') TATTAGTTGT TGTAATATTA TAACCACAAA TGCCAAATTT GGCGGCCGTG ATTATTCCGGT TGAACTCCCA AACTGCTTGT ATAAGCGGGC

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Mitochondrial genome - *Chromera velia* CCAP 1602/1 (KC899110)

	2530	2540	2550	2560	2570	2580	2590	2600	2610	
Consensus	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
CoxI_PCR	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_1	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_2	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_3	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_4	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
Illumina_5	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_1 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_2 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_3 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_4 (5')	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----
iPCR_2 (3')	AGTTGTTGTA	ATATTATAAC	CACAAATACC	AAATTTGGCG	GCCGTGATTA	TTCGGTTGAA	CTCCCAAAC	GCTTGTATAA	GCGGGCAATT	
iPCR_3 (3')	AGTTGTTGTA	ATATTATAAC	CACAAATACC	AAATTTGGCG	GCCGTGATTA	TTCGGTTGAA	CTCCCAAAC	GCTTGTATAA	GCGGGCAATT	
iPCR_4 (3')	AATTGGTGTT	GTCCAGGGAA	ATAATAATCT	GACTCATCAT	AGT-----	-----	-----	-----	-----	-----

	2620	2630	2640	
Consensus	-----	-----	-----	-----
CoxI_PCR	-----	-----	-----	-----
Illumina_1	-----	-----	-----	-----
Illumina_2	-----	-----	-----	-----
Illumina_3	-----	-----	-----	-----
Illumina_4	-----	-----	-----	-----
Illumina_5	-----	-----	-----	-----
iPCR_1 (5')	-----	-----	-----	-----
iPCR_2 (5')	-----	-----	-----	-----
iPCR_3 (5')	-----	-----	-----	-----
iPCR_4 (5')	-----	-----	-----	-----
iPCR_2 (3')	GGTGTGTGCC	AGGGAGATAA	TAATCTGACT	CATCATAGT
iPCR_3 (3')	GGTGTGTGCC	AGGGAGATAA	TAATCTGACT	CATCATAGT
iPCR_4 (3')	-----	-----	-----	-----

Figure S1: Alignment of the mitochondrial genome from *Chromera velia* CCAP 1602/1 based on five genomic nodes of the metagenome sequencing project (BioProject: PRJNA196886; Illumina_1 to Illumina_5 [Node186709, Node235449, Node461926, Node2236, Node 119218]) and four sequences obtained by inverse PCR amplification (iPCR_1 to iPCR_4). The deduced amino acid sequence of the sole mitochondrial gene, *coxI*, is highlighted in yellow, the start and stop codon in green and red, respectively. Overlapping Illumina sequences are shown in light gray. Homologous regions in variable alignment positions between Illumina and iPCR as well as iPCR regions are shown in light green and light red, respectively. The complete *coxI* gene was amplified with the two primers highlighted in light blue; the PCR-product was cloned and resequenced. The nucleotide consensus sequence of all genome and PCR sequences, which has been deposited under the accession number [KC899110](https://www.ncbi.nlm.nih.gov/nuccore/KC899110), is shown in bold.