

<b>A</b>	<b><i>Chromera velia</i></b>	
	CAMPEP_0184610696/1-136	1 MARTKQTARKSTGGKAPRKQLASKAARKTTPSTGGVKK38
	CAMPEP_0184616670/1-136	1 MARTKQTARKSTGGKAPRKQLASKAARKTTPSTGGVKK38
	Homo_sapiens-H3.3-gi 4885385/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKK38
	Homo_sapiens-H3.1-gi 4504285/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK38
	Arabidopsis_thaliana-H3.3-gi 7271058/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKK38
	Arabidopsis_thaliana-H3.1-gi 15238433/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK38
<b>B</b>	<b><i>Heterocapsa rotundata</i></b>	
	CAMPEP_0168685586/1-127	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPSQGGVKK 38
	CAMPEP_0168629108/1-136	1 MARTKHTARKAVGGKAPRSQLAAKAARKQMPVEGGIKK 38
	Homo_sapiens-H3.3-gi 4885385/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKK 38
	Homo_sapiens-H3.1-gi 4504285/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK 38
	Arabidopsis_thaliana-H3.3-gi 7271058/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKK 38
	Arabidopsis_thaliana-H3.1-gi 15238433/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK 38
<b>C</b>	<b><i>Symbiodinium sp. C1</i></b>	
	CAMPEP_0199619984/1-216	1 MARTKMEALKA SEGK GKAKKMKKERKSKGVPPQGFMTVQVEGDTSE 45
	CAMPEP_0199587754/1-156	1 MARTKMTAQKSA -GNKGRGELAAKAARKQAP - - - - -VVTMCK 37
	CAMPEP_0199634840/1-136	1 MARTKMTAQKSAGGNKQREDLAAKAARKQAP - - - - -VVTMCK 38
	CAMPEP_0199632446/1-277	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -ATGGVKK 38
	CAMPEP_0199582754/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -TAGGVKK 38
	CAMPEP_0199564138/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -AQGGVKK 38
	Homo_sapiens-H3.3-gi 4885385/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -STGGVKK 38
	Homo_sapiens-H3.1-gi 4504285/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -ATGGVKK 38
	Arabidopsis_thaliana-H3.3-gi 7271058/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -TTGGVKK 38
	Arabidopsis_thaliana-H3.1-gi 15238433/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAP - - - - -ATGGVKK 38
<b>D</b>	<b><i>Symbiodinium sp. C15</i></b>	
	CAMPEP_0192410354/1-204	1 MARGKRMSRQTTSP IEDHIERLR LQRMNSKAP EDRDQWQ 39
	CAMPEP_0192432788/1-178	1 MARTKMEALKA SEGK GKAKKMKKERKSKGVPPQGFMTVQ 38
	CAMPEP_0192450070/1-131	1 - - - - -MTAQKSAGGNKQR - EDLAAKAARKQAPVVTMCK 33
	CAMPEP_0192436512/1-136	1 MARTKQTARKSTGGKAPR - KQLATKAARKSAPSTGGVKK 38
	CAMPEP_0192431758/1-162	1 MARTKMTAQKSA -GNKGR - GELAAKAARKQAPAVVTMCK 37
	Homo_sapiens-H3.3-gi 4885385/1-136	1 MARTKQTARKSTGGKAPR - KQLATKAARKSAPSTGGVKK 38
	Homo_sapiens-H3.1-gi 4504285/1-136	1 MARTKQTARKSTGGKAPR - KQLATKAARKSAPATGGVKK 38
	Arabidopsis_thaliana-H3.3-gi 7271058/1-136	1 MARTKQTARKSTGGKAPR - KQLATKAARKSAPTTGGVKK 38
	Arabidopsis_thaliana-H3.1-gi 15238433/1-136	1 MARTKQTARKSTGGKAPR - KQLATKAARKSAPATGGVKK 38
<b>E</b>	<b><i>Alexandrium tamarense</i></b>	
	CAMPEP_0186368882/1-76	1 MARTKQTARKSSAGKAPRVQLAAKAARKQTPVSGGIKK 38
	CAMPEP_0186247602/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPAAAGGVKK 38
	CAMPEP_0186248598/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKK 38
	CAMPEP_0186315546/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPSAAGGVKK 38
	CAMPEP_0186245626/1-76	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPTAGGVKK 38
	CAMPEP_0186362848/1-136	1 MARTKQTARKSTGGKAPRSHLAAKAARKQTPVVGGIKK 38
	CAMPEP_0186241736/1-206	1 MARTKQTARMSTGSKAPRQVLAACAARKQAPISSGGVKK 38
	Homo_sapiens-H3.3-gi 4885385/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPSTGGVKK 38
	Homo_sapiens-H3.1-gi 4504285/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK 38
	Arabidopsis_thaliana-H3.3-gi 7271058/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPTTGGVKK 38
	Arabidopsis_thaliana-H3.1-gi 15238433/1-136	1 MARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKK 38

**Figure S8: Putative H3.3/H3.1 histone variants in dinoflagellates.** Histones H3.3 and H3.1 are distinguished by the sequence at position 31, which is S or T (in animals and fungi, respectively) in H3.3 and A in H3.1. Slightly different sequences are observed in other groups, for example in *Tetrahymena* the H3.3/H3.1 distinction is that the sequence is VS vs AT, respectively (Talbert et al. 2012). Putative H3.3/H3.1 pairs are observed in several dinoflagellate transcriptomes: *Heterocapsa rotundata* (B), *Symbiodinium sp. C1* (C), *Symbiodinium sp. C15* (D), and *Alexandrium tamarense* (E). Only H3.3 variants are observed in the *Chromera velia* transcriptome, thus caution with respect to false negatives have to be exercised when interpreting the presence/absence of H3.3/H3.1 variants.