

**Supplemental Table S1: Comparison of Illumina, 454 and Sanger sequence coverage exemplified for 16 cDNAs from *Chromera velia* CCAP 1602/1**

No	Gene	Introns	Coverage	Illumina Approach (current study)				454 Approach (Woehle et al. 2011)				Sanger Approach (unpublished)			
				Accession	Coverage	Length	Protein	Accession*	TSAs	Length	Protein	Accession*	ESTs	Length	Protein
1	PRK	10	19.2x	<a href="#">KC899087</a>	755x	2,767 bp	full length	<a href="#">JO788081.1</a>	1	1,846 bp	partial	<a href="#">HO866516.1</a>	3	845 bp	partial
2	SBP1	1	17.5x	<a href="#">KC899088</a>	1,999x	2,258 bp	full length	<a href="#">JO790107.1</a>	2	1,449 bp	partial	-	-	-	-
3	SBP2	4	18.4x	<a href="#">KC899089</a>	155x	1,225 bp	full length	-	-	-	-	-	-	-	-
4	SBP3-HDR	15	19.5x	<a href="#">KC899090</a>	505x	3,275 bp	full length	<a href="#">JO802140.1</a>	1	1,132 bp	partial <sup>3</sup>	-	-	-	-
5	FBP <sub>cyt1</sub>	7	17.2x	<a href="#">KC899091</a>	146x	2,172 bp	full length	<a href="#">JO798440.1</a>	2	2,142 bp	full length	-	-	-	-
6	FBP <sub>cyt2</sub>	9	18.1x	<a href="#">KC899092</a>	356x	2,513 bp	full length	<a href="#">JO800087.1</a>	2	1,267 bp	partial	-	-	-	-
7	FBP <sub>cyt3</sub>	7	18.8x	<a href="#">KC899093</a>	321x	2,801 bp	full length	<a href="#">JO788854.1</a>	3	805 bp	partial	<a href="#">HO866483.1</a>	3	799 bp	partial
8	FBP <sub>pla</sub>	11	18.8x	<a href="#">KC899094</a>	13,563x	3,364 bp	full length	<a href="#">JO790611.1</a>	5	760 bp	partial	<a href="#">HO866945.1</a>	2	820 bp	partial
9	FBA-I a	9	16.5x	<a href="#">KC899095</a>	1,243x	1,600 bp	full length	<a href="#">JO801881.1</a>	1	865 bp	partial	-	-	-	-
10	FBA-I b	4	17.6x	<a href="#">KC899096</a>	1,966x	1,996 bp	full length	<a href="#">JO795142.1</a>	1	1,438 bp	full length	<a href="#">HO866136.1</a>	3	711 bp	partial
11	FBA-I c	9	19.6x	<a href="#">KC899097</a>	105x	1,615 bp	full length <sup>1</sup>	-	-	-	-	-	-	-	-
12	FBA-I d	0	17.3x	<a href="#">KC899098</a>	111x	1,325 bp	full length <sup>2</sup>	<a href="#">JO787575.1</a>	1	1,544 bp	full length	-	-	-	-
13	FBA-II	2	19.3x	<a href="#">KC899099</a>	1,976x	2,647 bp	full length	<a href="#">JO805056.1</a>	2	606 bp	partial	<a href="#">HO866767.1</a>	2	829 bp	partial
14	GapC-I	0	20.2x	<a href="#">KC899100</a>	816x	1,994 bp	full length	<a href="#">JO786707.1</a>	1	1,989 bp	full length	<a href="#">HO865964.1</a>	4	843 bp	full length <sup>1</sup>
15	GapC	4	17.0x	<a href="#">KC899101</a>	2,598x	1,703 bp	full length	<a href="#">JO789461.1</a>	2	1,650 bp	partial	<a href="#">HO866153.1</a>	7	863 bp	partial
16	Not1	32	17.6x	<a href="#">KC899102</a>	307x	13,382 bp	full length	<a href="#">JO802605.1</a>	1	928 bp	partial	-	-	-	-

\* largest transcriptome shotgun assembly (TSA) or expressed sequence tag (EST); <sup>1</sup> cDNA merged from two overlapping TSAs; <sup>2</sup> cDNA merged from three TSAs in comparison with genomic contigs; <sup>3</sup> N-terminal SBP3 sequence not covered, C-terminal HDR sequence partial.